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Microbial and antimicrobial resistance patterns in pneumonia: A regional cross-sectional analysis

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Abstract
Background: The global burden of pneumonia is exacerbated by the emergence of antimicrobial resistance. This study aimed to characterize the microbial and resistance profiles of pneumonia cases in a regional context, focusing on CAP, HAP, and VAP.
Materials and Methods: A cross-sectional study was conducted over a year, including 150 adults with radiologically confirmed pneumonia. Respiratory and blood samples were analyzed using standard culture techniques. Antibiotic susceptibility testing followed CLSI guidelines, with resistance mechanisms such as ESBL and MRSA identified through phenotypic assays.
Results: Gram-negative bacteria were predominant, with *Klebsiella pneumoniae* accounting for 40% of CAP and 30% of VAP cases. ESBL production was observed in 30.76% of HAP and 25% of VAP isolates. Recovery rates were highest in CAP (63%) but lowest in VAP (50%), which also had the highest mortality rate (45%).
Conclusion: The study highlights the predominance of gram-negative organisms and rising antimicrobial resistance in pneumonia. Regional data on resistance trends are essential for improving empirical therapy and patient outcomes.

Keywords: Parental attitude, participation, sports, girls

Introduction
The rising prevalence of multidrug-resistant bacteria poses a significant challenge to global healthcare, particularly in the management of respiratory infections such as adult pneumonia. Methicillin-resistant *Staphylococcus aureus* (MRSA) and extended-spectrum beta-lactamase (ESBL)-producing organisms represent a critical public health threat due to their resistance to commonly used antibiotics, resulting in limited therapeutic options and increased morbidity and mortality rates. The detection and characterization of these resistant pathogens are vital for understanding their epidemiology and guiding effective antimicrobial stewardship programs. MRSA, a major nosocomial pathogen, has exhibited resistance to beta-lactam antibiotics due to the acquisition of the mecA gene, encoding a modified penicillin-binding protein (PBP2a) with low beta-lactam affinity [1, 2]. Similarly, ESBL-producing bacteria, predominantly *Escherichia coli* and *Klebsiella pneumoniae*, hydrolyze a broad range of beta-lactams, including third-generation cephalosporins, mediated by enzymes encoded by transferable resistance genes such as blaCTX-M, blaSHV, and blaTEM [3, 4].

Adult pneumonia is frequently complicated by these resistant pathogens, complicating empirical treatment and often necessitating the use of carbapenems or other broad-spectrum agents, which further exacerbate the cycle of resistance development [5, 6]. Studies conducted in various clinical settings before 2016 indicated a steady rise in the prevalence of MRSA and ESBL producers, highlighting the importance of regular surveillance and molecular characterization to identify resistance patterns and potential outbreaks [7, 8]. Molecular techniques, such as polymerase chain reaction (PCR), remain pivotal in the detection of resistance genes, whereas phenotypic methods, including disk diffusion and automated systems, aid in routine identification and susceptibility testing [9, 10].

The significance of characterizing bacterial isolates in adult pneumonia extends beyond clinical implications, as it informs infection control strategies and public health policies aimed at curbing the spread of these formidable pathogens.

This underscores the need for robust diagnostic frameworks and integrated approaches combining microbiological, molecular, and epidemiological data to combat antibiotic resistance effectively.

This study aims to provide a historical perspective on the resistance trends and molecular mechanisms underlying MRSA and ESBL production, emphasizing their impact on treatment outcomes and healthcare resource utilization.

Materials and Methodology

The study was a cross-sectional analysis conducted over one year, from October 2015 to September 2016, at the Department of Microbiology, I-Care Institute of Medical Sciences and Research. A total of 150 adult patients with clinically and radiologically confirmed pneumonia were included. The sample population comprised 100 cases of community-acquired pneumonia (CAP), 30 cases of hospital-acquired pneumonia (HAP), and 20 cases of ventilator-associated pneumonia (VAP).

Inclusion criteria included adults aged 18 years and above with clinically suspected and radiologically proven pneumonia. Patients with active tuberculosis or those who had taken antibiotics within two weeks prior to sample collection were excluded.

Respiratory samples were collected under sterile precautions and included sputum samples for CAP and HAP patients, while endotracheal aspirates (ETA) were obtained from patients with VAP who were on mechanical ventilation for more than 48 hours. For sputum samples, deeply expectorated or induced sputum was collected in leak-proof sterile containers. ETA samples were obtained using a suction catheter attached to a mucus extractor and were transported in sterile containers to the laboratory. Blood samples were collected from febrile pneumonia patients (≥37.8 °C) using sterile techniques.

