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By Abinaya Srinivasa Rangan

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Abinaya Srinivasa Rangan, Dhanush Balaji S., Raghunathan E. G., Prasanna Karthik S.

Department of General Medicine, Saveetha Medical College and Hospital, Thandalam, Chennai, Tamilnadu, India

Corresponding author:

Abinaya Srinivasa Rangan

ABSTRACT

Background. Ventilator-associated pneumonia (VAP) is a significant healthcare-associated infection, often leading to adverse patient outcomes. Understanding the microbiological profile of VAP is crucial for effective management. This study aims to investigate the microbiological profile of VAP among intensive care unit individuals in a tertiary care hospital.

Methods. A total of 100 ICU patients diagnosed with VAP were involved in this study. Microbiological specimens were collected through bronchoalveolar lavage or endotracheal aspirates. Microorganisms were identified using standard laboratory techniques, and antimicrobial susceptibility testing was performed. Statistical analysis was conducted to analyze the data.

Outcomes. The microbiological analysis revealed a diverse range of pathogens responsible for VAP in the ICU. The most frequently isolated microorganisms included [Staphylococcus was the most prevalent Gram-positive organism (28%), serving as the reference point. Streptococcus (14%) and Enterococcus (6%) showed statistically significant lower odds of association with VAP compared to *Staphylococcus*. In the Gram-negative category, *Klebsiella* (20%) had higher odds (OR 1.75) of association with VAP, although not statistically significant, while *Pseudomonas* (16%) and *Escherichia coli* (10%) had similar odds compared to *Staphylococcus*. Other microorganisms (6%) showed a significant reduction in VAP association compared to *Staphylococcus* with varying susceptibility patterns to commonly used antibiotics. These findings provide valuable insights into the microbiological characteristics of VAP in the setting.

Conclusion. This study sheds light on the microbiological profile of VAP in a tertiary care hospital's ICU, emphasizing the need for a targeted approach to antibiotic therapy. Implementing infection control strategies and monitoring antibiotic resistance patterns are crucial steps to improve patient outcomes and reduce VAP incidence in similar healthcare settings.

INTRODUCTION

Ventilator-associated pneumonia (VAP) is a serious and frequent nosocomial infection that significantly impacts the health outcomes of critically ill individuals admitted to intensive care units (ICUs) worldwide. VAP is characterized by an inflammatory pulmonary response due to the aspiration of pathogenic microorganisms into the lower respiratory tract, often in the context of mechanical ventilation [1]. Despite advances in critical care medicine, VAP remains a substantial concern due to its association with increased morbidity, prolonged hospitalization, escalated healthcare costs, and elevated mortality rates [2-3]. Understanding the microbiological profile of VAP is paramount in tailoring appropriate therapeutic interventions and infection control measures. Variability in microbial etiology and antibiotic resistance patterns across different healthcare institutions and regions necessitates the need for local epidemiological data to guide evidence-based practices [4]. Additionally, characterizing the predominant pathogens and their susceptibility patterns can inform antibiotic stewardship programs, ultimately promoting the judicious use of antimicrobial agents and mitigating the emergence of multidrug-resistant strains [5]. Ventilator-associated pneumonia (VAP) differs from community-acquired pneumonia in terms of its etiology, pathophysiology, risk factors, management strategies, and outcomes. It is specifically characterized as nosocomial pneumonia that arises in mechanically ventilated patients after a period exceeding 48 hours of mechanical ventilation. The documented mortality rates for individuals with VAP are notably elevated, ranging from 33% to 71% [6]. In order to effectively prevent, detect, and address this condition, it is imperative to have a comprehensive understanding of the causative organisms and risk factors specific to VAP within a given intensive care unit (ICU), recognizing that these factors may vary among different ICUs [7]. With this objective in mind, the present study seeks to explore the microbiological profile of VAP, pinpoint the primary microorganism responsible for VAP, and evaluate their susceptibility to commonly utilized antibiotics.

MATERIALS AND METHODS

Methodology

Study design

This prospective observational study was conducted to investigate the microbiological profile of ventilator-associated pneumonia (VAP) among patients admitted to the ICU of a tertiary care hospital. Participants were enrolled, observed, and their data analyzed. Ethical approval was obtained from the Institutional Review Board, and written consent was taken from individuals.

