RESEARCH PAPER

BACTERIAL ETIOLOGY OF PNEUMONIA AMONG MEDICAL ICU PATIENTS: A PROSPECTIVE OBSERVATIONAL STUDY

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ABSTRACT

Background

Pneumonia is a pulmonary infection caused by bacteria, viruses, or other microorganisms that results in inflammation of the alveoli and impairs normal gas exchange. It remains a major cause of morbidity and mortality globally, particularly among critically ill patients in intensive care settings. Hospital-acquired pneumonia (HAP) and ventilator-associated pneumonia (VAP) are frequently linked with prolonged hospital stays, increased healthcare costs, emergence of multidrug-resistant (MDR) organisms, and unfavorable clinical outcomes. The rising burden of antimicrobial resistance among hospital pathogens has further complicated the treatment of pneumonia, especially in tertiary care centers. This study was conducted to assess the bacteriological profile, antimicrobial resistance patterns, associated risk factors, and clinical outcomes of pneumonia in patients admitted to the Medical Intensive Care Unit (MICU) of a tertiary care hospital.

Methods

A one-year prospective observational study (2024–2025) was carried out in the Department of Microbiology in collaboration with the MICU at MMIMSR, Mullana, Haryana. A total of 826 respiratory specimens were processed, of which 173 showed significant bacterial growth. Bacterial identification and antimicrobial susceptibility testing were performed using the VITEK 2 Compact automated system in accordance with CLSI guidelines.

Results

Hospital-acquired pneumonia accounted for the highest proportion of cases (12.8%), followed by ventilator-associated pneumonia (6.5%). The most frequently isolated organisms were *Pseudomonas aeruginosa* (31.79%) and *Klebsiella pneumoniae* (30.06%). A large proportion of patients had a history of prior antibiotic use (83.8%) and associated comorbid conditions, most commonly hypertension (40%) and diabetes mellitus (30%). The overall mortality rate observed in the study was 17.3%.

Conclusion

The study highlights a predominance of multidrug-resistant Gram-negative bacilli in ICU-related pneumonia, particularly non-fermenting organisms such as *Pseudomonas aeruginosa* and *Acinetobacter baumannii*, along with *Klebsiella pneumoniae*. Gram-positive pathogens such as *Staphylococcus aureus* (including MSSA and MRSA) were also identified. Regular microbiological surveillance, prompt diagnosis, institution-specific antibiograms, and robust antimicrobial stewardship programs are crucial to improving clinical outcomes and controlling the spread of resistance.

Keywords

Pneumonia, Hospital-Acquired Pneumonia, Ventilator-Associated Pneumonia, Antimicrobial Resistance, Intensive Care Unit, Bacteriological Profile, Antibiogram.

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INTRODUCTION

Pneumonia is an acute infection of the lungs caused by bacteria, viruses, or other microorganisms, leading to inflammation of the alveoli and impaired gas exchange. It commonly presents with cough, fever, sputum production, dyspnoea, and chest pain, and disproportionately affects infants, the elderly, immunocompromised individuals, and critically ill patients [1,2]. Based on the mode and site of acquisition, pneumonia is classified into community-acquired pneumonia (CAP), hospital-acquired pneumonia (HAP), and ventilator-associated pneumonia (VAP). HAP, defined as pneumonia occurring ≥48 hours after hospital

admission, and VAP, a subset occurring after ≥48 hours of mechanical ventilation, are particularly associated with invasive procedures, prolonged hospitalization, and rising antimicrobial resistance [1,2].

In Southeast Asia and India, HAP remains a major healthcare concern due to high patient burden, inconsistent infection control practices, and limited antibiotic stewardship. Reported incidence rates in India range from 10–30 per 1,000 admissions, with HAP accounting for a significant proportion of hospital-acquired infections [3-4]. In Haryana, tertiary care centers report similar trends, with increasing cases driven by broad-spectrum antibiotic misuse and inadequate infection control measures . Mortality remains high, largely due to multidrug-resistant (MDR) pathogens and delayed appropriate therapy [2,5].

HAP develops through aspiration of contaminated secretions, hematogenous spread, or direct inoculation via invasive devices such as endotracheal tubes [2]. Critically ill and ventilated patients are particularly vulnerable due to impaired airway defenses. Clinically, it presents with fever, leucocytosis, purulent secretions, hypoxia, and new pulmonary infiltrates, although differentiation from non-infectious conditions may be challenging [6-8]. Hence, microbiological confirmation remains essential.

Diagnosis relies on clinical, radiological, and microbiological evaluation, with lower respiratory tract samples such as endotracheal aspirates (ETA) and bronchoalveolar lavage (BAL) serving as the diagnostic standard [9]. Culture and sensitivity testing, supported by automated systems such as Vitek 2.0, enables accurate pathogen identification and resistance profiling for targeted therapy.

Major risk factors for HAP include prolonged mechanical ventilation, prior antibiotic exposure, comorbidities, immunosuppression, and invasive procedures [10]. Prognosis is influenced by pathogen virulence, treatment delay, and host factors. Although scoring systems like PSI and CURB-65 are widely used in CAP, there is a lack of standardized prognostic tools for HAP [11].

The bacteriological profile of HAP is dominated by Gram-negative bacilli such as *Klebsiella pneumoniae*, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, and *Escherichia coli*, along with Gram-positive organisms like *Staphylococcus aureus* (including MRSA), which together account for a substantial proportion of infections [12,13]. These pathogens frequently exhibit multidrug resistance through mechanisms such as ESBL production, carbapenemase production, and target site modifications [2,14].

Antimicrobial resistance (AMR) has significantly complicated pneumonia management, particularly in ICU settings, where MDR organisms are associated with poor outcomes and increased mortality [15,16]. Although empiric broad-spectrum antibiotics are often initiated early, inappropriate continuation contributes to resistance, highlighting the importance of culture-guided de-escalation strategies [17].

Hospital antibiograms play a crucial role in guiding empirical therapy and monitoring local resistance trends, forming the backbone of antimicrobial stewardship programs [15,18]. In resource-limited settings like India, strengthening surveillance systems and implementing antibiogram-based antibiotic policies are essential to improve outcomes and reduce unnecessary antibiotic use [18].