Upon arrival, samples underwent macroscopic and microscopic examination, including Gram staining, to assess the quality and inflammatory response. Respiratory samples were processed on nutrient agar, blood agar, chocolate agar, and MacConkey agar. Culture plates were incubated at 37 °C, with blood and chocolate agar placed under 5-10% carbon dioxide.

Antibiotic susceptibility testing was performed using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar, interpreted according to CLSI 2015 guidelines. Methicillin resistance in *Staphylococcus aureus* was screened using cefoxitin disc diffusion, while ESBL production in Enterobacteriaceae was confirmed by combined disc diffusion tests with ceftazidime and ceftazidime-clavulanic acid.

Data were analyzed using SPSS software. Chi-square and Fisher's exact tests were applied for categorical variables, with a significance level set at $p<0.05$. Findings were summarized in statistical tables and charts, emphasizing their clinical implications and alignment with similar studies.

Results

This study investigates the demographic, clinical, microbiological, and resistance profiles of pneumonia cases, including community-acquired pneumonia (CAP), hospital-acquired pneumonia (HAP), and ventilator-associated pneumonia (VAP). A total of 150 patients were analyzed, focusing on risk factors, microbial growth, antibiotic resistance, and clinical outcomes to provide insights into disease patterns and inform treatment strategies.

Middle-aged adults (40-60 years) represented the highest proportion of CAP (46%) and VAP (60%), while HAP predominantly affected older individuals above 60 years (43.33%). Male patients were more affected across all pneumonia types, accounting for 68% in CAP, 66.66% in HAP, and 70% in VAP. Smoking was the most common risk factor, observed in 49% of CAP and 70% of VAP patients.

Table 1: Demographic and Risk Factors in Pneumonia Patients

Variable		CAP (n=100)	HAP (n=30)	VAP (n=20)
Age Group	20-40 years	18 (18%)	7 (23.33%)	2 (10%)
	40-60 years	46 (46%)	10 (33.33%)	12 (60%)
	>60 years	36 (36%)	13 (43.33%)	6 (30%)
Gender	Males	68 (68%)	20 (66.66%)	14 (70%)
	Females	32 (32%)	10 (33.33%)	6 (30%)
Risk Factors	Smoking	49 (49%)	16 (53.33%)	14 (70%)
	Diabetes Mellitus	39 (39%)	14 (46.66%)	11 (55%)
	COPD	22 (22%)	8 (26.66%)	5 (25%)
	Alcoholism	20 (20%)	13 (43.33%)	10 (50%)

Sputum and endotracheal aspirates showed high culture positivity, with rates of 55% in CAP and 100% in VAP. Blood culture positivity was lower, with 8% in CAP and 20% in VAP. *Klebsiella pneumoniae* was the predominant pathogen, accounting for 40% of CAP and 30% of VAP cases. ESBL production in *K. pneumoniae* was notable, especially in HAP (30.76%) and VAP (25%). MRSA was detected in 7.27% of CAP and 10% of VAP cases.

Table 2: Microbial Growth and Culture Positivity (n=150)

Sample	CAP (n=100)	HAP (n=30)	VAP (n=20)
Sputum/ETA Culture Positive	55 (55%)	26 (86.66%)	20 (100%)
Blood Culture Positive	8 (8%)	5 (16.66%)	4 (20%)
Gram-Negative Organisms	71 (71%)	24 (80%)	16 (80%)
Gram-Positive Organisms	29 (29%)	6 (20%)	4 (20%)

Table 3: Distribution of Organisms in Respiratory Samples (n=101)

Organism	CAP (n=55)	HAP (n=26)	VAP (n=20)
Klebsiella pneumoniae	22 (40%)	10 (38.46%)	6 (30%)
Staphylococcus aureus	15 (27.27%)	5 (19.23%)	5 (25%)
Pseudomonas aeruginosa	8 (14.54%)	3 (11.54%)	4 (20%)
Escherichia coli	6 (10.91%)	5 (19.23%)	3 (15%)
Acinetobacter baumannii	2 (3.64%)	3 (11.54%)	2 (10%)

Table 4: Antibiotic Resistance and Resistance Mechanisms in Key Isolates (n=101)

Resistance Mechanism	CAP (%)	HAP (%)	VAP (%)
ESBL (*K. pneumoniae*)	12 (21.82%)	8 (30.76%)	5 (25%)
Amp C (*K. pneumoniae*, *E. coli*)	1 (1.82%)	3 (11.54%)	2 (10%)
MBL (*P. aeruginosa*)	1 (1.82%)	0 (0%)	2 (10%)
MRSA (*S. aureus*)	4 (7.27%)	1 (3.84%)	2 (10%)

Recovery rates were highest in CAP (63%) and lowest in VAP (50%), which also showed the highest mortality rate (45%). HAP demonstrated moderate recovery (60%) but significant mortality (26.66%).

