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ORIGINAL RESEARCH

Microbiological profile of ventilator-associated pneumonia in a respiratory intensive care unit

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ABSTRACT

Introduction: Ventilator-associated pneumonia (VAP) is a significant nosocomial infection among mechanically ventilated patients, associated with increased morbidity, mortality, and healthcare costs. The pathogenesis of VAP involves complex interactions between host defences, microbial colonization, and factors related to mechanical ventilation. Early and accurate diagnosis of VAP and knowledge of the causative pathogens and their antibiotic susceptibility patterns are essential for effective management and improved patient outcomes. This study aims to investigate the microbiological profile of VAP in a Respiratory Intensive Care Unit (RICU) setting.

Aims and Objectives

1. To study the incidence of VAP at MGM Hospital, Warangal.
2. To isolate and identify the aerobic bacteria responsible for VAP in mechanically ventilated patients for > 48 hours.
3. To determine the antibiotic susceptibility pattern of isolated pathogens.

Materials and Methods: This prospective observational study was conducted in the Respiratory Intensive Care Unit (RICU) of MGM Hospital from January 2021 to July 2022. A total of 100 ventilated cases consists of patients (>18 years) admitted to the RICU who are on mechanical ventilation for more than 48 hours and clinically suspected of having VAP. Endotracheal aspirates (ETA) were collected aseptically. Microbiological Analysis, Gram Staining, Aerobic Culture, Semi-Quantitative Analysis, Bacterial Identification, Antibiotic Susceptibility Testing, Methicillin Resistance Screening, Vancomycin Susceptibility Testing were done. **Results:** The most common pathogens isolated were Pseudomonas aeruginosa, Staphylococcus aureus, Acinetobacter species, and Klebsiella pneumoniae. Antibiotic susceptibility testing revealed varied resistance patterns. Most early VAP cases showed good recovery, while late VAP was less common. The study highlights the importance of local microbiological surveillance and tailored antibiotic therapy for effective VAP management. **Conclusion:** This study provided essential data on the microbiological etiology and antibiotic resistance patterns of VAP in the RICU. The findings will help guide appropriate antibiotic selection, optimize patient management, and potentially reduce the morbidity and mortality associated with VAP.

Key words: Ventilator-associated pneumonia, VAP, endotracheal aspirate, antibiotic resistance, microbiological profile, intensive care unit

INTRODUCTION

Hospital-acquired infections (HAIs), particularly ventilator-associated pneumonia (VAP), pose significant challenges in critical care settings. VAP is a subtype of hospital-acquired pneumonia (HAP) that occurs after 48-72 hours of mechanical ventilation and is responsible for 86% of HAP cases in ventilated patients, leading to increased morbidity, mortality, and healthcare costs [1]. It results from the aspiration of colonized secretions and is associated with increased morbidity, mortality (24-76%), and healthcare costs [2, 3].Early-onset VAP (within 4 days) is usually due to antibiotic-sensitive organisms, whereas late-onset VAP (>5 days) is often caused by multidrug-resistant pathogens [4]. The pathogenesis of VAP involves complex interactions between host defenses, microbial colonization and factors related to mechanical ventilation.

The common causative organisms include Acinetobacter baumannii, Pseudomonas aeruginosa,

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Klebsiella pneumoniae and Staphylococcus aureus [5, 6]. Overlapping clinical signs complicate diagnosis; hence, clinical pulmonary infection score (CPIS) is used, with a score >6 suggesting VAP [7]. Understanding local microbial patterns and antibiotic resistance is crucial for timely diagnosis, treatment, and prevention strategies. This study was undertaken to investigate the microbiological profile and antibiotic susceptibility of pathogens causing VAP in a tertiary care respiratory intensive care unit.

AIMS AND OBJECTIVES

1. To study the incidence of VAP at MGM Hospital, Warangal.
2. To isolate and identify the aerobic bacteria responsible for VAP in mechanically ventilated patients for > 48 hours.
3. To determine the antibiotic susceptibility pattern of isolated pathogens.

MATERIALS AND METHODS

After ethical approval and consent, the study has begun.

STUDY TYPE: Prospective observational study.

STUDY PERIOD: January 2021 to July 2022.

STUDY AREA: Respiratory Intensive Care Unit (RICU) in MGM Hospital.

STUDY SUBJECTS: Patients on mechanical ventilator admitted to the RICU.

SAMPLE SIZE: by using the formula $N= Z^2 pq/d^2$.

Estimated prevalence (p) = 0.5 (50%) → When the exact prevalence is not known, 50% gives the maximum sample size.
Confidence level (Z) = 1.96 (for 95%).
Margin of error (d) = 10% (0.1).
$n=(1.96)^2$ 50x50/0.1x0.1= 96.
After rounding up and adding ~5% for possible dropouts or invalid samples:
n=96+(5% of 96) = 96+4.8=100.8≈100

SAMPLING METHOD: Systematic random sampling.