The present study aims to evaluate the bacteriological profile of pneumonia in the Medical ICU of a tertiary care hospital, with emphasis on pathogen distribution, antimicrobial susceptibility patterns, associated risk factors, and clinical outcomes. The findings are expected to support the development of institutional antibiograms, optimize antibiotic stewardship, and enhance infection control strategies to reduce HAP-related morbidity, mortality, and antimicrobial resistance.

REVIEW OF LITERATURE:

Pneumonia is an acute inflammatory condition of the lung parenchyma characterized by alveolar filling with inflammatory exudates, resulting in impaired gas exchange and clinical manifestations such as fever, cough, dyspnoea, and radiological consolidation. In severe cases, it may progress to acute respiratory distress syndrome (ARDS) and sepsis [1,9]. It is broadly classified into community-acquired pneumonia (CAP) and hospital-acquired pneumonia (HAP), with etiologies including bacteria, viruses, and fungi, and host immune status playing a key role in disease severity [1].

Globally, lower respiratory tract infections remain a leading cause of mortality, accounting for nearly 3–4 million deaths annually. Approximately 450 million pneumonia cases occur each year, with the highest burden in low- and middle-income countries [1]. HAP contributes significantly to healthcare-associated infections (≈22%), with incidence rates of 5–20 per 1,000 admissions and mortality reaching up to 50% in critically ill patients [2,13].

Pneumonia is classified into CAP, HAP, and ventilator-associated pneumonia (VAP) as per IDSA/ATS guidelines [2]. ICU-associated pneumonia represents a high-risk subgroup with mortality ranging from 11% to 56% [1,2]. Severity assessment tools such as PSI and CURB-65 are widely used for CAP, whereas standardized scoring systems for HAP remain limited [1, 9].

HAP develops due to aspiration of contaminated secretions, hematogenous spread, or device-related colonization, particularly in mechanically

ventilated patients [19]. Diagnosis relies on clinical, radiological, and microbiological correlation, with lower respiratory tract samples such as endotracheal aspirates and BAL being the gold standard [20]. Automated systems like VITEK 2 and molecular diagnostics have improved pathogen detection and resistance profiling.

The etiological spectrum varies by setting. CAP is most commonly caused by *Streptococcus pneumoniae* (20–60%) followed by *Haemophilus influenzae* (3–10%) [21]. *Staphylococcus aureus* (including CA-MRSA) causes severe necrotizing pneumonia, while *Klebsiella pneumoniae* is associated with severe disease in patients with comorbidities [22].

Atypical pathogens such as *Mycoplasma pneumoniae*, *Legionella pneumophila*, and *Chlamydia pneumoniae* contribute to a smaller proportion of cases but require specific therapy due to intrinsic beta-lactam resistance [9]. Viral causes including influenza, RSV, adenovirus, and SARS-CoV-2 are increasingly recognized in severe pneumonia and ICU admissions [23,1]. Fungal pneumonia, mainly caused by *Histoplasma capsulatum*, *Aspergillus spp.*, and *Pneumocystis jirovecii*, is seen in immunocompromised hosts and carries high mortality [24].

HAP and VAP are predominantly caused by aerobic Gram-negative bacilli and MRSA, accounting for nearly 80% of cases [25]. Major pathogens include *Pseudomonas aeruginosa*, *Acinetobacter baumannii*, *Klebsiella pneumoniae*, *E. coli*, and *S. aureus*. These organisms frequently exhibit multidrug resistance via ESBL and carbapenemaseproduction[2]. VAP is strongly associated with mechanical ventilation duration, biofilm formation, and aspiration. Early-onset VAP is typically caused by community flora such as *H. influenzae* and MSSA, while late-onset VAP is associated with MDR organisms [2,13].

Antimicrobial resistance (AMR) significantly complicates pneumonia management, especially in ICU settings, leading to poor outcomes and increased mortality [13]. Empirical broad-spectrum therapy is often required, but inappropriate continuation promotes resistance, making culture-guided de-escalation essential [2,1]. Hospital antibiograms are critical for guiding empirical therapy and monitoring resistance trends [2, 26].

Risk factors for pneumonia include advanced age, smoking, COPD, diabetes mellitus, alcoholism, immunosuppression, and chronic cardiac or neurological disease [27–30]. For HAP/VAP, major risks include prolonged hospitalization, prior antibiotic exposure, mechanical ventilation, and colonization with MDR organisms, with ventilation being the strongest risk factor for VAP [25, 31].

Diagnosis of VAP is based on clinical, radiological, and microbiological criteria. Johanson's criteria and CPIS are commonly used clinically, though with limited specificity. Microbiological confirmation using BAL or tracheal aspirates remains essential, supported by biomarkers such as CRP and procalcitonin. Radiological findings include new or progressive infiltrates and consolidation [32].

Respiratory specimens such as sputum, BAL, and tracheal aspirates are processed using conventional, automated (VITEK 2, MicroScan), and molecular methods (BioFire panel), while MALDI-TOF MS enables rapid species identification [33-34]. Proper sample transport and adherence to CLSI guidelines are essential for accuracy.

Beta-lactams remain the mainstay of therapy, while macrolides and fluoroquinolones provide coverage for atypical pathogens [9,35]. For MDR organisms, newer agents such as ceftazidime-avibactam and meropenem-vaborbactam are used, while vancomycin and linezolid are standard for MRSA pneumonia [9,2]. Daptomycin is contraindicated in pneumonia due to inactivation by surfactant, and aminoglycosides are not recommended as monotherapy due to poor lung penetration [36].

Resistance mechanisms include ESBL, CRE, and carbapenem-resistant non-fermenters such as *Pseudomonas aeruginosa* and *Acinetobacter baumannii*, requiring pathogen-specific therapy based on molecular or phenotypic detection methods [IDSA-guided therapy].

Prevention of VAP involves bundle-based strategies including hand hygiene, head elevation, sedation interruption, and oral care, along with antimicrobial stewardship programs. Hospital-acquired pneumonia remains associated with high morbidity and mortality, prolonged ICU stay, and increased healthcare costs [1,2].

The present study addresses the bacteriological profile, antimicrobial resistance patterns, and clinical outcomes of pneumonia in MICU patients. Limitations include lack of MIC comparison, shorter study duration, and absence of advanced molecular testing, while strengths include use of automated identification systems and generation of region-specific antibiogram data supporting empirical therapy and stewardship.

