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Original Research Article

Prospective study of bacteriological profile of indoor patient of respiratory diseases at tertiary care centre

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ABSTRACT

Background: Respiratory tract infections (RTIs) are a major cause of morbidity among hospitalized patients and are frequently associated with bacterial pathogens and antimicrobial resistance. Knowledge of the local bacteriological profile and antibiotic susceptibility pattern is essential for guiding appropriate empirical therapy and improving clinical outcomes.
Methods: This prospective observational study was conducted over a period of one year from 20 January 2025 to 30 December 2025 at Rajarshi Dashrath Autonomous State Medical College, Ayodhya, Uttar Pradesh. A total of 102 indoor patients admitted with respiratory diseases were included. Respiratory samples, predominantly sputum, were collected and processed using standard microbiological techniques. Bacterial isolates were identified, and antibiotic susceptibility testing was performed. Data were analysed using the descriptive statistics and expressed as frequencies and the percentages.
Results: Among the 102 patients studied, males constituted the majority. Gram-negative organisms were predominantly isolated. *E. coli* was the most common organism, followed by *K. pneumoniae* and *P. aeruginosa*. Most isolates showed higher sensitivity to broad-spectrum antibiotics such as carbapenems, aminoglycosides, and higher-generation cephalosporins, while resistance to commonly used first-line antibiotics was observed in several cases.
Conclusions: Gram-negative bacteria were the predominant pathogens among indoor patients with respiratory diseases. Regular monitoring of bacteriological patterns and antibiotic susceptibility is essential to guide rational antibiotic therapy and to curb the growing problem of antimicrobial resistance in tertiary care settings.

Keywords: Respiratory tract infections, Bacteriological profile, Antibiotic sensitivity, Gram-negative bacteria, Tertiary care hospital

INTRODUCTION

Respiratory tract infections (RTIs) remain one of the leading causes of morbidity and hospitalization worldwide, particularly in developing countries like India.[1] Indoor patients admitted with respiratory diseases often represent a vulnerable population due to advanced age, underlying chronic lung conditions, associated comorbidities, and repeated exposure to healthcare settings.[2] These factors predispose them to bacterial infections, prolonged hospital stay, and increased risk of antimicrobial resistance.

Lower RTIs such as pneumonia, acute exacerbations of chronic obstructive pulmonary disease (COPD), bronchiectasis, and post-tubercular sequelae are

commonly associated with bacterial pathogens.[3] The bacteriological spectrum of respiratory infections varies widely depending on geographical location, hospital environment, patient demographics, and antibiotic usage patterns.[4] In tertiary care centres, gram-negative organisms have increasingly emerged as predominant pathogens, replacing the traditionally common gram-positive bacteria.[5]

Among gram-negative bacilli, *P. aeruginosa* and *E. coli* are frequently isolated from hospitalized patients with respiratory diseases, particularly those with chronic lung pathology or prolonged hospitalization.[6] These organisms are of significant clinical concern due to their intrinsic resistance mechanisms and their ability to acquire multidrug resistance, leading to limited therapeutic options.[7] The irrational and empirical use of broad-spectrum antibiotics further accelerates the development of antimicrobial resistance, posing a serious public health challenge.[8]

Knowledge of the local bacteriological profile and antibiotic sensitivity pattern is essential for guiding empirical therapy, reducing treatment failure, and preventing the emergence of resistant strain.[9] Periodic surveillance studies conducted at the institutional level help clinicians choose appropriate antibiotics while awaiting culture reports and aid in formulating hospital antibiotic policies.[10] Despite the high burden of respiratory diseases, there is limited recent data from tertiary care centres in Uttar Pradesh regarding the bacteriological profile of indoor patients with respiratory illnesses.

Despite existing literature, there is a paucity of recent region-specific data from eastern Uttar Pradesh focusing exclusively on indoor patients with respiratory diseases. Variations in microbial flora and antibiotic resistance patterns across institutions necessitate continuous local surveillance. Therefore, this study was designed to generate updated institutional data to support evidence-based empirical therapy and antimicrobial stewardship practices.

Therefore, the present prospective study was undertaken to evaluate the bacteriological profile and antibiotic sensitivity pattern among indoor patients admitted with respiratory diseases at a tertiary care centre. The findings of this study aim to provide valuable insights into prevalent respiratory pathogens and their antimicrobial susceptibility, thereby contributing to rational antibiotic use and improved patient management.

METHODS

Study design

This was a prospective observational study conducted to evaluate the bacteriological profile and antibiotic sensitivity pattern among indoor patients admitted with respiratory diseases at a tertiary care centre.

Study setting

The study was carried out at Rajarshi Dashrath Autonomous State Medical College, Ayodhya, Uttar Pradesh, which serves as a tertiary care teaching hospital catering to patients from both urban and rural populations.

