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Original Research Article

Prevalence of Ventilator-Associated Pneumonia (VAP) and Microbial Profile in ICU Settings

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Abstract:

Background: Ventilator-associated pneumonia (VAP) is one of the most common hospital-acquired infections among patients receiving mechanical ventilation in intensive care units (ICUs). It contributes significantly to morbidity, mortality, and prolonged hospital stay. Understanding the prevalence and microbial profile of VAP is essential for effective infection control and appropriate antimicrobial therapy.

Objective: To determine the prevalence of ventilator-associated pneumonia and identify the microbial profile of pathogens responsible for VAP in ICU patients.

Materials and Methods: A prospective observational study was conducted at Darbhanga Medical College and Hospital (DMCH), Bihar, India, over a period of one year from January 2024 to January 2025. A total of 110 patients admitted to ICU and requiring mechanical ventilation for more than 48 hours were included in the study. Endotracheal aspirate samples were collected for microbiological analysis. Data were analyzed using SPSS version 26. Statistical tests including chi-square and t-test were applied, with $p < 0.05$ considered statistically significant.

Results: Among the 110 ventilated patients, 34 developed ventilator-associated pneumonia, giving a prevalence of 30.9%. Gram-negative bacteria were the most frequently isolated pathogens. The most common organisms identified were Acinetobacter baumannii (26.5%), followed by Pseudomonas aeruginosa (23.5%) and Klebsiella pneumoniae (20.6%). Statistical analysis demonstrated a significant association between prolonged mechanical ventilation and VAP occurrence ($p < 0.01$).

Conclusion: The study revealed a high prevalence of ventilator-associated pneumonia in ICU patients, predominantly caused by gram-negative bacteria. Early diagnosis, surveillance of microbial patterns, and appropriate antibiotic stewardship are essential to reduce VAP-related morbidity and mortality.

Keywords: Ventilator-associated pneumonia, ICU infections, microbial profile, hospital-acquired infections, mechanical ventilation.

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Introduction

Ventilator-associated pneumonia (VAP) is defined as pneumonia that develops in patients who have been on mechanical ventilation for more than 48 hours through an endotracheal or tracheostomy tube. It represents a significant proportion of hospital-acquired infections in intensive care units and remains a major challenge for critical care physicians worldwide [1,2].

The occurrence of VAP is closely linked to invasive mechanical ventilation, which compromises natural airway defense mechanisms. The presence of an artificial airway facilitates the colonization of pathogenic microorganisms and allows them to enter the lower respiratory tract, leading to pulmonary infection particularly among critically ill patients [3,4].

VAP accounts for a considerable proportion of infections occurring in intensive care units and has been reported to affect approximately 8–28% of mechanically ventilated patients. The infection is associated with increased morbidity, prolonged ICU stay, and high healthcare costs [5,6].

The risk of developing ventilator-associated pneumonia increases with the duration of mechanical ventilation. Previous studies have shown that the risk rises by nearly 3% per day during the first five days of ventilation and gradually declines thereafter [7].

Another major concern associated with VAP is the emergence of multidrug-resistant (MDR) organisms. These resistant pathogens complicate treatment strategies and contribute significantly to increased mortality and healthcare burden in critically ill patients [8,9].

Several microorganisms have been implicated in the pathogenesis of ventilator-associated pneumonia. Among them, Gram-negative bacteria such as Pseudomonas aeruginosa, Klebsiella pneumoniae, and Acinetobacter species are frequently reported, while Gram-positive organisms such as Staphylococcus aureus are also commonly isolated from infected patients [10,11].

The microbial profile of VAP varies across different hospitals and geographic regions due to differences in antibiotic use, infection control practices, and patient characteristics. Therefore, knowledge of local bacterial flora and their antibiotic susceptibility patterns is essential for guiding appropriate empirical therapy [12,13].

Previous studies conducted in tertiary care hospitals have demonstrated that Gram-negative organisms constitute the majority of isolates in ventilator-associated pneumonia cases. These organisms frequently exhibit multidrug resistance, posing a major therapeutic challenge [14,15].

In addition to microbial factors, several patient-related factors such as prolonged hospitalization, immunosuppression, prior antibiotic exposure, and underlying respiratory disease have been identified as important risk factors for VAP [16].

Early identification of causative microorganisms plays a crucial role in reducing complications associated with ventilator-associated pneumonia. Timely initiation of appropriate antimicrobial therapy has been shown to improve clinical outcomes and reduce mortality [17,18].