Aim& OBJECTIVE: To evaluate the bacteriological profile, antimicrobial resistance patterns, associated risk factors, and clinical outcomes of pneumonia in critically ill patients admitted to the Medical Intensive Care Unit (MICU) of a tertiary care hospital.

MATERIALS AND METHODOLOGY

Study Design and Setting

This prospective observational study was conducted in the Department of Microbiology in collaboration with the Medical Intensive Care Unit (MICU) at Maharishi Markandeshwar Institute of Medical Sciences and Research (MMIMSR), Mullana, Ambala, Haryana.

Study Population and Duration

The study included patients admitted to the MICU with clinically suspected pneumonia. The study was carried out over a period of 12 months (2024–2025).Ethical approval was obtained from the Institutional Ethics Committee (Ethical clearance no: 3269).

Inclusion Criteria

1. MICU patients diagnosed with pneumonia based on clinical, radiological, and microbiological criteria.
2. Patients of all age groups and either gender.
3. Patients providing informed consent.

Exclusion Criteria

1. Patients with non-respiratory primary diagnoses (e.g., surgical site infection, primary sepsis, or other systemic infections).
2. Fungal isolates.
3. Viral pneumonia cases.

Sample Size and Data Collection

All consecutive eligible patients fulfilling inclusion criteria during the study period were included. Data were collected using a pre-designed semi-structured proforma, including demographic details, comorbidities, antibiotic exposure, and hospital course.

Specimen Collection and Processing

Respiratory samples were obtained using both invasive and non-invasive methods, including endotracheal aspirate (ETA), bronchoalveolar lavage (BAL), and other bronchoscopic techniques. Samples were processed within 2 hours of collection whenever possible.

Gram staining was used for preliminary evaluation. A good-quality sample was defined by low epithelial cell contamination and presence of neutrophils and bacteria. Samples with significant epithelial contamination were considered unsuitable.

Culture and Identification

Samples were cultured on standard media (Blood agar, MacConkey agar, Chocolate agar) and incubated at 35–37°C for 18–72 hours. Quantitative and semi-quantitative culture methods were used with diagnostic thresholds:

- ETA $\geq 10^5$ CFU/mL
- BAL $\geq 10^4$ CFU/mL
- PSB $\geq 10^3$ CFU/mL

Bacterial identification was performed using the VITEK 2 Compact automated system (bioMérieux, France) based on standardized inoculum (0.5 McFarland), biochemical reactions, and database matching.

Antimicrobial Susceptibility Testing (AST)

AST was performed using VITEK 2 system following CLSI guidelines. Specific AST cards were used depending on organism type (Gram-positive cocci, Enterobacterales, non-fermenters, and ICU isolates). Results were interpreted as Sensitive, Intermediate, or Resistant as per CLSI criteria.

Standard quality control strains included *E. coli* ATCC 25922, *Pseudomonas aeruginosa* ATCC 27853, and *Staphylococcus aureus* ATCC 43300.

Classification of Resistance

Isolates were classified as:

- **MDR:** Resistance to ≥1 agent in ≥3 antimicrobial classes
- **XDR:** Susceptibility limited to ≤2 antimicrobial classes
- **PDR:** Resistance to all antimicrobial classes

Outcome Measures

1. Bacteriological profile of pneumonia in MICU patients.
2. Antimicrobial resistance patterns.
3. Associated risk factors.
4. Clinical outcomes including duration of stay, mechanical ventilation requirement, and mortality.

Statistical Analysis

Data were entered in Microsoft Excel and analyzed using IBM SPSS v26. Descriptive statistics (frequency, percentage, mean, standard deviation) were applied.

RESULTS:

A total of **826 non-duplicate respiratory samples** (including endotracheal aspirates, BAL, mini-BAL, and sputum) received from the Medical ICU were analyzed for culture and antimicrobial susceptibility testing. Of these, **173 samples showed positive bacterial growth**, giving an overall pneumonia positivity rate of **20.9%**. Among confirmed cases, **Hospital-Acquired Pneumonia (HAP)** constituted the majority with **106 cases (12.8%)**, followed by **Ventilator-Associated Pneumonia (VAP)** with **54 cases (6.5%)**, and **severe Community-Acquired Pneumonia (CAP)** with **13 cases (1.57%)**. During the study period, **496 patients required mechanical ventilation**, accounting for **16,360 ventilator days**. Based on 54 VAP cases, the calculated **VAP incidence density was 3.3 per 1,000 ventilator days**, indicating a measurable burden of ventilator-associated infection in the ICU setting.

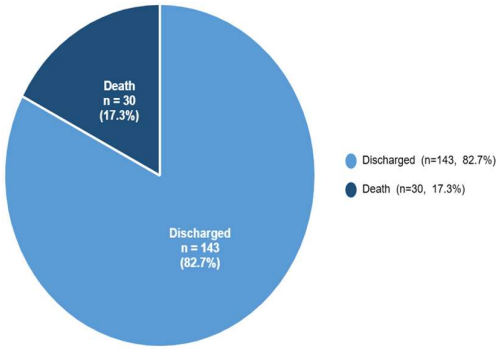
In our study The age distribution shows a marked predominance of elderly patients in the study population. The largest proportion belonged to the **61–70 years group (25.4%)**, followed closely by **51–60 years (23.1%)**, together accounting for nearly half of all cases. The **71–80 years group**

(17.9%) also formed a substantial segment. In comparison, middle-aged individuals (**41–50 years: 15.6%**) were less represented, while younger age groups contributed minimally, including **31–40 years (10.4%)**, **21–30 years (5.2%)**, and **10–20 years (2.3%)**, indicating a clear shift of disease burden toward older age groups as shown in Table 1.

Table 1:**Agewisedistributionofpatients(N=173)**

AGE	FREQUENCY	PERCENTAGE (%)
10-20years	4	2.3
21-30years	9	5.2
31-40years	18	10.4
41-50years	27	15.6
51-60years	40	23.1
61-70years	44	25.4
71-80years	31	17.9
Total	173	100.0

The gender distribution demonstrates a clear male predominance in the study population. Out of 173 patients, **133 were males (76.9%)** and **40 were females (23.1%)**, indicating that the majority of cases occurred in male patients.