Study duration

The study was conducted over a period of one year, from 20 January 2025 to 30 December 2025.

Study population

The study population comprised indoor patients admitted to the medical wards with a clinical diagnosis of respiratory diseases during the study period.

Sample size

A total of 102 patients were included in the study.

Eligibility criteria

Patients aged 18 years and above admitted with clinical features suggestive of respiratory diseases and from whom respiratory samples could be obtained were included after obtaining informed consent. Patients who did not provide consent, those with contaminated or inadequate samples, and patients who had received antibiotics for more than 72 hours prior to sample collection were excluded from the study.

Sample collection

Respiratory samples, predominantly sputum, were collected under aseptic precautions. Patients were instructed to provide early morning deep expectorated sputum samples in sterile, wide-mouthed containers. Samples were assessed for adequacy, and those showing salivary contamination were excluded. All specimens were transported promptly to the microbiology laboratory for processing.

Microbiological processing

Samples were subjected to Gram staining and cultured using standard microbiological techniques. The specimens were inoculated onto blood agar and MacConkey agar media and incubated aerobically at 37°C for 24 to 48 hours. Bacterial isolates were identified based on colony characteristics, Gram reaction, and conventional biochemical tests.

Antibiotic susceptibility testing

Antibiotic susceptibility testing was performed using the Kirby-Bauer disc diffusion method on Mueller–Hinton agar. Interpretation of sensitivity patterns was done according to standard laboratory guidelines. A panel of

antibiotics representing beta-lactams, aminoglycosides, fluoroquinolones, and carbapenems was tested as per institutional protocol.

Data collection and analysis

Clinical and microbiological data recorded in predesigned proforma and entered into Microsoft excel. Data analysis was performed using descriptive statistical methods, and results were expressed as frequencies and percentages.

Ethical considerations

The study was conducted after obtaining approval from the institutional ethics committee of Rajarshi Dashrath Autonomous State Medical College, Ayodhya. Written informed consent was obtained from all participants prior to their inclusion in the study.

RESULTS

A total of 102 indoor patients admitted with respiratory diseases were included in the present prospective study. All collected respiratory samples were processed and yielded bacterial growth.

Demographic characteristics of study population

The study population comprised predominantly male patients. Out of 102 patients, 69 (67.6%) were males and 33 (32.4%) were females, with a male-to-female ratio of approximately 2.1:1. Most patients belonged to the elderly age group, reflecting a higher burden of respiratory infections among older individuals.

Table 1: Gender distribution of study participants, (n=102).

Gender	N	Percentage (%)
Male	69	67.6
Female	33	32.4
Total	102	100

Distribution of respiratory samples

All samples obtained for bacteriological analysis were sputum samples. Adequate quality samples were included, and none were rejected due to contamination.

Table 2: Type of respiratory sample collected.

Sample type	N	Percentage (%)
Sputum	102	100
Total	102	100

Bacteriological profile of isolates

Gram-negative organisms constituted the majority of isolates. *E. coli* was the most frequently isolated organism, followed by *K. pneumoniae* and *P. aeruginosa*. Gram-positive organisms such as *E. faecalis* and *S. aureus* were isolated in fewer cases. A single isolate of *Acinetobacter* species was also identified.

Table 3: Distribution of bacterial isolates among study participants

Organism isolated	N	Percentage (%)
E. coli	33	32.4
K. pneumoniae	31	30.4
P. aeruginosa	25	24.5
E. faecalis	8	7.8
S. aureus	4	3.9
***Acinetobacter* spp.**	1	1.0
Total	102	100

Antibiotic sensitivity pattern

Most gram-negative isolates demonstrated higher sensitivity to broad-spectrum antibiotics such as piperacillin, cefepime/cefepirome, amikacin, meropenem, and imipenem. *E. coli* isolates showed good sensitivity to third- and fourth-generation cephalosporins and carbapenems, while *P. aeruginosa* isolates were predominantly sensitive to antipseudomonal beta-lactams and aminoglycosides. Gram-positive organisms showed sensitivity to commonly used antibiotics, though resistance to the first-line agents was noted in the some cases.

Gender-wise distribution of bacterial isolates

The gender-wise analysis of bacterial isolates revealed a higher prevalence of infections among male patients compared to females across all major organisms. *E. coli* was the most common isolate in both genders, with 22 cases (31.9%) observed in males and 11 cases (33.3%) in females. *K. pneumoniae* was isolated in 21 male patients (30.4%) and 10 female patients (30.3%).

