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Optimizing Diagnosis and Antibiotic Therapy in Ventilator-Associated Pneumonia: A Comparative Study of Tracheal Secretion Cultures in Critically Ill Patients

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Abstract

Invasive mechanical ventilation in pneumonia patients often leads to complications, including ventilator-associated pneumonia (VAP), which is associated with specific bacterial pathogens and antibiotic resistance. Tracheal secretion cultures are essential for identifying bacterial patterns and assessing antibiotic resistance in these patients. This study aims to analyze the bacterial patterns and antibiotic resistance in tracheal secretion cultures of pneumonia patients undergoing invasive mechanical ventilation in a hospital setting. This cross-sectional study involved 95 samples from patients receiving care in the intensive care unit (ICU) who met predefined inclusion and exclusion criteria. Samples were collected through endotracheal aspiration or bronchoalveolar lavage procedures. Bacterial identification was conducted using both conventional and automated methods, while antibiotic resistance was assessed using the disk diffusion method. The study found that Gram-negative bacteria, primarily *Acinetobacter baumannii* and *Pseudomonas aeruginosa*, dominated the bacterial cultures. These pathogens are known for their high adaptability in hospital environments and their association with prolonged hospitalization and increased mortality. High resistance to β-lactam antibiotics and fluoroquinolones was observed, although antibiotics like amikacin and meropenem remained effective. Chi-square analysis showed a significant correlation between bacterial species and antibiotic resistance patterns. The findings highlight the importance of accurate microbiological diagnosis to guide appropriate empirical therapy and emphasize the need for strict antibiotic stewardship programs and continuous resistance surveillance in ICU settings. Further studies are necessary to optimize infection control and antibiotic therapy protocols for patients requiring prolonged mechanical ventilation.

INTRODUCTION

Ventilator-associated pneumonia (VAP) is one of the most common nosocomial infections observed in patients undergoing intensive care with invasive mechanical ventilation (Xu et al., 2019). The incidence of VAP is linked to increased morbidity, mortality, and significant economic burden on healthcare systems (Darvishi-Khezri et al., 2016). The primary cause of this infection is the colonization of pathogenic bacteria in the lower respiratory tract, often facilitated by mechanical ventilation (Díaz et al., 2020). At Adam Malik Hospital, there has been a rising trend in the number of pneumonia cases requiring invasive mechanical ventilation, posing challenges in effectively managing antimicrobial therapy.

A major issue in managing VAP is the development of antibiotic resistance, which often arises due to inappropriate empirical antibiotic use (Ahuatzin-Flores et al., 2024). Previous studies have highlighted that the pathogens responsible for VAP typically show diverse and evolving resistance patterns (Bassetti et al., 2018). Common causative bacteria such as Pseudomonas aeruginosa, Acinetobacter baumannii, and Klebsiella pneumoniae are known to exhibit high resistance rates to first-line antibiotics (Mojica et al., 2022). However, recent data on pathogen patterns and antibiotic resistance at Adam Malik Hospital in 2024 is limited, necessitating further research to gain a more accurate understanding of these factors in pneumonia patients undergoing invasive mechanical ventilation at this hospital.

The rising antibiotic resistance of VAP-causing bacteria requires urgent attention, especially in clinical microbiology and infectious disease therapy (Chaudhury & Kumar, 2016). Without a clear understanding of bacterial resistance patterns, treatments may be ineffective, potentially worsening patient conditions. Addressing antibiotic resistance is also crucial for infection prevention and the development of more rational antibiotic use policies (Baker et al., 2019). This study seeks to provide the latest data that can guide the development of more effective antimicrobial therapy strategies and better inform clinical practice (Stogios & Savchenko, 2020).

This research aims to analyze bacterial patterns and antibiotic resistance from tracheal secretion cultures in pneumonia patients undergoing invasive mechanical ventilation at Adam Malik Hospital in 2024. The findings of this study are expected to offer new insights into the distribution of infectious microorganisms and their resistance levels, which could serve as a basis for optimizing antibiotic therapy strategies in hospital settings (Alnimr, 2023). Furthermore, this study contributes to antibiotic resistance mitigation efforts by providing data-driven recommendations for medical professionals (Modi & Kovacs, 2020).

RESEARCH METHOD

This cross-sectional analytical observational study was conducted to evaluate the research objectives. Ethical approval was granted by the Health Research Ethics Committee of the Faculty of Medicine, Universitas Sumatera Utara (approval number 6259/UN5.2.1.1.45/PT.01.04/2024). Patient confidentiality was strictly maintained, and all data were used exclusively for research purposes without disclosing individual identities.

