International Journal of Pharmacy and Pharmaceutical Sciences

Print ISSN: 2656-0097 | Online ISSN: 0975-1491 Vol 17, Issue 2, 2025

Original Article

BACTERIAL PROFILE, ANTIMICROBIAL SUSCEPTIBILITY PATTERNS, AND ASSOCIATED FACTORS OF COMMUNITY-ACQUIRED PNEUMONIA AMONG ADULT PATIENTS IN SOUTH INDIA: A CROSS-SECTIONAL STUDY

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Received: 07 Oct 2024, Revised and Accepted: 02 Jan 2025

ABSTRACT

Objective: This study aimed to analyze the bacterial profile, antibiotic sensitivity patterns, and prevalence of multidrug resistance in community-acquired pneumonia patients at a tertiary care hospital in Bangalore, India.

Methods: Bacterial isolates were identified using standard microbiological techniques and their antibiotic sensitivity was determined using the Kirby-Bauer disk diffusion method.

Results: A total of 215 sputum samples were processed, of which 150 tested positive for bacteria. *Klebsiella pneumoniae* (32%) was the most common isolate, followed by Acinetobacter spp. (20.66%), and *Pseudomonas aeruginosa* (16%). Notable antibiotic resistance, particularly against third-generation cephalosporins, was observed, with 17.2% of g-negative isolates exhibiting multidrug resistance, primarily due to Extended-Spectrum Beta-Lactamase (ESBL) production.

Conclusion: These findings highlight the need for more effective empirical treatment strategies for CAP.

Keywords: Community-acquired pneumonia (CAP), Antibiotic resistance, Bacterial profile, Multidrug resistance

DOI: https://dx.doi.org/10.22159/ijpps.2025v17i2.52891 Journal homepage: https://innovareacademics.in/journals/index.php/ijpps

INTRODUCTION

Pneumonia is largely categorized into Community-Acquired Pneumonia (CAP) and Hospital-Acquired Pneumonia (HAP), which are caused by many pathogens, including bacteria, viruses, and fungi. This state remains a foremost cause of morbidity and mortality, principally in low-income countries [1, 2].

The Infectious Diseases Society of America (IDSA) defines CAP as pneumonia within 48 h of hospital admission or in individuals who have not recently been hospitalized [2]. In Europe, there are between 1.6 and 10.6 manifestations of CAP per 1,000 adults [3]. Nearly one million deaths in Asia are annually endorsed by CAP [4]. Nearly 200,000 people die from CAP each year in sub-Saharan Africa [5], but the occurrence in Ethiopia is between 38.7% and 45% [6].

CAP is usually initiated by bacterial pathogens, such as *Streptococcus pneumoniae*, *Klebsiella pneumoniae*, and *Staphylococcus aureus*. Of these, *S. pneumoniae* is responsible for almost 30% of cases worldwide [1]. Pneumolysins and capsules are virulence factors that pathogens like *S. pneumoniae* evade the immune system's recognition and reaction [7].

Multidrug-resistant (MDR) bacteria have evolved as a result of antibiotic abuse, and Antimicrobial Resistance (AMR) is growing predominantly in low-resource settings [8]. Empirical therapy options are convoluted by the resistance of routinely administered antibiotics [8, 9]. CAP is often managed empirically in nations with limited diagnostic resources, such as Ethiopia and India [6]. This attitude can lead to poor outcomes for ideal patients. Updated treatment references and reduced CAP-related death rates need to be considered for regional bacterial profiles and resistance patterns [5, 9].

To advance empirical treatment options, this study aimed to define the bacterial profile, antimicrobial susceptibility patterns, and associated variables of CAP in geriatric patients from South India.

MATERIALS AND METHODS

Study design and setting

This cross-sectional study was conducted at a tertiary care teaching hospital in Bangalore, South India, from January 2018 to June 2019. This study included adult patients who were clinically diagnosed with CAP.

Population and sampling

Patients aged ≥ 18 y diagnosed with CAP who consented to participate were included in the study. Individuals who were currently on antibiotics or had been recently hospitalized were excluded. A systematic random sampling method was used to select the 215 participants.

Data collection

Clinical and sociodemographic data were collected using a standardized questionnaire. Sputum samples were collected, transported to the laboratory, and processed within 30 min.

Laboratory procedures

Sputum samples were tested macroscopically and microscopically and then cultured. Bacterial identification was performed by colony morphology, Gram staining, and biochemical tests.