The residence-wise distribution shows a strong predominance of rural patients. Out of 173 cases, **128 patients (74.0%) were from rural areas**, while **45 patients (26.0%) belonged to urban areas**, indicating that most cases were drawn from rural populations.

The symptom profile shows that **breathlessness was the most frequent complaint**, reported in **162 patients (93.6%)**, closely followed by **cough in 159 patients (92%)**. In contrast, **chest pain was relatively uncommon**, occurring in only **11 patients (6.4%)**, indicating that respiratory distress symptoms were far more prominent than pleuritic pain in the study population.

The history of prior antibiotic use indicates that most patients had been exposed to antibiotics before admission. Out of 173 cases, **145 patients (83.8%) reported antibiotic use within the previous 3 months**, whereas only **28 patients (16.2%) had no such history**, suggesting a high rate of recent antibiotic exposure in the study population.

The comorbidity profile shows a substantial burden of chronic illnesses among the study population. **Diabetes mellitus was the most common condition**, present in **87 patients (50.3%)**, followed by **hypertension in 52 patients (30.1%)**. A notable proportion of patients had **no comorbidities (34 cases, 19.7%)**. Other conditions included **post-COVID status (15, 8.7%)**, **COPD (12, 6.9%)**, and **post-tuberculosis sequelae (2, 1.2%)**, indicating that metabolic and cardiovascular disorders were the dominant comorbidities in the cohort as shown in Table 2.

Table2:Co-morbiditiesassociatedwiththepatients

Co-morbidities	Frequency	Percentage (%)
Diabetes mellitus	87	50.3
Hypertension	52	30.1
No Comorbidity	34	19.7
Post TB	2	1.2
Post COVID	15	7.4
COPD	12	5.9

The treatment outcome analysis shows that the majority of patients had a favorable outcome. Out of 173 cases, **143 patients (82.7%) were discharged**, whereas **30 patients (17.3%) died**, indicating a significant mortality burden in the study population despite a higher discharge rate as shown in Figure 1.

Figure 1: **Outcomeofthetreatmentofpatients(N=173)**

The microbiological profile shows a clear predominance of Gram-negative organisms in the study population. **Pseudomonas aeruginosa was the most frequently isolated pathogen** (55 cases, 31.79%), followed closely by **Klebsiella pneumoniae** (52 cases, 30.06%). **Acinetobacter baumannii** was the third most common isolate (30 cases, 17.34%), while **Escherichia coli** accounted

for 15 cases (8.67%). Among Gram-positive cocci, **Staphylococcus aureus (MSSA and MRSA combined)** was identified in 11 cases (6.36%), with **MRSA in 5 cases (2.89%) and MSSA in 6 cases (3.47%)**, while **Streptococcus pneumoniae** was isolated in 9 cases (5.20%), all associated with community-acquired pneumonia. **Stenotrophomonas maltophilia** was rarely detected (1 case, 0.58%). Overall, the data demonstrate dominance of Gram-negative bacilli, particularly non-fermenters such as Pseudomonas and Acinetobacter, with Gram-positive organisms contributing a smaller proportion of infections as shown ion table 3

Table 3: **Prevalenceofbacterialisolatesamongpneumoniapatients (N=173)**

ORGANISMISOLATED	FREQUENCY	PERCENTAGE (%)
PSEUDOMONASAERUGINOSA	55	31.79
KLEBSIELLAPNEUMONIAE	52	30.06
ACINETOBACTERBAUMANII	30	17.34
E.COLI	15	8.67
STAPHYLOCOCCUS AUREUS(MRSA)	5	2.89
STREPTOCOCCUSPNEUMONIAE	9	3.47
STENOTROPHOMONAS MALTOPHILIA	1	0.58
STAPHYLOCOCCUS AUREUS(MSSA)	6	5.20
TOTAL	173	100.0

The distribution of pneumonia types shows that **Hospital-Acquired Pneumonia (HAP) formed the majority of cases (106 patients)**, followed by **Ventilator-Associated Pneumonia (VAP) with 54 patients**, and **Community-Acquired Pneumonia (CAP) with 13 patients**.

In the **VAP group**, Gram-negative bacilli were predominant, with **Klebsiella pneumoniae and Acinetobacter baumannii each isolated in 18 cases (33.3%)**, followed by **Pseudomonas aeruginosa in 13 cases (24.1%)**, while **Escherichia coli (7.4%)** and **Stenotrophomonas maltophilia (1.9%)** were less frequent.

In **HAP patients**, **Pseudomonas aeruginosa was the leading pathogen (39.6%)**, followed by **Klebsiella pneumoniae (32.1%)**. **Acinetobacter baumannii (11.3%)**, **Escherichia coli (10.4%)**, and **MRSA (6.6%)** were also identified.

In contrast, **CAP cases were predominantly caused by Gram-positive organisms**, with **Streptococcus pneumoniae accounting for 69.2% of isolates**, followed by **MRSA (30.8%)**, and no Gram-negative bacilli were isolated. Overall, Gram-negative organisms predominated in HAP and VAP, whereas CAP was mainly associated with Gram-positive pathogens as depicted in table 4.

Table 4: **PatternofBacterialIsolatesinVAP,HAP,andCAP(Totaln= 173)**

Causative Organism	Total (N= 173)	VAP (n= 54)		HAP (n=106)		CAP (n= 13)	
		n	%	n	%	n	%
GRAMPOSITIVE COCCI(GPC)							
Streptococcus pneumoniae	**9 (5.2%)**	—	—	—	—	9	5.20%
Staphylococcus aureus(MSSA)	**6 (3.46 %)**	2	1.15 %	4	2.31 %	-	-
Staphylococcus aureus(MRSA)	**5 (2.89 %)**	1	0.57 %	4	2.31 %	-	-
GRAMNEGATIVEBACILLI (GNB)							
Pseudomonas aeruginosa	**55 (31.8%)**	13	7.51 %	42	24.27 %	—	—
Klebsiella pneumoniae	**52 (30.1%)**	18	10.4 %	34	19.6 %	—	—
Acinetobacter baumannii	**30 (17.3%)**	18	10.4 %	12	6.93 %	—	—
Escherichiacoli	**15 (8.7%)**	4	2.31 %	11	6.35 %	—	—
Stenotrophomonas maltophilia	**1 (0.6%)**	1	0.57 %	—	—	—	—
Total	**173 (100%)**	**57**	**32.91%**	**107**	**61.77 %**	**9**	**5.20 %%**

Our study also revealed that The antimicrobial susceptibility profile revealed a high level of multidrug resistance among Gram-negative isolates. **Pseudomonas aeruginosa (n=55)** showed complete resistance (100%) to Gentamicin, Amikacin, Ertapenem, Ceftriaxone, Cefuroxime, Piperacillin/Tazobactam, Cotrimoxazole, and Ciprofloxacin. High resistance was also observed for carbapenems, with **Imipenem resistance in 96.4% and Meropenem in 92.7% of isolates**.