This study enrolled 95 pneumonia patients who were receiving invasive mechanical ventilation in the Intensive Care Unit (ICU) at Adam Malik Hospital in 2024. Inclusion criteria included patients aged ≥18 years, diagnosed with pneumonia, and undergoing invasive mechanical ventilation, with complete and documented tracheal secretion culture results. Exclusion criteria comprised patients with incomplete medical records, those with lung infections unrelated to Ventilator-Associated Pneumonia, and patients who had received antibiotic therapy for more than 48 hours prior to the tracheal secretion culture. After obtaining informed consent and providing a detailed explanation of the study procedures, relevant data were collected from the medical records of patients who had undergone tracheal secretion culture during the study period. The study aimed to analyze the bacterial patterns and antibiotic resistance found in these cultures.

Tracheal secretion samples were collected from patients through endotracheal aspiration procedures. Cultures were then performed in the microbiology laboratory of Adam Malik Hospital, using selective and differential growth media following standard protocols. Bacterial identification was carried out using both conventional methods, such as Gram staining and biochemical tests, and automated systems like VITEK or MALDI-TOF. Antibiotic resistance testing was conducted using the Kirby-Bauer disc diffusion method, in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines.

Data analysis was conducted using statistical software. Descriptive analysis was performed on the culture results and antibiotic resistance data, with pathogenic bacteria types and their antibiotic resistance patterns presented in tables and graphs. Chi-square or Fisher's exact test was used to analyze differences in resistance patterns, with a significance level set at $p < 0.05$.

RESULTS AND DISCUSSION

This study involved 95 subjects with a varied age distribution. The majority of the patients were aged over 60 years (47.4%), followed by the 41-60 years age group (35.8%). The 21-40 years and <20 years age groups accounted for 9.5% and 7.4%, respectively.

In terms of gender, males were more dominant with 59 subjects (62.1%), while females accounted for 36 subjects (37.9%). Regarding the medical history, 24 subjects (25.3%) had no comorbidities, while 71 subjects (74.7%) had at least one comorbid condition. The most common comorbidities found were stroke (24.2%), followed by kidney disorders (13.7%), cancer (12.6%), and type 2 diabetes mellitus (8.4%). Some patients also had a combination of diseases, such as diabetes mellitus and kidney disorders (7.4%) and diabetes mellitus and stroke (2.1%).

Table 1. Analysis of Tracheal Secretion Culture Based on Bacterial Species

	Total	
Bacteria in Tracheal Secretions	**(n)**	**(%)**
Pseudomonas aeruginosa	19	20.0
Staphylococcus aureus	7	7.4
Stenotrophomonas maltophilia	2	2.1
Acinetobacter baumannii	27	28.5
Acinetobacter nosocomialis	1	1.1
Klebsiella pneumoniae	9	9.5
Escherichia coli	7	7.4
Klebsiella pneumoniae ssp pneumoniae	5	5.3
Serratia marcescens	1	1.1
Corynebacterium striatum	1	1.1
Achromobacter xylosoxidans	1	1.1
No bacterial growth	15	15.8
Total	95	100

Table 1 shows the results of the tracheal secretion culture analysis based on the identified bacterial species. Acinetobacter baumannii was the most dominant pathogen, found in 28.5% of samples, followed by Pseudomonas aeruginosa (20.0%) and Klebsiella pneumoniae (9.5%). Staphylococcus aureus and Escherichia coli were detected in 7.4% of samples, while Klebsiella pneumoniae ssp. pneumoniae was found in 5.3% of cases. Other less commonly found bacteria included Stenotrophomonas maltophilia (2.1%), Acinetobacter nosocomialis, Serratia marcescens, Corynebacterium striatum, and Achromobacter xylosoxidans, each detected in only 1.1% of samples. Additionally, 15.8% of the samples showed no bacterial growth.

This study demonstrates that Acinetobacter baumannii and Pseudomonas aeruginosa are the most frequently found bacteria in patients with pneumonia requiring invasive mechanical ventilation. The presence of several bacterial species with low prevalence suggests variation in the microbial colonization of the lower respiratory tract in critically ill patients.

Table 2. Analysis of Tracheal Secretion Culture Based on Bacterial Gram Classification

Bacterial Classification	Total (n)	Total (%)
Gram positive	8	8.4
Gram negative	72	75.8
No data	15	15.8
Total	95	100

Table 2 shows that the majority of bacteria identified in tracheal secretion cultures were Gram-negative, accounting for 72 samples (75.8%). Meanwhile, Gram-positive bacteria were found in 8 samples (8.4%). A total of 15 samples (15.8%) showed no bacterial growth. These findings confirm that Gram-negative bacteria are the dominant pathogens in pneumonia patients with invasive mechanical ventilation. This result is consistent with previous studies that have reported a high prevalence of Gram-negative bacteria in lower respiratory tract infections among critically ill patients.

