



Original Research Article

ETIOLOGICAL PROFILE AND ANTIBIOTIC SUSCEPTIBILITY TREND OF COMMUNITY ACQUIRED PNEUMONIA AMONG GERIATRIC PATIENTS “A CROSS SECTIONAL STUDY FROM A TERTIARY CARE TEACHING HOSPITAL”.

Article History:

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Received: 12-11-2025

Revised: 25-11-2025

Accepted: 09-12-2025

Published: 31-12-2025

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Abstract: **Background:** Community-acquired pneumonia (CAP) remains a leading cause of morbidity and mortality among the geriatric population, particularly in developing countries. Age-related immune decline, comorbidities, and increasing antimicrobial resistance complicate disease management. **AIM:** The present study aimed to determine the bacterial etiology and antimicrobial susceptibility patterns of community-acquired pneumonia among geriatric patients attending a tertiary care teaching hospital in Western Uttar Pradesh. **Materials and Methods:** A hospital-based observational study was conducted over 12 months (July 2024–June 2025). A total of 349 respiratory samples, including sputum, bronchoalveolar lavage (BAL), and pleural fluid, were processed using standard microbiological techniques. Bacterial identification was performed by conventional and automated method by VITEK® 2 Compact system. Antimicrobial susceptibility testing was carried out by the Kirby–Bauer disk diffusion method, interpreted according to CLSI 2024 guidelines. Statistical analysis was performed using SPSS version 23.0. **Results:** Of the 349 samples, 128 (36.67%) showed significant bacterial growth. Gram-negative bacilli constituted 97.6% of isolates, while Gram-positive cocci accounted for only 2.4%. *Pseudomonas* species (42.97%) were the most frequently isolated organisms, followed by *Klebsiella* species (22.66%). *Pseudomonas aeruginosa* showed high sensitivity to amikacin (82.81%) and poor sensitivity to ceftazidime (15.63%). Carbapenems demonstrated better efficacy against most Gram-negative isolates. No statistically significant association was observed between gender and culture positivity ($p = 0.064$). **Conclusion:** The study highlights a marked predominance of multidrug-resistant Gram-negative pathogens in geriatric CAP patients. Continuous regional surveillance and judicious antibiotic use are essential for effective empirical management.

Keywords: Community-acquired pneumonia, Geriatric patients, Gram-negative bacilli, Antibiotic resistance, Western Uttar Pradesh

INTRODUCTION

Pneumonia is an acute infection of the lung parenchyma and remains a major cause of morbidity and mortality worldwide, particularly among the elderly. Individuals aged ≥ 65 years are disproportionately affected and represent a large proportion of hospital admissions and infection-related deaths. Lower respiratory tract infections (LRTIs), including pneumonia, account for a substantial global disease burden^[1], with WHO estimates reporting over 429 million cases and nearly

94 million disability-adjusted life years annually. With the expanding geriatric population, the incidence of pneumonia is expected to rise further.

Community-acquired pneumonia (CAP) is a common form of LRTI and occurs outside healthcare settings. Elderly individuals are especially vulnerable due to immunosenescence, aspiration risk, and comorbid conditions such as chronic obstructive pulmonary disease, diabetes mellitus, and renal disorders^[2]. *Streptococcus pneumoniae* remains the most frequently isolated pathogen, followed by

Klebsiella pneumoniae, *Haemophilus influenzae*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Legionella* spp., and *Staphylococcus aureus*^[3]. While *S. pneumoniae* generally remains susceptible to β -lactams, third-generation cephalosporins, and respiratory fluoroquinolones, increasing resistance to penicillins and macrolides has been reported^[4,5]. Gram-negative pathogens, particularly in elderly patients with comorbidities, frequently exhibit resistance to ampicillin and first-generation cephalosporins, with emerging ESBL production, though sensitivity to carbapenems and piperacillin–tazobactam is largely preserved. MRSA, though less common, remains clinically significant.

Accurate diagnosis relies on clinical assessment, radiological findings, and microbiological evaluation of respiratory samples. Timely initiation of appropriate antimicrobial therapy is critical; however, rising antimicrobial resistance complicates empirical treatment decisions. Given regional variations in pathogen distribution and resistance patterns, ongoing local surveillance is essential^[6,7].

This study aims to evaluate the bacterial etiology and antimicrobial susceptibility patterns of community-acquired pneumonia among geriatric patients attending a tertiary care teaching hospital in western Uttar Pradesh, to aid in evidence-based empirical therapy.

Given the variability in bacterial patterns and resistance trends across regions, continuous surveillance is necessary to guide empirical therapy.