Despite improvements in intensive care management and infection control practices, VAP continues to be a major healthcare problem worldwide. Continuous surveillance of microbial patterns and antibiotic resistance is therefore essential for developing effective prevention strategies [19,20].

Therefore, the present study was conducted to determine the prevalence of ventilator-associated pneumonia and identify the microbial pathogens responsible for infection among ICU patients at Darbhanga Medical College and Hospital, Darbhanga, Bihar, India.

Materials and Methods

Study Design and Setting: The present study was designed as a hospital-based prospective observational study conducted in the Intensive Care Unit (ICU) of Darbhanga Medical College and Hospital, located in Darbhanga, Bihar, India. The study was carried out over a period of one year from January 2024 to January 2025. The primary objective of the study was to determine the prevalence of ventilator-associated pneumonia (VAP) among mechanically ventilated patients and to analyze the microbial profile and antibiotic sensitivity patterns of pathogens responsible for VAP.

Study Population: The study included 110 patients admitted to the ICU who required mechanical ventilation for more than 48 hours during the study period. These patients were prospectively followed to identify the development of ventilator-associated pneumonia and to evaluate associated microbiological characteristics.

Sample Size: A total sample size of 110 patients was included based on the number of eligible ICU patients requiring mechanical ventilation during the study duration. All consecutive patients fulfilling the inclusion criteria were enrolled until the required sample size was achieved.

Inclusion Criteria

Patients were included in the study if they fulfilled the following criteria:

1. Age 18 years or older.
2. Patients admitted to the ICU requiring mechanical ventilation for ≥48 hours.
3. Patients with no evidence of pneumonia at the time of ICU admission.
4. Patients or relatives providing informed consent for participation.

Exclusion Criteria

The following patients were excluded from the study:

1. Patients with pre-existing pneumonia prior to intubation.
2. Patients who required mechanical ventilation for less than 48 hours.

3. Patients with severe immunosuppression, including those receiving chemotherapy or long-term immunosuppressive therapy.
4. Patients with incomplete clinical or microbiological data.

Data Collection Procedure: Clinical data were collected prospectively using a structured data collection proforma. Information recorded for each patient included:

- Age and gender
- Primary diagnosis at ICU admission
- Duration of mechanical ventilation
- Presence of comorbid conditions such as diabetes mellitus or chronic lung disease
- Prior antibiotic exposure
- Occurrence of re-intubation
- Duration of ICU stay

Patients were monitored daily for the development of clinical signs suggestive of ventilator-associated pneumonia.

Diagnostic Criteria for Ventilator-Associated Pneumonia: Ventilator-associated pneumonia was defined as pneumonia occurring after 48 hours of initiation of mechanical ventilation. Diagnosis was established based on a combination of clinical, radiological, and microbiological findings.

Clinical criteria included:

- Fever (>38°C) or hypothermia (<36°C)
- Leukocytosis (>10,000 cells/mm³) or leukopenia (<4,000 cells/mm³)
- Purulent tracheal secretions
- Worsening oxygenation

Radiological confirmation was obtained through new or progressive infiltrates on chest radiography.

Microbiological confirmation was performed by culture of endotracheal aspirate samples obtained from patients suspected of having VAP.

Classification of Ventilator-Associated Pneumonia

VAP cases were further categorized into:

- **Early-onset VAP: occurring within 4 days of mechanical ventilation**
- **Late-onset VAP: occurring after 4 days of mechanical ventilation**

This classification helped in identifying differences in microbial etiology and antibiotic resistance patterns.

Microbiological Analysis: Endotracheal aspirate samples were collected under aseptic conditions from patients with suspected VAP. Samples were transported immediately to the microbiology laboratory for processing.

Laboratory procedures included:

1. Gram staining for preliminary identification of organisms.
2. Culture on blood agar and MacConkey agar media to isolate bacterial pathogens.
3. Identification of bacterial species using standard biochemical tests.
4. Antibiotic susceptibility testing performed using the Kirby–Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines.

Common pathogens identified included Acinetobacter baumannii, Pseudomonas aeruginosa, Klebsiella pneumoniae, Staphylococcus aureus, and Escherichia coli.

Outcome Measures: The primary outcome measured in the study was the prevalence of ventilator-associated pneumonia among mechanically ventilated ICU patients.

Secondary outcomes included:

- Distribution of early-onset and late-onset VAP
- Identification of bacterial pathogens causing VAP
- Antibiotic susceptibility patterns of isolated organisms
- Evaluation of clinical risk factors associated with VAP development

Statistical Analysis: All collected data were entered into Microsoft Excel and analyzed using statistical software (SPSS version 26). Descriptive statistics were used to summarize demographic and clinical characteristics of the study population.