Table 5: Outcomes in Pneumonia Patients (n=150)

Outcome	CAP (n=100)	HAP (n=30)	VAP (n=20)
Recovered	63 (63%)	18 (60%)	10 (50%)
Expired	10 (10%)	8 (26.66%)	9 (45%)
Lost Follow-Up	27 (27%)	4 (13.33%)	1 (5%)

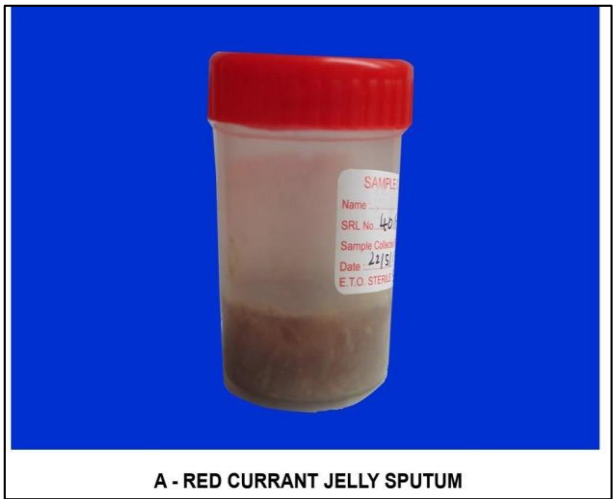

Fig 1: Sputum samples

Discussion

Pneumonia is a major global health concern, with community-acquired pneumonia (CAP), hospital-acquired pneumonia (HAP), and ventilator-associated pneumonia (VAP) contributing significantly to morbidity and mortality. This study was undertaken to investigate the demographic characteristics, microbial profiles, and resistance mechanisms of these pneumonia types, addressing a gap in region-specific data. By analyzing 150 cases, the study aimed to provide actionable insights into pneumonia management and antimicrobial stewardship.

The findings of this study align with other research showing the predominance of gram-negative pathogens in pneumonia cases. Similar studies, such as that by Kollef *et al.* [11], highlighted *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* as the leading pathogens in nosocomial pneumonia, corroborating the current study's findings of 40% and 14.54% isolation rates, respectively, in CAP. Additionally, *Staphylococcus aureus* was a significant gram-positive organism, consistent with observations by Richards *et al.* [12], who reported its role in severe pneumonia across healthcare settings.

However, the rates of ESBL-producing *K. pneumoniae* in this study, particularly in HAP (30.76%) and VAP (25%), are higher than those reported by Paterson *et al.* [13], who documented rates below 20% in nosocomial settings. This could reflect evolving resistance trends in the studied population, emphasizing the need for local antimicrobial resistance surveillance. Similarly, MRSA prevalence in this study (10% in VAP) was slightly lower than the 15% reported by Cosgrove *et al.* [14], suggesting possible differences in infection control practices.

Mortality rates were notably higher in VAP (45%), aligning with trends reported by Vincent *et al.* [15], who identified VAP as the most severe pneumonia type due to critical illness and multidrug-resistant pathogens. Recovery rates in CAP (63%) were comparable to global averages, highlighting the effectiveness of early diagnosis and treatment.

Conclusion

This study identifies gram-negative organisms, particularly *Klebsiella pneumoniae*, as dominant pathogens in pneumonia cases. The significant prevalence of multidrug-resistant strains, including ESBL-producing and methicillin-resistant organisms, emphasizes the critical need for tailored treatment and robust infection prevention measures. The higher mortality in VAP underlines the complexity of managing critically ill patients, while the moderate outcomes in CAP reflect effective community-level interventions. These findings highlight the importance of localized antimicrobial surveillance to guide empirical treatment strategies.

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Conflicts of Interest

The authors declare no conflict of interest in this study.

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