Similarly, **Klebsiella pneumoniae (n=52)** exhibited 100% resistance to most tested antibiotics including aminoglycosides, cephalosporins, fluoroquinolones, and beta-lactam/beta-lactamase inhibitor combinations, with **Imipenem and Meropenem resistance rates of 94.2% and 92.3% respectively**.

Acinetobacter baumannii (n=30) demonstrated extensive resistance across all major antibiotic classes, including 100% resistance to carbapenems, cephalosporins, fluoroquinolones, and cotrimoxazole, with only partial susceptibility remaining to aminoglycosides (Gentamicin 86.7%, Amikacin 93.3% resistance).

Escherichia coli (n=15) also showed high resistance, with 100% resistance to multiple agents including cephalosporins, fluoroquinolones, and cotrimoxazole. Carbapenem resistance remained substantial but comparatively lower, with **Imipenem resistance in 66.7% and Meropenem in 60% of isolates**.

In contrast, **Stenotrophomonas maltophilia (n=1)** showed susceptibility to Minocycline and Levofloxacin, while remaining resistant to Chloramphenicol as shown in table 5.

Overall, the findings indicate a predominant burden of multidrug-resistant Gram-negative pathogens with significant carbapenem resistance, particularly among non-fermenting organisms.

Table 5: **Antimicrobialresistanceamonggram-negativeorganisms(N=153)**

Organism	**n (%)**	**Gen n(%)**	**AK n(%)**	**Imi n(%)**	**Mero n(%)**	**ER Tn (%)**	**CTR n (%)**	**CXM n (%)**	**Pip/Taz n(%)**	**(t n (%)**	**Cipro (%)**
Pseudomonas aeruginosa	55 (35.9%)	55 (100)	55 (100)	53 (96.4)	51 (92.7)	55 (100)	55 (100)	55 (100)	55 (100)	55 (100)	55 (100)
Klebsiella pneumoniae	52 (34.0%)	52 (100)	52 (100)	49 (94.2)	48 (92.3)	52 (100)	52 (100)	52 (100)	52 (100)	52 (100)	52 (100)
Acinetobacter baumannii	30 (19.6%)	26 (86.7)	28 (93.3)	30 (100)	30 (100)	30 (100)	30 (100)	30 (100)	30 (100)	30 (100)	30 (100)
	15 (9.8%)	15 (100)	13 (86.7)	10 (66.7)	9 (60)	15 (100)	15 (100)	15 (100)	13 (86.7)	15 (100)	15 (100)
Stenotrophomonas maltophilia**	1 (0.7%)	Minocycline 1(100) (S)	Levofloxacin 1(100) (S)	Chloramphenicol 1(100) (R)							

AntibioticResistance;AK=Amikacin;IMI=Imipenem;MER=Meropenem;ERT=Ertapenem;CTR=Ceftriaxone;CXM= Cefuroxime; Pip/Taz = Piperacillin/Tazobactam; COT = Trimethoprim/Sulfamethoxazole; CIP = Ciprofloxacin; CR = Carbapenem-Resistant;CRPA=Carbapenem-ResistantPseudomonasaeruginosa;CRKP= Carbapenem-ResistantKlebsiella pneumoniae; CRAB = Carbapenem-Resistant Acinetobacter baumannii; CRE = Carbapenem-Resistant Enterobacteriaceae.

*Stenotrophomonasmaltophilia**(n=1):StandardGram-negativeantibioticpanelnotapplicabledueto intrinsicresistanceto carbapenems and most beta-lactams. Isolate tested on organism-specific drugs — Minocycline — S, Levofloxacin — S, Chloramphenicol — R*

The analysis of last-line antibiotic susceptibility among 153 Gram-negative isolates revealed variable resistance patterns across different organisms. **Pseudomonas aeruginosa** showed

reduced susceptibility to tigecycline, with 26.14% of isolates showing intermediate response and 9.8% resistance, while for colistin, 29.41% were intermediate and 6.53% resistant.

In **Klebsiella pneumoniae**, the majority of isolates demonstrated reduced susceptibility to tigecycline, with 96.2% intermediate and 3.8% resistant. For colistin, 33.3% were intermediate and 0.65% resistant, indicating comparatively better activity than tigecycline.

Acinetobacter baumannii showed marked resistance to tigecycline, with 93.3% of isolates resistant and only 6.6% intermediate. Colistin susceptibility was also reduced, with 83.3% intermediate and 16.6% resistant isolates.

In **Escherichia coli**, tigecycline resistance was relatively low, with 6.53% intermediate and 3.26% resistant isolates. However, colistin activity was limited, with 93.3% intermediate and 0.65% resistant isolates as depicted in table 6.

Overall, the findings highlight concerning variability in susceptibility to last-resort agents, particularly colistin and tigecycline, among multidrug-resistant Gram-negative pathogens.

Table 6: SusceptibilitytoTigecyclineandColistinamonggramnegative organism

Bacteria	**n**	**Tigecycline**		**Colistin**	
		I n (%)	R n (%)	I n (%)	R n (%)
Pseudomonas aeruginosa	55	40(26.14%)	15 (9.8%)	45 (29.41%)	10(6.53%)
Klebsiella pneumoniae	52	50 (96.2%)	2 (3.8%)	51 (33.3%)	1 (0.65%)
Acinetobacter baumannii	30	2(6.6%)	28(93.3%)	25 (83.3%)	5 (16.6%)
E. coli	15	10(6.53%)	5(3.26%)	14 (93.3%)	1 (0.65%)

Antimicrobial susceptibility testing among Gram-positive isolates demonstrated notable resistance patterns. In **Streptococcus pneumoniae (n=9)**, resistance was highest to benzylpenicillin (66.7%) followed by ampicillin (44.4%), while lower to moderate resistance (11.1–33.3%) was observed for other tested beta-lactams and gentamicin.