The geriatric population requires special attention due to their higher vulnerability and poorer outcomes. The present study aims to determine the bacterial etiology and antibiotic susceptibility trends of CAP among geriatric patients at tertiary care teaching hospital in western UP., with the goal of supporting evidence-based empirical treatment guidelines.

MATERIALS AND METHODS

This hospital-based observational study was conducted over a period of 12 months (July 2024–June 2025) at the Department of Microbiology, Sharda Hospital, Greater Noida. A total of 349 respiratory samples, including sputum, bronchoalveolar lavage (BAL), and pleural fluid, were collected from patients clinically diagnosed with pneumonia settings. Samples were processed following standard microbiological procedures. Gram staining was performed, and specimens were cultured on appropriate media. Bacterial isolates were identified using standard biochemical tests. **Isolates that could not be conclusively identified using conventional methods were further identified using the automated identification system (VITEK® 2 Compact).** Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar, and results were interpreted according to Clinical and Laboratory Standards Institute (CLSI) 2024 guidelines. As all data were obtained from the hospital Laboratory Information System (LIS), individual patient consent was not required for this study.

Statistical Analysis and Calculation of p-value

Data were entered into Microsoft Excel and analysed using SPSS version 23.0. Categorical variables were summarized as frequencies and percentages. The association between sex (male and female) and culture positivity was evaluated using a 2×2 contingency table comparing positive and negative culture results between the two groups. Statistical significance was assessed using the chi-square (χ^2) test. The analysis produced a chi-square value of 17.23 with 1 degree of freedom and a corresponding p-value of <0.001. A p-value less than 0.05 was considered statistically significant.

RESULTS

A total of 349 samples were received for culture and sensitivity testing, of which sputum constituted the majority (207/349) (59.3%), followed by BAL (98/349) (28.1%) and pleural fluid (44/349) (12.6%). Samples were collected from both inpatient and outpatient departments. (Shown in fig 01)

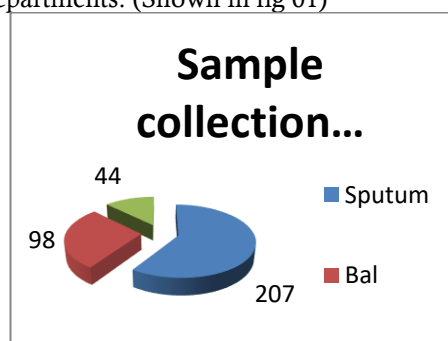


Fig 01: Distribution of sample collection

Out of the total 349 patients, the age group of 50–60 years constituted the highest proportion with 91 patients (31.6%), followed by 60–70 years with 66 patients (22.9%), 80–90 years with 51 patients (17.7%), 70–80 years with 46 patients (15.9%), 40–50 years with 33 patients (11.5%), and >90 years with 1 patient (0.3%). This represents the demographic distribution of the study population. (Table 01)

Table 01: Demographic distribution of study population

Age	No. of patients	Percentage %
40-50	39	11.18%
50-60	117	33.52%
60-70	91	26.07%
70-80	46	13.18%
80-90	55	15.76%
>90	1	0.29%

Out of 349 respiratory samples, 36.67% (128/349) showed pure bacterial growth, whereas 221 samples (63.33%) were reported as non-pathogenic organisms/oropharyngeal commensals. Among the culture-positive isolates, the majority were obtained from sputum samples (104) (81.25%), followed by BAL (19) (14.84%) and pleural fluid (5) (3.91%). (Table 02)

Table 02: Sample wise distribution of the pure growth isolates

Specimen	No. of isolates (n=128)	Percentage (%)
Sputum	104	81.25%
Bal	19	14.84%
Pleural fluid	5	3.91%

Out of 349 total samples, 128 were isolates 110 (85.94%) were from (IPD) and 18 (14.06%) were from (OPD)

Demographic Profile

Out of 349 samples gram-negative bacilli represented the predominant group among the 128 culture-positive samples, accounting for 125 isolates (97.6%), whereas Gram-positive cocci were detected in only 3 isolates (2.4%). Most of the patients from whom Gram-negative bacilli (GNB) were isolated belonged to the age group of 40–90 years (30.65%), followed by 40–50 years (28.31%), 50–60 years (27.27%), 60–70 years (8.05%), and >80 years (5.71%). (Table 03-04) (shown in fig 02).

Table 03: Distribution of isolates according to age.