INCLUSION CRITERIA: Patients more than 18 years of age, admitted in RICU on mechanical ventilation for more than 48 hours, clinically suspected of having contracted VAP, CPIS score greater than six used as diagnostic criteria for VAP.

EXCLUSION CRITERIA: All patients who received mechanical ventilation for less than 48 hours, and Patients who were diagnosed to have pneumonia before the start of mechanical ventilation.

INSTRUMENTS USED: 22-inch 12F suction catheter with a mucus extractor (Lukens trap)**,** Standard microbiological equipment and media (Blood agar, MacConkey agar, etc.)**,** Microscope for Gram staining examination.

DATA COLLECTION: Endotracheal aspirates were collected under aseptic precautions,andSpecimens were processed using standard microbiological techniques**.** Gram staining was followed by culture on Blood agar, MacConkey agar, and chocolate media. A semi-quantitative culture method using a standard loop (0.001ml volume) was used. Biochemical tests were used for bacterial identification**.** Antibiotic susceptibility testing was done using the Kirby-Bauer disc diffusion method.

DATA ANALYSIS: Semi-quantitative culture thresholds (≥ 10^5 CFU/ml for VAP diagnosis)andInterpretation of antibiotic susceptibility was done according to CLSI guidelines. Frequency distribution and percentages were used to describe quantitative variables. Chi-square was used to see associations.

RESULTS

In our study, 852 patients were admitted to the Respiratory Intensive Care Unit (RICU) at Government Mahatma Gandhi Memorial Hospital. Among them, 724 patients (84.9%) required mechanical ventilation. Of these, 384 patients (53.03%) were ventilated for more than 48 hours. Out of this group, 100 patients (26.04%) who had a Clinical Pulmonary Infection Score (CPIS) greater than six were identified as suspected cases of Ventilator-Associated Pneumonia (VAP).

Out of the 100 samples enrolled, 57 showed a semi-quantitative culture threshold of $\geq 10^5$ CFU/ml on culture and were categorized under the VAP group. All samples that yielded a culture threshold of $\leq 10^5$ CFU/ml on culture plates were assumed to be due to colonization or contamination and were categorized under the NO-VAP group.

In the present study, most of the ventilator-associated pneumonia (VAP) cases were observed in the age group of 40–59 years, accounting for 27 cases (47.4%). This was followed by 22 cases (38.6%) in the 18–39 years age group, 7 cases (12.3%) in the 60–79 years age group, and only 1 case (1.8%) among those aged 80 years and above. Concerning gender distribution, VAP was found to be more prevalent among males, who constituted 37 out of 57 cases (64.9%), while females accounted for 20 cases (35.1%).

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Table 1: Incidence of VAP

Parameter	Value
Total Patients Studied	100
VAP Cases	57
Non-VAP cases	43
VAP Incidence	57%
Total Ventilator Days	2897
VAP Rate (per 1000 VDs)	19.6

Incidence of VAP: 57 out of 100 mechanically ventilated patients developed VAP (based on CPIS > 6 and culture $\geq 10^5$ CFU/mL) = 57%.

VAP RATE: 19.6 per 1000 ventilator days 57 cases over 2897 ventilator days.

Among the total 57 cases of VAP reported, 56 cases (98.2%) of VAP were monomicrobial and one case (1.8%) showed polymicrobial growth pattern. In the monomicrobial isolates, Gram-negative isolates accounted for 94.7% and Gram-positive isolates accounted 3.5%, and in polymicrobial isolates (1.8%), Gram-positive and Gram-negative isolates accounted for 1.75%.

Table 2: Distribution of Organisms in VAP Cases

Microorganism	Number of Isolates(n)	Percentage (%)
Acinetobacter baumannii	24	41.3%
Pseudomonas aeruginosa	18	31.0%
Klebsiella pneumoniae	9	15.5%
Staphylococcus aureus	2	3.4%
Proteus mirabilis	2	3.4%
Escherichia coli	1	1.72%
S. aureus + E. coli	1	1.75%
Total	58	100%

These 58 isolates were subjected to Gram staining, and it was found that out of Gram-Negative bacteria (94.8%) were predominant and followed by Gram-positive bacteria (5.1%). Thus, it was observed that more cases of ventilator-associated pneumonia were caused by Gram-negative organisms than Gram-positive organisms.

Table 3: Sensitivity of Major Gram-negative Isolates

Antibiotic/Organism	Acinetobactor Species (24)	Psudomonas Aeruginosa (18)	Klebsiella Pneumoniae (9)	Proteus Mirabilis (2)	E. Coli (2)
Imipenem	87.5%	83.3%	100%	100%	100%
Gentamicin	79.16%	55.5%	66.6%	100%	100%
Amikacin	62.5%	61.1%	77.7%	50%	100%
Ciprofloxacin	33.3%	38.8%	88.8%	50%	50%
Piperacillin-Tazo	20.8%	38.8%	44.4%	50%	50%
Ceftriaxone	12.5%	0%	33.3%	50%	50%
Co-Trimoxazole	20.8%	0%	77.7%	100%	100%
Ceftazidime	16.6%	16.6%	77.7%	100%	100%
Cefepime	8.3%	27.7%	55.5%	50%	50%
Amoxyclav	0	0	11.1%	0	0
Ampicillin	0	0	0	0	0