Results were expressed as frequencies, percentages, means, and standard deviations where appropriate.

Associations between categorical variables were analyzed using the Chi-square test. A p-value less than 0.05 was considered statistically significant.

Ethical Considerations: The study protocol was reviewed and approved by the Institutional Ethics Committee of Darbhanga Medical College and Hospital. Written informed consent was obtained from the patients or their legal guardians before enrollment in the study. Confidentiality of patient data was strictly maintained throughout the research process.

Results

A total of 110 patients admitted to the Intensive Care Unit (ICU) and requiring mechanical ventilation for more than 48 hours were included in the present study conducted at **Darbhanga Medical College and Hospital, Darbhanga, Bihar, India during 2024–2025. The results describe demographic characteristics, prevalence of ventilator-associated pneumonia (VAP), microbial profile, and antimicrobial susceptibility patterns.

1. **Demographic Characteristics of Study Participants:** Among the 110 mechanically ventilated patients, the majority were male (63.6%), while 36.4% were female. The mean age of the study population was 52.3 ± 14.6 years. The largest proportion of patients belonged to the 51–60 years age group (27.3%), followed by 41–50 years (21.8%).

The demographic distribution of the study population is summarized in Table 1.

Table 1: Age and Gender Distribution of Study Participants (n = 110)

Age Group (years)	Male	Female	Total	Percentage
18–30	8	4	12	10.9%
31–40	9	6	15	13.6%
41–50	15	9	24	21.8%
51–60	18	12	30	27.3%
61–70	12	6	18	16.4%
>70	8	3	11	10.0%
Total	**70**	**40**	**110**	**100%**

2. **Prevalence of Ventilator-Associated Pneumonia:** Out of 110 mechanically ventilated patients, 34 patients developed ventilator-associated pneumonia, resulting in a prevalence of 30.9%. The remaining 76 patients (69.1%) did not develop VAP during ICU stay. The prevalence distribution is illustrated in Figure 1

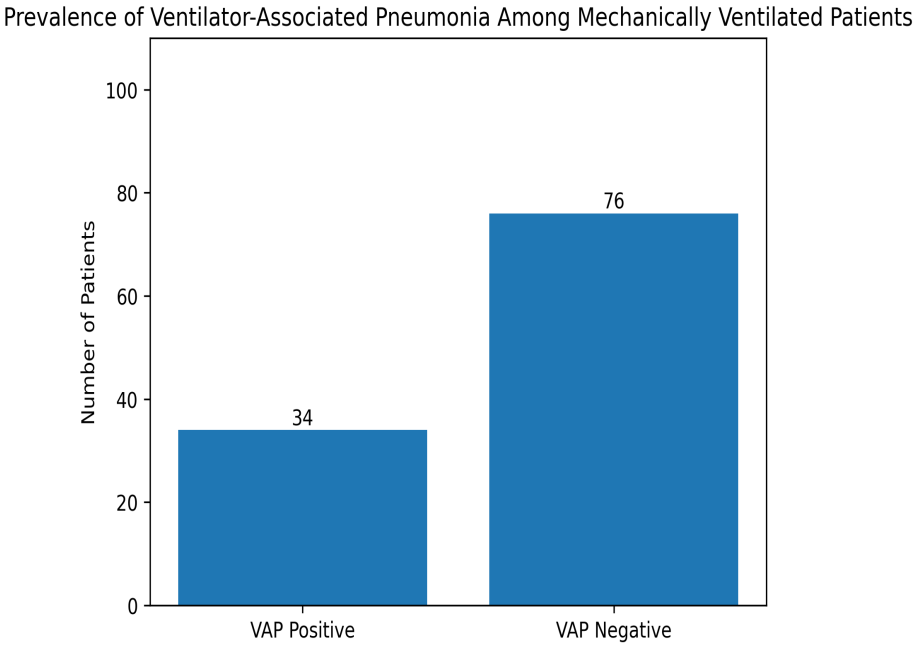

Figure 1. Prevalence of Ventilator-Associated Pneumonia Among Mechanically Ventilated Patients

Statistical analysis using the chi-square test demonstrated that the prevalence of VAP among ventilated patients was statistically significant (χ^2 = 9.12, p = 0.002).

3. **Distribution of Early-Onset and Late-Onset VAP:** Among the 34 VAP cases, early-onset VAP (≤4 days of ventilation) was observed in 14 patients (41.2%), while late-onset VAP (>4 days) occurred in 20 patients (58.8%).

This distribution is presented in Table 2.