Age in Years	No. of isolates (N)	Positivity rate (%)
40-50	9	7.0%
50-60	39	30.47%
60-70	30	23.44%
70-80	17	13.28%
80-90	33	25.78%

Table 04: Distribution of isolates according to gender

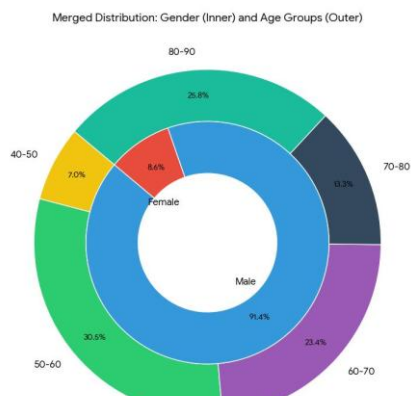


Fig 02: Distribution of age and gender

Gender	Count	Percentage (%)
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Male	117	91.41%
female	11	8.59%

There was no statistically significant association between gender and culture positivity among geriatric patients with community-acquired pneumonia ($\chi^2 = 3.43$, $p = 0.064$). Although culture positivity was higher among males compared to females, the difference did not reach the statistical significance at the conventional 5% level. (Table 05)

Table 05: Association between Gender and Culture Positivity

Gender	Culture positive	Culture negative	Total	P - value
Male	120 (38.9%)	188 (61.1%)	308	
Female	6 (20.0%)	24 (80.0%)	30	
Total	126 (37.3%)	212 (62.7%)	338	0.064

Out of the 128 culture-positive samples, the majority of isolates were Gram-negative bacilli (GNB), accounting for 125 isolates (97.6%), while Gram-positive cocci (GPC) were identified in 3 isolates (2.4%). Thus, Gram-negative organisms constituted the predominant bacterial group in the study population. (Shown in Fig 03)

Distribution of GNB Organisms (N=128)

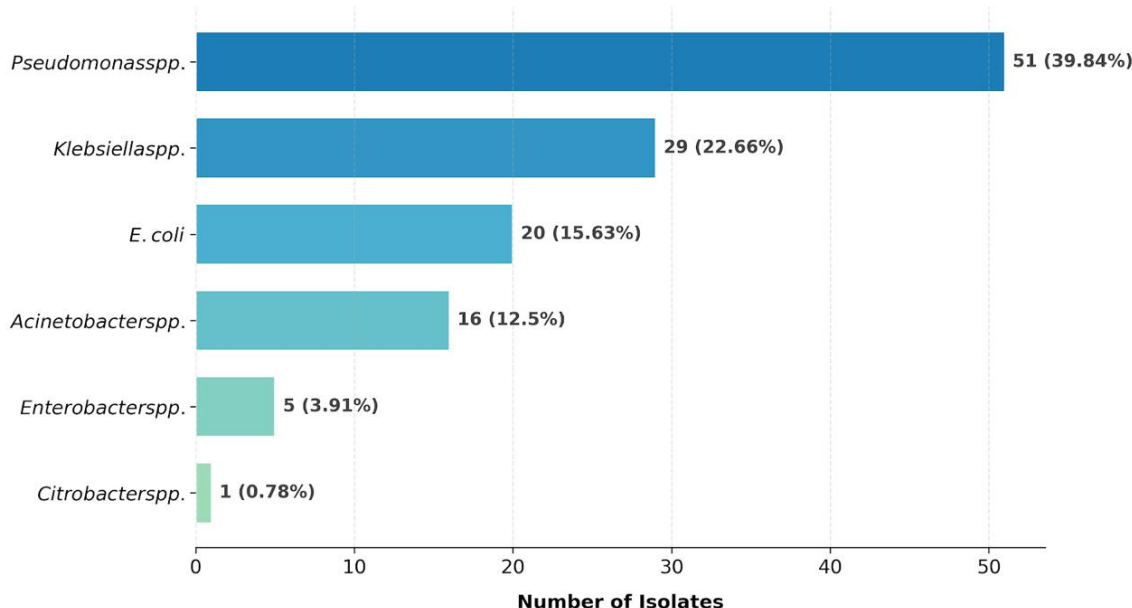


Fig 03: Distribution of gram negative organism.

Out of the 128 microbial isolates recovered during the study period, *Pseudomonas* species were the most predominant pathogens, accounting for 55 isolates (42.97%), followed by *Klebsiella* species with 29 isolates (22.66%). A higher prevalence of these organisms was observed among inpatients (IPD) compared to outpatients (OPD). The predominance of these Gram-negative bacteria highlights their significant role in respiratory infections, particularly among hospitalized patients.