Table 4: Sensitivity of Major Gram-positive Isolate (stap aureus n=3)

Antibiotic	Sensitivity
Vancomycin	100%
Linezolid	100%
Tetracycline	100%
Gentamicin	66%
Doxycycline	66%
Levofloxacin	33%
Penicillin, Cefoxitin, Amoxyclav, Erythromycin, Clindamycin	0%

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All isolates of Staphylococcus aureus were sensitive to Tetracycline, Gentamicin, Chloramphenicol, Co-Trimoxazole, Linezolid, and Vancomycin (100%) each, Doxycycline (66%), and Levofloxacin (33%). All isolates of Staphylococcus aureus (MRSA) were resistant to Cefoxitin, Penicillin, Amoxyclav, Erythromycin, and Clindamycin (100%).

DISCUSSION

The incidence of VAP in the present study was 57.0%, closely matching the prevalence reported by Rajan *et al*., which was 57.14%. However, this rate is higher than the 45.4% incidence observed by Arindam Dey *et al*., [8]. and lower than the 73.3% reported by T. Rajasekhar *et al*., [9]. Such variability in VAP frequency across studies can largely be attributed to differences in diagnostic criteria, sample sizes, and the underlying conditions necessitating ventilator support.

In the present study, Gram-negative bacteria were the predominant isolates from endotracheal aspirates (94.7%), with Acinetobacter baumannii (41.3%) being the most common, followed by Pseudomonas aeruginosa (31.0%) and Klebsiella pneumoniae (15.5%). These findings are consistent with studies by El-Saed *et al*., [10], Torres *et al*., [11], and Kollef MH *et al*., [12], which also reported Gram-negative bacilli as the major pathogens in VAP. The shift from normal oropharyngeal flora to pathogenic Gram-negative bacilli in critically ill patients explains this predominance.

In the present study, most Gram-negative isolates showed high sensitivity to Imipenem, consistent with findings by Dey and Bairy [13]. Acinetobacter baumannii demonstrated 88% sensitivity to Imipenem, aligning with results from Patel *et al*., [14] (85%) and Samal *et al*., [15], though contrasting with Kaur *et al*., [16] who reported only 11.4% sensitivity. Sensitivity to Co-trimoxazole was 20.8%, which closely matches Rajesh *et al*., [17] who reported 19.35%.

Among Pseudomonas aeruginosa isolates, 84% were sensitive to Imipenem-similar to the findings by Kaur *et al*., [16] (88.5%). Gentamicin sensitivity in P. aeruginosa was 55.5%, comparable to 59.9% reported by Rajesh *et al*., [17].

Klebsiella pneumoniae isolates showed 100% sensitivity to Imipenem, followed by high sensitivity to Ciprofloxacin (88.8%), Co-trimoxazole, Amikacin, and Ceftazidime (each 77.7%), and Gentamicin (66.6%). These isolates were entirely resistant to Ampicillin, with low sensitivity to Amoxyclav (11.1%).

All Escherichia coli isolates were 100% sensitive to Imipenem, Gentamicin, Amikacin, Co-trimoxazole, and Ceftazidime, and 50% sensitive to Ceftriaxone, Piptaz, Ciprofloxacin, and Cefepime. They showed complete resistance to Ampicillin and Amoxyclav.

Similarly, Proteus mirabilis isolates were 100% sensitive to Imipenem, Gentamicin, Ceftazidime, and Co-trimoxazole and showed 50% sensitivity to Ceftriaxone, Cefepime, Piptaz, Amikacin, and Ciprofloxacin, while being completely resistant to Ampicillin and Amoxyclav.

In contrast, Staphylococcus aureus was the most common Gram-positive isolate (5.2%) in our study and showed 100% resistance to Cefoxitin, indicating MRSA. This is in agreement with earlier studies by Akca O *et al*., [8] and others, where MRSA was commonly isolated in VAP cases. The emergence of resistant organisms may be attributed to prolonged hospital stay, mechanical ventilation, and prior use of broad-spectrum antibiotics. Colonization versus true infection was distinguished in our study using CPIS and culture thresholds, supporting the clinical relevance of isolated pathogens.

CONCLUSION & RECOMMENDATION

This study highlights a high incidence of ventilator-associated pneumonia (57%) in the RICU at MGM Hospital. The predominant pathogens were Gram-negative bacteria, especially Acinetobacter baumannii, Pseudomonas aeruginosa, and Klebsiella pneumoniae. Gram-positive isolates such as Staphylococcus aureus showed complete resistance to Cefoxitin, indicating MRSA. These findings underscore the importance of early diagnosis, appropriate microbiological surveillance, and tailored antibiotic therapy for effective VAP management and reduction in morbidity.

CONFLICT OF INTEREST: No.

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