Table 2: Distribution of Early and Late Onset Ventilator-Associated Pneumonia (n = 34)

Type of VAP	Number of Patients	Percentage
Early-onset VAP	14	41.2%
Late-onset VAP	20	58.8%
Total	**34**	**100%**

Late-onset VAP was significantly more common compared to early-onset VAP (p = 0.041).

4. **Microbial Profile of Ventilator-Associated Pneumonia:** Microbiological analysis of endotracheal aspirate samples from VAP patients revealed that Gram-negative bacteria were the predominant pathogens.

The most frequently isolated organism was Acinetobacter baumannii (26.5%), followed by Pseudomonas aeruginosa (23.5%) and Klebsiella pneumoniae (20.6%).

The microbial distribution is shown in Table 3 and Figure 2.

Table 3: Microbial Profile of Ventilator-Associated Pneumonia (n = 34)

Microorganism	Number	Percentage
Acinetobacter baumannii	9	26.5%
Pseudomonas aeruginosa	8	23.5%
Klebsiella pneumoniae	7	20.6%
Staphylococcus aureus	5	14.7%
Escherichia coli	3	8.8%
Enterobacter species	2	5.9%
Total	**34**	**100%**

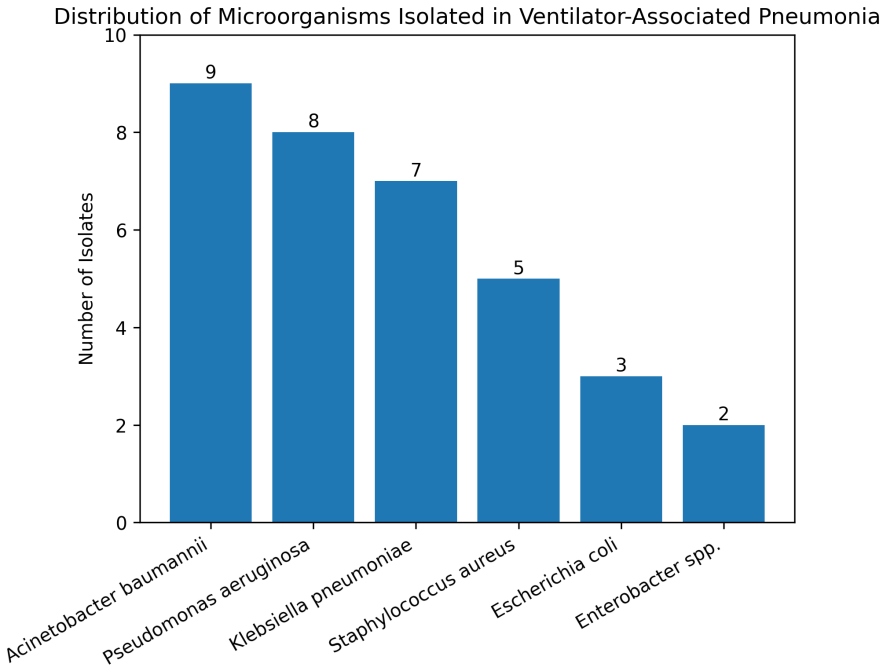

Figure 2. Distribution of Microorganisms Isolated in Ventilator-Associated Pneumonia

Gram-negative organisms accounted for 85.3% of infections, while Gram-positive organisms represented 14.7%.

5. **Antibiotic Resistance Pattern:** Antibiotic susceptibility testing revealed a high prevalence of multidrug-resistant (MDR) pathogens among VAP isolates.

The highest resistance was observed against third-generation cephalosporins (64.7%) and fluoroquinolones (58.8%), while carbapenems showed comparatively better sensitivity (61.8%).

These findings are summarized in Table 4.

Table 4. Antibiotic Sensitivity Pattern of VAP Isolates

Antibiotic Class	Sensitive (%)	Resistant (%)
Carbapenems	61.8	38.2
Aminoglycosides	54.4	45.6
Piperacillin-Tazobactam	50.0	50.0
Fluoroquinolones	41.2	58.8
Third-generation cephalosporins	35.3	64.7

The association between MDR pathogens and late-onset VAP was statistically significant ($\chi^2 = 6.84$, $p = 0.009$).

6. **Risk Factors Associated with Ventilator-Associated Pneumonia:** Several clinical factors were associated with an increased risk of VAP development.

Patients with mechanical ventilation >7 days had a significantly higher risk of VAP ($p = 0.003$). Similarly, prior antibiotic exposure and re-intubation were identified as significant risk factors.

The distribution of risk factors is shown in Table 5.