Among **Staphylococcus aureus isolates**, both MRSA and MSSA exhibited substantial resistance. The **MRSA isolates (n=5)** showed high-level multidrug resistance, with 80% resistance to most beta-lactams, fluoroquinolones, macrolides, and tetracyclines. Concerningly, resistance was also observed against key reserve agents including teicoplanin (60%), vancomycin (40%), and linezolid (40%).

The **MSSA isolates (n=6)** also demonstrated significant resistance, with 66.6% resistance to benzylpenicillin, piperacillin-tazobactam, gentamicin, erythromycin, clindamycin, and cotrimoxazole. Additionally, 50% resistance was noted to other penicillins, ciprofloxacin, and tetracycline.

Overall, the findings indicate considerable antimicrobial resistance even among Gram-positive pathogens, including reduced susceptibility to several first-line and last-resort agents.

Table 7: **Antimicrobialresistanceamonggram-positiveorganisms(N= 20)**

Organism	***Streptococcus pneumoniae***	***S. aureus (MRSA)***	***S.aureus (MSSA)***
n	**9**	**5**	6
Cefoxitin	NT	5	0
Benzylpenicillin	6(66.7%)	4(80%)	4(66.6%)
Amoxicillin	3(33.3%)	5	5
Ampicillin	4(44.4%)	5	3(50%)
Amoxiclav	3 (33.3%)	4(80%)	3(50%)
Piperacillin/ Tazobactam	1(11.1%)	5	4(66.6%)
Oxacillin	2(22.2%)	4(80%)	3(50%)
Gentamicin	3(33.3%)	5	4(66.6%)
Ciprofloxacin	1(11.1%)	4((80%)	3(50%)
Erythromycin	0	4(80%)	4(66.6%)
Inducible Clindamycin	NT	3(60%)	1(16.6%)
Clindamycin	1(11.1%)	5	4(66.6%)
Linezolid	0	2(40%)	0
Teicoplanin	0	3(60%)	0
Vancomycin	0	2(40%)	0
Doxycycline	0	4(80%)	1(16.6%)
Minocycline	0	4(80%)	1(16.6%)

Tetracycline	0	5	3(50%)
Rifampicin	0	4(80%)	2(33.3%)
Cotrimoxazole	0	2(40%)	4(66.6%)

The analysis of antimicrobial resistance phenotypes revealed that extensively drug-resistant (XDR) organisms were the predominant category, accounting for 102 isolates (64.6%), followed by pan-drug resistant (PDR) isolates at 41 cases (25.9%), and multidrug-resistant (MDR) isolates at 15 cases (9.5%). Notably, no Gram-negative isolate was classified as non-MDR, highlighting a uniformly high resistance burden.

Among individual pathogens, Pseudomonas aeruginosa (n=55) was mainly XDR (69.1%), with 20.0% PDR and 10.9% MDR. Klebsiella pneumoniae (n=52) also showed extensive resistance, with 63.5% XDR and 28.8% PDR, leaving only 7.7% as MDR; together, XDR and PDR accounted for 92.3% of isolates, indicating a critically resistant profile.

Acinetobacter baumannii (n=30) demonstrated the highest level of extreme resistance, with 40.0% PDR and 53.3% XDR, and only 6.7% MDR isolates, making it the most resistant organism in this study. Escherichia coli (n=15) showed predominantly XDR phenotype (60.0%), with MDR and PDR each contributing 20.0%.

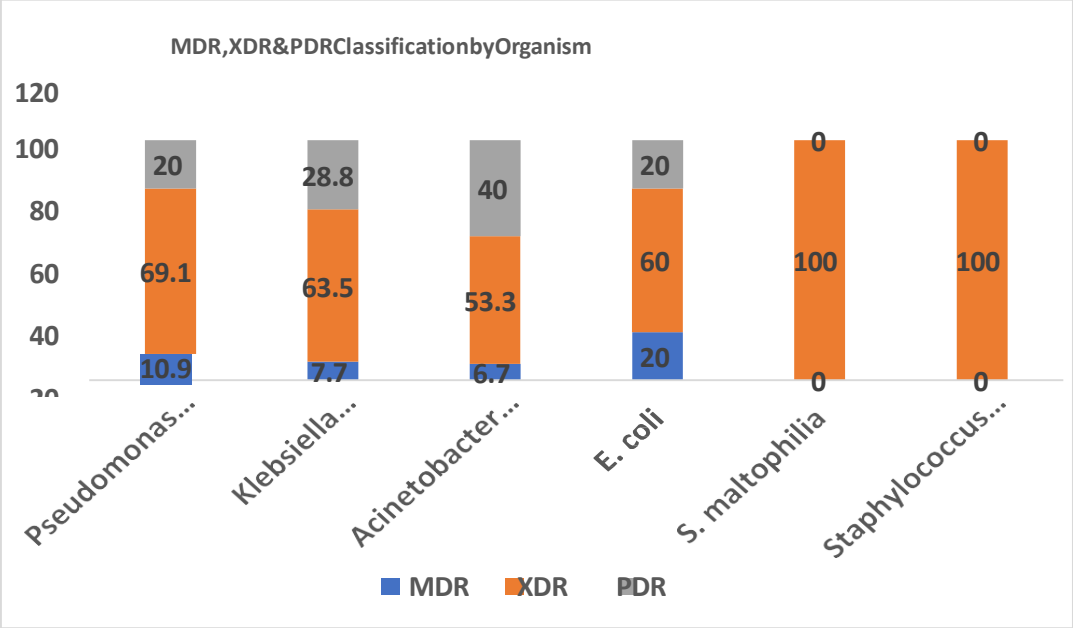
The single Stenotrophomonas maltophilia isolate and all MRSA isolates (n=5) were classified as 100% XDR, with no MDR or PDR phenotypes observed as shown in Table 8 and Figure 3.