Among the isolated organisms, *Pseudomonas aeruginosa* showed the highest sensitivity to amikacin (82.81%) and the lowest sensitivity to ceftazidime (15.63%). *Pseudomonas* spp. demonstrated maximum sensitivity to gentamicin (96.67%), while ceftazidime showed poor activity (10.00%). *Escherichia coli* isolates were most sensitive to imipenem and meropenem (70.83%) and exhibited complete resistance to ampicillin (0.00%). *Klebsiella pneumoniae* showed highest sensitivity to imipenem (36.36%) and marked resistance to cefuroxime and aztreonam (2.27%), whereas *Klebsiella* spp. were most sensitive to tetracycline (45.16%) and resistant to cefuroxime (12.90%). *Acinetobacter* spp. showed notable sensitivity to minocycline (63.71%) with minimal sensitivity to ceftazidime (0.81%). *Enterobacter* spp. were most sensitive to tetracycline (41.94%) and resistant to ceftriaxone and ceftazidime (9.68%). *Citrobacter koseri* showed highest sensitivity to imipenem, meropenem, and amikacin (61.54%), while ciprofloxacin showed low activity (15.38%). *Enterococcus* spp. demonstrated maximum sensitivity to high-level gentamicin (87.05%), with fosfomycin showing low sensitivity (19.03%). (Table 06, fig 04)

Table 06: Antibiotics Showing Highest Sensitivity and Resistance Among Isolated Organisms

Organism	Most Sensitive Antibiotic (Sensitivity%)	Most Resistant Antibiotic (Sensitivity%)
<i>Pseudomonas aeruginosa</i>	Amikacin (82.81%)	Ceftazidime (15.63%)
<i>Pseudomonas spp.</i>	Gentamicin (96.67%)	Ceftazidime (10.00%)
<i>Escherichia coli</i>	Imipenem / Meropenem (70.83%)	Ampicillin (0.00%)
<i>Klebsiella pneumoniae</i>	Imipenem (36.36%)	Cefuroxime / Aztreonam (2.27%)
<i>Klebsiella spp.</i>	Tetracycline (45.16%)	Cefuroxime (12.90%)
<i>Acinetobacter spp.</i>	Minocycline (63.71%)	Ceftazidime (0.81%)
<i>Enterobacter spp.</i>	Tetracycline (41.94%)	Ceftriaxone / Ceftazidime (9.68%)
<i>Citrobacter koseri</i>	Imipenem / Meropenem / Amikacin (61.54%)	Ciprofloxacin (15.38%)
<i>Enterococcus spp.</i>	High-level Gentamicin (87.05%)	Fosfomycin (19.03%)

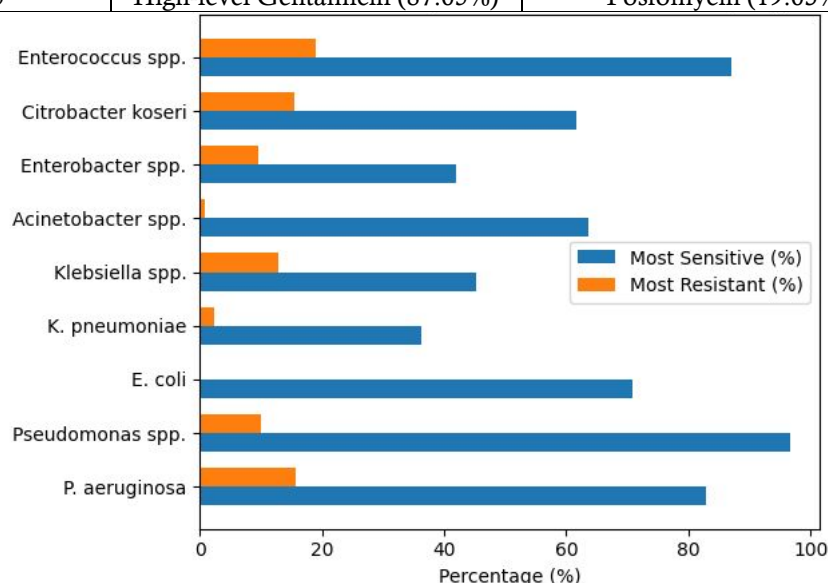


Fig 04: Distribution of isolated organisms according to antibiotic sensitivity and resistance.