Antimicrobial susceptibility testing

Antimicrobial susceptibility was determined using the Kirby-Bauer disk diffusion method, following the Clinical and Laboratory Standards Institute (CLSI) guidelines. The antibiotics tested were penicillin, ceftriaxone, and ciprofloxacin [10].

Data management and analysis

Data were analyzed using SPSS version 26. Logistic regression was applied to evaluate the associations between CAP and various risk factors, with $p<0.05$ considered statistically significant.

Ethical considerations

The Institutional Review Board approved the study ethically, and informed consent was obtained from all subjects. Data privacy was maintained.

RESULTS

This study was conducted at a tertiary care teaching hospital in Bangalore between January 2018 and June 2019 and involved 215

respiratory samples. Of the 215 sputum samples, 195 met Bartlett's criteria for culturing. Among these, 150 were culture-positive: 140 (93.4%) had pure bacterial isolates, 10 (6.6%) had mixed infections, and 45 samples showed normal upper respiratory flora.

Table 1: Distribution of age and sex in LRTI cases (n=150)

Age group	Female (%)	Male (%)	Total
60-79 Y	42.8%	57.2%	136
≥80 Y	57.2%	42.8%	14
Total	66	84	150

The table outlines age and gender distribution, emphasizing the groups most affected by Lower Respiratory Tract Infections (LRTIs). Of the 150 patients, 56% were male, and 96.66% were within the 60–79 age group.

Table 2: Frequently identified bacterial isolates in LRTI cases stratified by age

Organism	60-79 Y	≥80 Y	Total
Klebsiella pneumoniae	40	8	48(32%)
Acinetobacter spp.	31	0	31(20.66)
Pseudomonas aeruginosa	22	2	24 (16)
Escherichia coli	17	1	18(12)
Staphylococcus aureus	9	2	11(7.3)
Haemophilus influenza	10	0	10 (6.66)
Streptococcus pneumoniae	7	1	8 (5.33)

The table shows the main bacterial isolates by age, emphasizing the most common organisms. *Klebsiella pneumoniae* was the most dominant, accounting for 31.5% of isolates, trailed by *Acinetobacter* spp (20.4%), *Pseudomonas aeruginosa* (15.4%), and *Escherichia coli* (11.7%).

Table 3: Antibiotic resistance patterns of *Enterobacteriaceae* and non-fermenters

Antibiotic	*Enterobacteriaceae* (n=70)	Non-fermenters (n=58)
PI	58.8% (*K. pneumoniae*)	24% (*P. aeruginosa*)
	84.2% (*E. coli*)	63.6% (*A. baumanii*)
AMC	68.4% (*K. pneumoniae* and *E. coli*)	63.6% (Both Non-Fermenters)
CIP	33.3% (*K. pneumoniae*)	12% (*P. aeruginosa*)
	78.9% (*E. coli*)	42.2% (*A. baumanii*)
CPZ	58.8% (*K. pneumoniae*)	44% (*P. aeruginosa*)
	89.5% (*E. coli*)	78.9% (*A. baumanii*)
CTX	60.8% (*K. pneumoniae*), 89.5% (*E. coli*)	40% (Both Non-Fermenters)
CZ	58.8% (*K. pneumoniae*), 84.2% (*E. coli*)	64% (Both Non-Fermenters)
CAZ	64.5% (*K. pneumoniae*)	28% (*P. aeruginosa*)
	73.7% (E. coli)	66.7% (*A. baumanii*)
PIT	27.5% (*K. pneumoniae*)	8% (*P. aeruginosa*)
	21.1% (*E. coli*)	48.5% (*A. baumanii*)
AT	54.9% (*K. pneumoniae*)	24% (*P. aeruginosa*)
	73.7% (*E. coli*)	57.6% (*A. baumanii*)
GEN	17.6% (*K. pneumoniae*)	16% (*P. aeruginosa*)
	15.8% (*E. coli*)	48.5% (*A. baumanii*)
IMP	17.6% (*K. pneumoniae*)	8% (*P. aeruginosa*)
	5.3% (*E. coli*)	42.4% (*A. baumanii*)
AK	9.8% (*K. pneumoniae*)	12% (*P. aeruginosa*)
	10.5% (*E. coli*)	48.5% (*A. baumanii*)

PI-Piperacillin, AMC-Amoxicillin-Clavulanic acid, CIP-Ciprofloxacin, CPZ-Cefoperazone, CTX-Ceotaxime, CZ-cefazoline, CAZ-Ceftazidime, PIT-Piperacillin Tazobactam, AT-Aztreonem, GEN-Gentamycin, IMP-Imipenem, AK-Amikacin.