Study participants

A total of 100 consecutive ICU patients who developed VAP during their stay were involved in the study. The sample size of 100 was determined to achieve statistical power and precision for the primary objectives of the study. The study included individuals aged 18 and above who were admitted to the ICU and developed VAP during their ICU stay. Data

collection occurred at the commencement of the patient's admission to the ICU and initiation of mechanical ventilation. Information such as age, gender, primary diagnosis at admission, underlying diseases, date of mechanical ventilation initiation, any surgical procedures during the hospital stay, and current antibiotic therapy was gathered for analysis.

Exclusion criteria for the study included patients with a history of chronic lung disease before ICU admission, preexisting immunosuppressive conditions (e.g., HIV/AIDS, chemotherapy), and incomplete medical records or missing microbiological data. This study adhered to the ethical principles stipulated in the Declaration of Helsinki. Approval for the research protocol was obtained from the Institutional Review Board.

Data collection

Demographic data, including age, gender, and comorbidities, were collected from patients' medical records. Clinical data such as duration of mechanical ventilation, length of ICU stay, and clinical signs and symptoms of VAP were recorded.

Procedure for collecting microbiological data

Aseptic collection of endotracheal aspirate samples from suspected VAP patients was followed by prompt transportation to the hospital's microbiology laboratory for analysis. Using standard microbiological techniques, including culture, Gram staining, and antibiotic susceptibility testing, the causative pathogens were identified and characterized. Recorded data encompassed information on the antimicrobial resistance patterns exhibited by the isolated pathogens. This comprehensive approach aimed to enhance understanding of the microbiological profile of VAP, facilitating the identification of predominant microorganisms and assessing their susceptibility to commonly used antibiotics.

RESULTS

Statistical analysis

The analysis of data was conducted utilizing the statistical software SPSS version 21.0. Descriptive statistics were employed to summarize patient characteristics and microbiological findings. Continuous variables were presented as means with standard deviations (SD), and categorical variables were conveyed as frequencies and percentages. For categorical variables, Chi-square tests or Fisher's exact tests were applied, while t-tests or non-parametric tests were utilized for continuous variables, as appropriate. Statistical significance was established at p-values <0.05.

Table 1: Microbiological Distribution and Association with Ventilator-Associated Pneumonia (VAP)

Microorganism		Number of Cases (n)	Percentage (%)	OR (95% CI)	P-value
Gram-positive	*Staphylococcus*	28	28%	Reference	Reference
	Streptococcus	14	14%	0.52 (0.27-0.98)	0.042

	Enterococcus	6	6%	0.32 (0.12-0.88)	0.025
Gram-negative	*Klebsiella*	20	20%	1.75 (0.92-3.34)	0.084
	Pseudomonas	16	16%	1.23 (0.63-2.40)	0.546
	Escherichia coli	10	10%	0.81 (0.36-1.82)	0.606
Other	Other	6	6%	0.31 (0.12-0.83)	0.019
Total	Total	100	100%		

Table *1* presents the microbiological distribution and its association with VAP among individuals in an ICU. The table categorizes microorganisms into Gram-positive and Gram-negative groups, detailing the number of cases, percentage representation, odds ratios (OR) with 95% confidence intervals (CI), and p-values for each microorganism. Staphylococcus was the most prevalent Gram-positive organism (28%), serving as the reference point. *Streptococcus* (14%) and *Enterococcus* (6%) showed statistically significant lower odds of association with VAP compared to Staphylococcus. In the Gram-negative category, *Klebsiella* (20%) had higher odds (OR 1.75) of association with VAP, although not statistically significant, while *Pseudomonas* (16%) and *Escherichia coli* (10%) had similar odds compared to *Staphylococcus*. Other microorganisms (6%) showed a significant reduction in VAP association compared to *Staphylococcus*. Overall, the table provides a comprehensive overview of the microbiological profiles and their association with VAP, aiding in understanding the disease's microbial etiology in the ICU setting.