Overall, the data demonstrate a severe burden of advanced antimicrobial resistance, with dominance of XDR and PDR organisms across both Gram-negative and Gram-positive pathogens.

Table8:DistributionofMDR,XDR,IsbyOrganismina Private Tertiary ICU

Organism	**Total (n)**	**MDRn (%)**	**XDRn (%)**	**PDRn (%)**
Pseudomonas aeruginosa	55	6 (10.9%)	38 (69.1%)	11 (20.0%)
Klebsiella pneumoniae	52	4 (7.7%)	33 (63.5%)	15 (28.8%)
Acinetobacter baumannii	30	2 (6.7%)	16 (53.3%)	12 (40.0%)
E. coli	15	3 (20.0%)	9 (60.0%)	3 (20.0%)
S. maltophilia	1	0 (0%)	1 (100%)	0 (0%)
Staphylococcus aureus(MRSA)	5	0 (0%)	5 (100%)	0 (0%)

Figure 3:



ISCUSSION:

In the present study, 173 of 826 non-duplicate respiratory samples from the MICU were culture positive, indicating a pneumonia prevalence of 20.9%. Among these, HAP was most common (61.3%), followed by VAP (31.2%) and CAP (7.5%). The VAP incidence rate was 3.3 per 1,000 ventilator days (54 cases/16,360 ventilator days).

This VAP rate is lower than several Indian ICU reports, where rates range from 12.35 to 52.34 per 1,000 ventilator days [3], and is also lower than the ICMR multicentre median of 5.1 per 1,000 ventilator days [4]. Choudhuri et al. (2017) reported a markedly higher incidence of 28.3 per 1,000 ventilator days in a tertiary ICU [5]. The comparatively lower rate in the present study may reflect better adherence to ventilator care bundle practices such as head-end elevation, sedation interruption, and oral hygiene measures. International data similarly show variability, with European benchmarks around 10.8 per 1,000 ventilator days [1]. Early studies by Rello et al. also highlighted the substantial ICU burden associated with VAP [37].

The higher proportion of HAP compared to VAP is consistent with IDSA/ATS 2016 guidelines, which describe HAP as a major healthcare-associated infection with significant mortality [2]. Global data from WHO and GBD 2023 further confirm that lower respiratory tract infections remain a leading infectious cause of death, particularly in LMICs including India [38].

Demographic Profile of the Study Population

The study population showed a clear age shift toward older adults, with the highest proportion in the 61–70-year group (25.4%), followed by 51–60 years (23.1%), together accounting for 66.4% of cases. This aligns with established evidence that advanced age is a major risk factor for pneumonia. Torres et al. (2013) identified age >65 years as a key risk factor for CAP [38], while Yende et al. (2018) demonstrated increasing pneumonia incidence with advancing age [39]. Indian ICU studies, including Choudhuri et al. (2017), also report similar age trends [5], and national analyses confirm a higher disease burden among elderly populations [40,41].

Male predominance (76.9%) is consistent with published ICU data, where higher exposure to smoking, alcohol use, and occupational risk factors contributes to increased susceptibility [31,37]. A substantial rural representation (74%) reflects delayed access to care, empirical antibiotic use at peripheral centers, and higher environmental exposure including biomass fuel use.

Clinical Presentation and Comorbidities

Breathlessness was the most common symptom (93.6%), followed by fever (92%) and cough (63.5%), while chest pain was least frequent (6.4%). This reflects the underlying pathophysiology of pneumonia, where alveolar inflammation leads to impaired gas exchange and respiratory distress [42]. Reduced reporting of chest pain is typical in ICU settings due to altered consciousness and ventilation support, as also noted by Garin et al. (2022) [43].

Diabetes mellitus was the most common comorbidity (50.3%), followed by hypertension (30.1%), indicating a significant cardiometabolic burden. This is consistent with evidence linking diabetes to increased susceptibility and severity of pneumonia [44,45].Similar findings have been reported in Indian ICU cohorts [46].

A notably high proportion of patients (83.8%) had prior antibiotic exposure, a well-recognized risk factor for MDR pathogen emergence as per IDSA/ATS guidelines [2]. This likely reflects inappropriate antibiotic use and over-the-counter availability in the community. Such widespread prior exposure strongly contributes to selection pressure and resistance development.

Pneumonia Classification: HAP, VAP, and CAP

HAP was the predominant category (61.3%), followed by VAP (31.2%) and CAP (7.5%). This pattern is expected in MICU populations due to prolonged hospitalization, invasive procedures, and mechanical ventilation. IDSA/ATS guidelines report HAP as a major contributor to healthcare-associated infections with high mortality [2].

Comparable Indian data by Patel et al. (2021) also show HAP predominance in ICU settings [12]. VAP pathogenesis involving biofilm formation and aspiration through endotracheal tubes explains its high association with MDR organisms [2,13]. The observed VAP rate of 3.3 per 1,000 ventilator days is lower than reported WHO benchmarks (~10.47), suggesting relatively better infection control practices in the study setting.

The low CAP proportion (7.5%) reflects ICU-based selection, where only severe CAP cases requiring intensive care are admitted, consistent with IDSA/ATS severity criteria [23,35]. CAP patients typically represent the most severe end of disease spectrum in ICU cohorts.

Bacteriological Profile

Gram-negative bacilli predominated (88.4%), with Pseudomonas aeruginosa (31.8%) and Klebsiella pneumoniae (30.1%) being the most common isolates, followed by Acinetobacter baumannii (17.3%). Gram-positive cocci accounted for only 11.6%.

This pattern is consistent with global ICU pneumonia data, where Gram-negative organisms dominate HAP/VAP cases [35]. Similar findings have been reported in Indian ICUs, where non-fermenters are major pathogens [25]. In CAP cases within the present study, Streptococcus pneumoniae remained predominant, consistent with global CAP epidemiology [38, 46].

Within HAP, P. aeruginosa was most common, followed by K. pneumoniae, similar to other Indian studies [47]. In VAP, K. pneumoniae and A. baumannii were co-dominant, reflecting their strong association with ventilator-associated biofilm infections [5,25].