Enterobacteriaceae displayed resistance to third-generation cephalosporins, with a maximum resistance of 68.6% to cefotaxime. Non-fermenters also exhibited considerable resistance, especially first-generation cephalosporins (64%). Meropenem was the most effective antibiotic for both groups, with sensitivity rates of 90% for *Enterobacteriaceae* and 81.1% for non-fermenters. A total of 17.2% of g-negative bacteria had multidrug resistance, including *Acinetobacter* spp. Accounting for 39.4%. The most dominant resistance mechanism was Extended-Spectrum Beta-Lactamases (ESBL) production (32.8%), followed by carbapenemase production (14.1%). Of the 14 *Staphylococcus aureus* isolates, 35.7% were methicillin-resistant (MRSA) and 64.3% were methicillin-sensitive (MSSA). *Enterococcus faecalis* showed no resistance to linezolid or teicoplanin.

DISCUSSION

This study was conducted at a tertiary care teaching hospital in Bengaluru from January 2018 to June 2019 and examined sputum samples in 215 geriatric patients [11]. The growing elderly population in India, expected to reach 157.7 million by 2050, emphasizes a significant concern. LRTIs pose a serious risk to the elderly owing to weakened immune systems and age-related liabilities. In 2015, LRTIs and Chronic Obstructive Pulmonary Disease (COPD) were the third and fourth leading causes of mortality worldwide, respectively [12].

According to the demographics, 136 out of 150 individuals were aged 60-79, whereas 14 were 80 y or older. The male-to-female ratio was 1.3:1, implying a greater prevalence among males, likely due to lifestyle factors such as smoking and alcohol use. These results align with the findings of Prabhudev *et al.* [13]. Bacteriological assessment of sputum samples revealed *K. pneumoniae* to be the most prevalent isolate (32%), followed by *Acinetobacter spp*. (20.66%), and *P. aeruginosa* (16%). Comparable results were reported by Cut *et al.*, possibly because of the collective pathogens found in similar patient populations and settings, in addition to similar diagnostic approaches [14].

The antibiotic resistance profile indicated that Enterobacteriaceae isolated from sputum samples were resistant to amoxicillin (68.4%) and cefotaxime (68.6%), but exhibited high sensitivity to Meropenem and Amikacin (90% each). These results are consistent with those of Choi *et al.* [15]. Non-fermenting bacteria display resistance to Cefazolin and Cefoperazone. MDR was observed in 17.2% of g-negative bacteria in sputum samples, including *Acinetobacter spp*. The highest MDR rate was 39.4%. These findings are consistent with those reported by Bitew *et al.* [16]. The antibiotic resistance and MDR observed in Enterobacteriaceae and non-fermenting bacteria are likely due to antibiotic misuse and the pathogens' intrinsic resistance mechanisms.

Beta-lactamase production, ESBL, AmpC, and carbapenemases, was prevalent, with 32% of isolates producing ESBL and 5.5% producing AmpC enzymes, consistent with the findings from the Pasha SAR study [17]. Clinically, LRTIs are primarily associated with acute exacerbation of COPD (AECOPD) (54%), pneumonia (42%), and bronchitis (7.4%). Most patients (88%) had elevated white blood cell counts, indicating an infection. This predominance of beta-lactamase production and the association of LRTIs with these clauses can be ascribed to high-risk populations, bacterial resistance mechanisms, and the inflammatory response observed in elevated white blood cell counts [18].

LIMITATIONS OF THE STUDY

This cross-sectional design constrains the causal conclusions. The sample of 215 patients may not signify a larger South Indian population, hypothetically directing selection bias by excluding those on antibiotics or recently hospitalized. Furthermore, dependence on sputum samples may cause infections caused by viruses and fungi. Ultimately, this study did not examine the impact of socioeconomic factors and comorbidities on clinical effects and antibiotic resistance.

CONCLUSION

This study emphasizes the predominance of Acinetobacter spp. and Klebsiella pneumoniae in CAP and their considerable drug resistance. These results emphasize the need for enhanced surveillance and customized treatment protocols based on local resistance patterns to increase clinical management and diminish the morbidity and mortality associated with CAP.

ACKNOWLEDGEMENT

We are thankful to the authorities of the ESIC-MC-PGIMSR, Bangalore, for allowing us to conduct this study. We also thank the participants for their support in completing the study.

FUNDING

Nil

AUTHORS CONTRIBUTIONS

Conception/design, Provision of study material Collection of data, Data analysis and interpretation, Manuscript writing: Dr Rahil Pasha S A

CONFLICTS OF INTERESTS

The authors declare no conflict of interest concerning the research and publication of this article.

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