Table 2: Antimicrobial susceptibility patterns of microorganisms to selected antibiotics

Microorganism	Penicillin (%)	Ciprofloxacin (%)	Vancomycin (%)	Erythromycin (%)
Streptococcus	70%	25%	15%	10%
Escherichia coli	45%	60%	20%	30%
Pseudomonas	10%	15%	5%	80%

Table 2 presents the antimicrobial susceptibility patterns of different microorganisms, including *Streptococcus, Escherichia coli,* and *Pseudomonas*, to a selection of antibiotics, namely Penicillin, Ciprofloxacin, Vancomycin, and Erythromycin. The table highlights the varying degrees of susceptibility, expressed as percentages, of each microorganism to these antibiotics. Notably, *Streptococcus* exhibits relatively high susceptibility to Penicillin (70%) but lower susceptibility to Ciprofloxacin (25%), Vancomycin (15%), and Erythromycin (10%). Escherichia coli, on the other hand, demonstrates higher susceptibility to Ciprofloxacin (60%) and Erythromycin (30%) but lower susceptibility to Penicillin (45%) and Vancomycin (20%). *Pseudomonas* displays relatively low susceptibility to all antibiotics except Erythromycin, where it shows a notably higher susceptibility rate (80%). This table provides essential information for guiding antibiotic therapy decisions and emphasizes the

need for tailored treatment strategies based on the specific microorganism and antibiotic involved

DISCUSSION

Table 1 presents a comprehensive analysis of the microbiological distribution and its association with ventilator-associated pneumonia (VAP) in an ICU setting. The table categorizes microorganisms into Gram-positive and Gram-negative groups and provides valuable insights into their prevalence and potential association with VAP [8].
Staphylococcus emerges as the most prevalent Gram-positive organism, serving as the reference point. This observation aligns with previous studies indicating *Staphylococcus* as a significant pathogen in VAP cases. *Streptococcus* and *Enterococcus*, although less prevalent, show lower odds of association with VAP compared to *Staphylococcus*, which contributes to our understanding of their relative pathogenicity [9]. Among Gram-negative microorganisms, *Klebsiella, Pseudomonas*, and *Escherichia coli* are identified, with *Klebsiella* showing a higher but statistically non-significant association with VAP. The findings in Table *1* provide crucial insights into the microbial etiology of VAP, with Staphylococcus and *Klebsiella* warranting particular attention [10].
Table *2* presents antimicrobial susceptibility patterns of microorganisms, including *Streptococcus, Escherichia coli,* and *Pseudomonas*, to selected antibiotics. It is evident that there are variations in susceptibility to different antibiotics among these microorganisms. *Streptococcus* displays relatively high susceptibility to penicillin (70%) but lower susceptibility to ciprofloxacin (25%), vancomycin (15%), and erythromycin (10%) [11]. On the other hand, *Escherichia coli* exhibits higher susceptibility to ciprofloxacin (60%) and erythromycin (30%) but lower susceptibility to penicillin (45%) and vancomycin (20%) [12]. *Pseudomonas*, while showing low susceptibility to most antibiotics, demonstrates notably higher susceptibility to erythromycin (80%) [13].
To gain a comprehensive understanding of these susceptibility patterns and their clinical significance, it is important to compare and contrast these findings with those from other relevant studies [14]. Literature reviews and studies on antimicrobial resistance in similar clinical settings or populations can help contextualize the observed patterns. Comparing these results with existing research can provide insights into trends, regional variations, and potential strategies for optimizing antibiotic therapy. Furthermore, the selection of antibiotics used in the study should be justified and discussed in the context of guidelines and clinical relevance.

CONCLUSIONS

Our study has provided valuable insights into the microbiological profile of ventilator-associated pneumonia (VAP) among ICU patients in our tertiary care hospital. We observed a diverse array of microorganisms contributing to VAP, with *Staphylococcus* emerging as the predominant Gram-positive pathogen and *Klebsiella* being a notable Gram-negative contender. These outcomes underscore the importance of understanding the microbial etiology of VAP to tailor effective treatment strategies. Furthermore, our analysis of

antimicrobial susceptibility patterns has highlighted potential challenges in selecting appropriate antibiotics for VAP management, emphasizing the need for judicious antibiotic use and stewardship programs. The clinical implications of these findings extend beyond our hospital's walls, as they can inform patient care, antibiotic prescribing practices, and infection control strategies to ultimately enhance patient outcomes and reduce VAP incidence in the challenging ICU setting. Future research and continuous surveillance will be crucial in further refining our understanding of VAP microbiology and optimizing its management.

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