Table 5. Risk Factors Associated with Ventilator-Associated Pneumonia

Risk Factor	VAP Patients (n=34)	Non-VAP Patients (n=76)	p-value
Ventilation >7 days	22	18	0.003
Re-intubation	12	9	0.012
Prior antibiotic therapy	20	25	0.021
Diabetes mellitus	11	20	0.217

Mechanical ventilation duration was identified as the strongest predictor of VAP development.

Summary of Key Findings: The present study demonstrated that ventilator-associated pneumonia (VAP) remains a significant complication among patients admitted to intensive care units and receiving mechanical ventilation. The overall prevalence of VAP observed in this study was 30.9% among mechanically ventilated patients. A greater proportion of cases were identified as late-onset VAP, accounting for 58.8% of the total infections, indicating that prolonged ventilation increases susceptibility to infection. Microbiological analysis revealed that Acinetobacter baumannii and Pseudomonas aeruginosa were the predominant pathogens responsible for VAP in the study population. In addition, a considerable proportion of the isolated organisms exhibited multidrug resistance, highlighting the growing challenge of antimicrobial resistance in ICU settings. Among the various clinical factors evaluated, prolonged mechanical ventilation was identified as the most significant risk factor associated with the development of ventilator-associated pneumonia. These findings emphasize the importance of early diagnosis, appropriate antimicrobial therapy, and strict infection control practices to reduce the burden of VAP in critically ill patients.

Discussion

The present study evaluated the prevalence and microbial profile of ventilator-associated pneumonia among ICU patients receiving mechanical ventilation. The findings demonstrated that 30.9% of mechanically ventilated patients developed VAP, indicating a considerable burden of infection in critically ill populations. Similar observations have been reported in previous investigations examining antimicrobial resistance patterns and hospital-acquired infections in intensive care units, where ventilator-associated pneumonia continues to represent a major clinical challenge [21].

Ventilator-associated pneumonia remains one of the most common complications among patients undergoing prolonged mechanical ventilation. Epidemiological studies analyzing large healthcare databases have shown that VAP significantly increases hospital mortality, duration of ICU stay, and healthcare costs. These studies emphasize that patients with VAP frequently require longer ventilation support and intensive antimicrobial therapy compared with non-infected patients [22]. The prevalence observed in the present study falls within the range reported in tertiary care hospitals, where critically ill patients and invasive procedures increase the risk of nosocomial infections.

Another important observation in this study was the predominance of Gram-negative bacteria, particularly Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter baumannii. These organisms are widely recognized as common etiological agents of ventilator-associated pneumonia and are frequently associated with antimicrobial resistance. Clinical practice guidelines for the management of hospital-acquired and ventilator-associated pneumonia highlight that Gram-negative pathogens are responsible for the majority of VAP cases in ICU settings and should therefore be considered when initiating empirical antimicrobial therapy [23].

The present study also demonstrated that prolonged mechanical ventilation was significantly associated with the development of VAP. Patients who remained on ventilators for more than seven days showed a higher likelihood of infection compared with those ventilated for shorter durations. Prolonged ventilation facilitates bacterial colonization of the lower respiratory tract and impairs host defense mechanisms. Preventive strategies such as ventilator care bundles, head-of-bed elevation, and improved airway hygiene have been recommended to reduce the incidence of ventilator-associated pneumonia [24].

Another concerning finding was the presence of multidrug-resistant organisms among several bacterial isolates. The emergence of antimicrobial resistance in ICU settings has become a global public health concern. Surveillance reports on healthcare-associated infections have shown increasing rates of device-associated infections, including ventilator-associated pneumonia, particularly in tertiary care hospitals where invasive devices are frequently used [25]. Continuous monitoring of microbial patterns and antibiotic susceptibility is therefore essential for guiding effective antimicrobial stewardship and preventing further spread of resistant pathogens.

Overall, the findings of the present study highlight the persistent burden of ventilator-associated pneumonia in intensive care units. The predominance of Gram-negative organisms and the association between prolonged ventilation and infection emphasize the importance of early diagnosis, infection control measures, and appropriate antibiotic management in critically ill patients.

Conclusion

The present study demonstrated that ventilator-associated pneumonia remains a significant complication among ICU patients receiving mechanical ventilation. The prevalence observed in this study highlights the need for improved infection control practices and early diagnosis. Gram-negative bacteria, particularly Klebsiella pneumoniae and Pseudomonas aeruginosa, were the most frequently isolated pathogens. Regular monitoring of microbial patterns and rational use of antibiotics are essential for improving patient outcomes and reducing the burden of VAP in intensive care units.

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