Antimicrobial Resistance in Gram-Negative Organisms

A severe resistance profile was observed among Gram-negative pathogens. P. aeruginosa and K. pneumoniae showed near-universal resistance to most antibiotic classes, including carbapenems (imipenem resistance 92–96%). A. baumannii demonstrated complete resistance to most tested agents.

These findings align with ICMR-AMR surveillance data reporting high carbapenem resistance in ICU isolates across India [4].Similar trends have been reported by Goel et al. (2019) and Mathur et al. (2022) [48,49]. Global pooled CRPA prevalence has been reported to be lower (34.7%), highlighting the high resistance burden observed in the present ICU .

Mechanisms such as carbapenemase production, efflux pump overexpression, and porin loss likely contribute to this resistance profile [14]. Many isolates meet criteria for difficult-to-treat resistant (DTR) phenotypes, leaving extremely limited therapeutic options. Reduced susceptibility to last-line agents such as tigecycline and colistin was also observed, further limiting treatment options.

MDR, XDR, and PDR Classification

Extensively drug-resistant (XDR) organisms predominated (62.4%), followed by PDR (23.7%) and MDR (8.7%). Notably, no isolate was fully susceptible.

A. baumannii showed the highest PDR proportion (40%), consistent with WHO classification of CRAB as a critical priority pathogen [49]. K. pneumoniae showed a very high combined XDR/PDR burden (92.3%), reflecting widespread carbapenemase-producing strains in India [14]. P. aeruginosa was predominantly XDR (69.1%), with significant DTR phenotype representation.

These findings align with North Indian ICU surveillance data but exceed many international reports, indicating strong regional antibiotic selection pressure [48,50].

Gram-Positive Cocci: Distribution and Resistance

Gram-positive organisms constituted a small proportion of isolates (11.6%), mainly S. aureus and S. pneumoniae. S. pneumoniae showed moderate resistance to penicillin and ampicillin but retained susceptibility to reserve agents, consistent with CAP literature [38,46].

MRSA isolates showed high multidrug resistance, while MSSA also demonstrated notable resistance to commonly used antibiotics. However, MRSA prevalence (2.9%) was below the IDSA/ATS threshold for routine empirical coverage (>20%) [2]. Despite this, high prior antibiotic exposure (83.8%) warrants cautious interpretation. National surveillance data report higher MRSA prevalence in ICU settings (30–40%) [4], supporting culture-guided therapy.

Treatment Outcomes and Mortality

Overall mortality was 17.3%, with 82.7% of patients discharged. This is lower than reported

ICU pneumonia mortality in other studies, which range from 21% to over 30% [50,51]. Indian studies also report higher mortality in VAP populations [5].

The lower mortality in this study may reflect differences in endpoint definition (in-hospital vs 28/90-day mortality). CAP patients had comparatively better outcomes due to lower MDR burden and predominance of S. pneumoniae, consistent with previous reports.

CONCLUSION:

Pneumonia continues to be a major cause of morbidity and mortality in intensive care settings, particularly due to the rising burden of multidrug-resistant organisms that significantly limit therapeutic options. The present study was conducted to evaluate the bacteriological profile, antimicrobial resistance patterns, associated risk factors, and clinical outcomes of pneumonia cases admitted to the Medical Intensive Care Unit (MICU) of a private tertiary care hospital in North India.

A total of 173 patients with confirmed HAP, VAP, or CAP were included. Standard microbiological methods, automated identification (VITEK 2), and CLSI/EUCAST-based antimicrobial susceptibility testing were used, along with MDR/XDR/PDR classification as per (2024)/ECDC-CDC consensus criteria.

The study population was predominantly elderly, male, and from rural areas, with a high burden of comorbidities—particularly diabetes mellitus and hypertension. A striking finding was the very high rate of prior antibiotic exposure, highlighting widespread community and peripheral healthcare antibiotic use. Clinically, breathlessness and fever were the most common presenting features, while HAP was the predominant clinical category, followed by VAP and CAP.

Microbiologically, Gram-negative bacilli overwhelmingly dominated, with *Pseudomonas aeruginosa*, *Klebsiella pneumoniae*, and *Acinetobacter baumannii* as the leading pathogens. Resistance patterns revealed an alarming scenario, with near-universal resistance to multiple antibiotic classes, including carbapenems, and reduced susceptibility even to last-resort agents such as colistin and tigecycline. Gram-positive isolates showed comparatively lower prevalence, but MRSA demonstrated significant multidrug resistance, including reduced susceptibility to key reserve antibiotics.

Phenotypic analysis confirmed that XDR organisms were predominant, followed by PDR and MDR strains, with no Gram-negative isolate being fully susceptible. *A. baumannii* showed the highest proportion of PDR, while *K. pneumoniae* exhibited the highest combined XDR/PDR burden. Overall mortality was 17.3%, reflecting the severity of illness and resistance profile in this ICU cohort.

In conclusion, this study highlights a critical antimicrobial resistance crisis in a North Indian MICU, where most Gram-negative pneumonia pathogens exhibit XDR or PDR phenotypes, severely restricting effective empirical therapy. The findings underscore the urgent need for robust antimicrobial stewardship programs, strict infection control practices, and routine institution-specific antibiogram-guided therapy. Additionally, integration of molecular diagnostics and inclusion of newer β-lactam/β-lactamase inhibitor combinations in routine susceptibility testing are essential to improve future management strategies and patient outcomes in such high-risk ICU settings.

LIMITATIONS:

The study is limited by its single-centre design, relatively small sample size, and lack of molecular confirmation of resistance mechanisms such as blaNDM, blaKPC, blaOXA-48, blaVIM, and blaIMP genes. Additionally, susceptibility testing for newer agents such as ceftazidime–avibactam, ceftolozane–tazobactam, imipenem–relebactam, and sulbactam–durlobactam was not performed.

Based on these findings, implementation of routine molecular carbapenemase detection (PCR or rapid immunoassays such as NG-Test CARBA 5) is strongly recommended. Inclusion of newer β-lactam/β-lactamase inhibitor combinations in routine AST panels is also essential for appropriate therapeutic guidance in XDR/PDR infections. Strict enforcement of quantitative culture thresholds is further recommended to distinguish colonisation from true infection and improve antibiotic targeting.

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