Pseudomonas aeruginosa showed similar male predominance with 17 cases (24.6%) in males and 8 cases (24.2%) in females. Gram-positive organisms such as *E. faecalis* and *S. aureus* were less frequently isolated in both genders. A single case of *Acinetobacter* species was observed in a male patient.

Overall, male patients demonstrated a higher burden of bacterial respiratory infections, reflecting the male predominance noted in the study population (Table 4).

Gender-wise distribution of E. coli

On separate analysis of *E. coli* isolates, males accounted for the majority of cases with 22 (66.7%), while females contributed 11 cases (33.3%). This finding indicates a higher occurrence of *E. coli* respiratory infections among male patients (Figure 3).

Table 4: Gender-wise distribution of *E. coli.*

Organism	Male	Female	Total
E. coli	22	11	33
Klebsiella	21	10	31
Pseudomonas	17	8	25
Enterococcus	5	3	8
Staph aureus	3	1	4
Acinetobacter	1	0	1
Total	69	33	102

DISCUSSION

The present prospective study evaluated the bacteriological profile of indoor patients admitted with respiratory diseases at a tertiary care centre. The findings demonstrate a predominance of gram-negative organisms, with *E. coli*, *K. pneumoniae*, and *P. aeruginosa* being the most frequently isolated pathogens. This bacteriological pattern reflects the changing epidemiology of respiratory infections in hospitalized patients and highlights the increasing role of gram-negative bacilli in lower RTIs.[11]

Male predominance observed in the present study is consistent with earlier reports, which have attributed this trend to higher exposure to environmental pollutants, smoking, and occupational hazards among males, as well as a greater prevalence of chronic respiratory illnesses in this group.[12] The higher incidence of infections in elderly patients further emphasizes the role of age-related immune decline and the presence of comorbid conditions, which predispose to severe respiratory infections requiring hospitalization.[13]

The predominance of *E. coli* and *K. pneumoniae* in respiratory samples has been increasingly reported from tertiary care centres, particularly among patients with prolonged hospital stay and underlying lung pathology.[14] These organisms are often associated with healthcare-associated infections and pose significant therapeutic challenges due to their ability to acquire extended-spectrum beta-lactamase and carbapenem resistance mechanisms.[15] The isolation of *P. aeruginosa* in a substantial proportion of cases in the present study is clinically significant, as this organism is well known for its intrinsic resistance and association with severe pulmonary infections, especially in hospitalized and immunocompromised patients. [16]

Antibiotic susceptibility patterns observed in this study revealed higher sensitivity of gram-negative isolates to broad-spectrum agents such as carbapenems, aminoglycosides, and higher-generation cephalosporins. Similar sensitivity patterns have been documented in other Indian studies, suggesting that these antibiotics remain effective therapeutic options for severe respiratory infections in tertiary care settings.[17] However, the observed resistance to commonly used first-line antibiotics is concerning and underscores the consequences of empirical and indiscriminate antibiotic use.[18]

The predominance of gram-negative organisms observed in this study reflects a shift in the microbiological spectrum of respiratory infections in hospitalized patients, likely influenced by antibiotic selection pressure and increased healthcare exposure. This trend highlights the urgent need for stringent antibiotic stewardship programs and infection control practices. Tailoring empirical therapy based on local antibiograms can significantly reduce morbidity, hospital stay, and the emergence of multidrug-resistant organisms.

The findings of this study reinforce the importance of routine bacteriological surveillance and antibiotic sensitivity testing in hospitalized patients with respiratory diseases. Culture-guided therapy not only improves clinical outcomes but also plays a crucial role in antimicrobial stewardship by minimizing unnecessary exposure to broad-spectrum antibiotics.[19] Periodic institutional studies such as the present one provide valuable data for updating hospital antibiotic policies and addressing growing burden of antimicrobial resistance.[20]

Limitations

This study has certain limitations. The sample size was relatively small and conducted at a single tertiary care centre, which may limit the generalizability of the findings. Only sputum samples were analyzed, and other respiratory specimens such as bronchoalveolar lavage were not included. Additionally, molecular methods for detection of resistance mechanisms were not performed, which could have provided more detailed insights into antimicrobial resistance patterns.

CONCLUSION

The present prospective study demonstrates that gram-negative organisms are the predominant causative agents of respiratory infections among indoor patients in a tertiary care hospital. *E. coli*, *K. pneumoniae*, and *P. aeruginosa* were the most frequently isolated pathogens. The observed antibiotic susceptibility pattern indicates better sensitivity to higher-generation antibiotics, while resistance to commonly used agents remains a significant concern. These findings emphasize the importance of routine bacteriological surveillance and culture-guided antibiotic therapy. Periodic institutional studies are essential for updating antibiotic policies, promoting rational antimicrobial use, and reducing the burden of antimicrobial resistance.

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