DISCUSSION

Community-acquired pneumonia (CAP) continues to be a major cause of morbidity and mortality among the geriatric population, particularly in developing countries where comorbidities, delayed healthcare access, and inappropriate antibiotic use are common. The present study provides valuable insight into the bacterial etiology and antimicrobial susceptibility trends of CAP among elderly patients in Western Uttar Pradesh, highlighting an alarming predominance of Gram-negative pathogens and multidrug resistance. In the present study, Gram-negative bacilli (GNB) constituted 97.6% of the isolates, with *Pseudomonas aeruginosa* emerging as the most common pathogen, followed by *Klebsiella pneumoniae*, *Escherichia coli*, and *Acinetobacter* species. This finding contrasts with classical literature, where *Streptococcus pneumoniae* is traditionally considered the most frequent cause of CAP. However, recent studies from India and other developing regions increasingly report a shift toward

Gram-negative organisms, particularly in elderly patients with multiple comorbidities and frequent healthcare exposure [8,9]. The predominance of *Pseudomonas aeruginosa* (approximately 40–43%) in the present study aligns with findings from tertiary-care-based studies in North India, which report isolation rates ranging from 30–45% in geriatric CAP cases [10]. This trend may be attributed to advanced age, underlying chronic lung disease, repeated antibiotic exposure, and frequent hospital visits, all of which predispose patients to colonization and infection by non-fermenting Gram-negative bacilli. *Klebsiella pneumoniae*, the second most common isolate in this study (22.66%), is well-recognized for causing severe pneumonia in elderly individuals, often associated with alcoholism, diabetes, and chronic lung disease. In the present study, community-acquired pneumonia (CAP) among geriatric patients was predominantly caused by Gram-negative bacilli, with *Pseudomonas* species (42.97%) and *Klebsiella* species (22.66%) being the

most frequently isolated pathogens, whereas Gram-positive cocci represented only 2.4% of isolates [11]. This observation is consistent with Goyal et al. [12], who reported a similar predominance of Gram-negative organisms in elderly CAP patients in India, suggesting a regional trend in pathogen distribution among the geriatric population. The higher prevalence of *Pseudomonas* and *Klebsiella* may be attributable to age-related immune senescence, comorbidities such as diabetes and chronic lung disease, and increased exposure to healthcare environments, which can predispose older adults to infections with opportunistic Gram-negative bacteria [12,13].

Antibiotic susceptibility patterns in the current study revealed that *Pseudomonas* isolates were highly sensitive to amikacin and gentamicin, while *E. coli* and *Klebsiella* species showed strong sensitivity to imipenem. These findings are in agreement with Mandal et al. [13] and Jain et al. [14], who also reported preserved susceptibility of Gram-negative respiratory pathogens to aminoglycosides and carbapenems despite widespread resistance to cephalosporins and penicillins. This underscores the continued relevance of these antibiotics for empirical therapy in geriatric CAP, particularly in regions with high resistance rates.

Regarding demographic factors, no statistically significant association was observed between gender and culture positivity ($p=0.064$), which is in line with the findings of Sharma et al. [15]. This suggests that gender may not be a major determinant of bacterial etiology in elderly CAP, and empirical therapy decisions should be guided primarily by local microbiological trends and resistance patterns rather than patient sex.

Overall, these results highlight the critical importance of continuous local surveillance of CAP pathogens and their antibiotic susceptibilities in geriatric populations. Given the regional variations in pathogen prevalence and resistance, such data are essential for optimizing empirical therapy, reducing treatment failures, and minimizing the development of further antimicrobial resistance [12,13,14].

CONCLUSION

The present study highlights that community-acquired pneumonia (CAP) among geriatric patients in western Uttar Pradesh is predominantly caused by Gram-negative bacilli, with *Pseudomonas* species (42.97%) and *Klebsiella* species (22.66%) being the most frequent isolates. Gram-positive cocci were comparatively rare (2.4%). Sputum samples represented the majority of positive cultures, and most isolates were obtained from hospitalized patients. Antibiotic susceptibility patterns

demonstrated that *Pseudomonas aeruginosa* and *Pseudomonas* spp. were highly sensitive to amikacin and gentamicin, respectively, while showing significant resistance to ceftazidime. Other Gram-negative organisms exhibited variable sensitivity to carbapenems, tetracycline, and minocycline, with widespread resistance to first-line cephalosporins and penicillins. These findings underscore the predominance of multidrug-resistant Gram-negative bacteria in elderly CAP patients, emphasizing the need for regular local surveillance and evidence-based empirical therapy to optimize clinical outcomes in this vulnerable population.

Limitations of this study

The study did not investigate the underlying factors or molecular mechanisms contributing to antimicrobial resistance among the isolates. Anaerobic bacteria and fungal pathogens were not evaluated, potentially underestimating the complete microbial spectrum involved in chronic suppurative otitis media.

DECLARATIONS

Conflicts of interest: There is no any conflict of interest associated with this study

Consent to participate: There is consent to participate.

Consent for publication: There is consent for the publication of this paper.

Authors' contributions: Author equally contributed the work.

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