Table 3. Antibiotic Resistance Patterns of Tracheal Secretion Bacteria

Antibiotic	Resistant (n)	Resistant (%)	Sensitive (n)	Sensitive (%)	No data (n)	No data (%)	No data (n)	No data (%)
Amikacin	28	29.5	43	45.3	24	25.3	0	0
Amoxicilin Clavulunate	28	29.5	9	9.5	56	58.9	2	2.1
Ampicilin	45	47.4	2	2.1	48	50.5	0	0
Ampicillin-Sulbactam	19	20.00	10	10.5	63	66.3	3	3.2
Aztreonam	36	37.9	12	12.6	41	43.2	6	6.3
Cefazolin	43	45.3	8	8.4	44	46.3	0	0
Cefepime	42	44.2	23	24.2	27	28.4	3	3.2
Cefoxitin	24	25.3	6	6.3	62	65.3	3	3.2
Ceftazidime	45	47.4	20	21.1	23	24.2	7	7.4
Ceftriaxone	49	51.6	10	10.5	35	36.8	1	1.1
Cephalexin	8	8.4	0	0	87	91.6	0	0
Chloramphenicol	26	27.4	6	6.3	63	66.3	0	0
Ciprofloxacin	56	58.9	18	18.9	19	20.0	2	2.1
Clindamycin	4	4.2	3	3.2	44	92.6	0	0
Daptomycin	0	0	2	2.1	93	97.9	0	0
Doxycycline	0	0	2	2.1	93	97.9	0	0
Ertapenem	27	28.4	17	17.9	51	53.7	0	0
Erythromycin	2	2.1	4	4.2	89	93.7	0	0
Fosfomycin	10	10.5	0	0	85	89.5	0	0
Gentamicin	35	36.8	24	25.3	33	34.7	3	3.2
Imipenem	19	20	12	12.6	62	65.3	2	2.1
Levofloxacin	4	4.2	4	4.2	87	91.6	0	0
Linezolid	0	0	6	6.3	89	93.7	0	0

	Resistant		**Sensitive**		**No data**		**No data**	
Antibiotic	**(n)**	**(%)**	**(n)**	**(%)**	**(n)**	**(%)**	**(n)**	**(%)**
Meropenem	40	42.1	29	30.5	25	26.3	1	1.1
Moxifloxacin	4	4.2	3	3.2	88	92.6	0	0
Mupirocin High level	0	0	2	2.1	93	97.9	0	0
Nitrofurantoin	19	20.0	13	13.7	60	63.2	3	3.2
Norfloxacin	10	10.5	5	5.3	79	83.2	1	1.1
Oxacillin	1	1.1	2	2.1	92	96.8	0	0
Penicillin G	1	1.1	1	1.1	93	97.9	0	0
Piperacillin Tazobactam	38	40.0	30	31.6	22	23.2	5	5.3
Quinupristin dalfopristin	2	2.1	2	2.1	91	95.8	0	0
Rifampin	0	0	2	2.1	93	97.9	0	0
Teicoplanin	0	0	2	2.1	93	97.9	0	0
Tetracycline	24	25.3	13	13.7	56	58.9	2	2.1
Ticarcillin Calvulanate	21	22.1	9	9.5	59	62.1	6	6.3
Tigecycline	24	25.3	22	23.2	37	38.9	12	12.6
Tobramycin	17	17.9	11	11.6	62	65.3	5	5.3
Trimethoprim Sulfamethoxazole	36	37.9	30	31.6	29	30.5	0	0
Vancomycin	1	1.1	7	7.4	87	91.6	0	0

The sensitivity test results indicate varying resistance patterns to different antibiotics. Several antibiotics exhibit high resistance rates, including Ciprofloxacin (58.9%), Ceftriaxone (51.6%), Ceftazidime (47.4%), and Ampicillin (47.4%), highlighting a significant prevalence of resistant bacteria against these agents.

On the other hand, some antibiotics demonstrate higher sensitivity rates, such as Amikacin (45.3%), Meropenem (30.5%), and Piperacillin-Tazobactam (31.6%), which remain effective in inhibiting bacterial growth. A significant proportion of antibiotics show unavailable data, such as Cephalexin (91.6%), Daptomycin (97.9%), and Rifampin (97.9%), indicating limited use of these antibiotics in this study sample.

These findings suggest that antibiotic selection for ventilator-associated pneumonia therapy should consider the high resistance rates to β-lactam and fluoroquinolone antibiotics, as well as the effectiveness of carbapenems and aminoglycosides.

Table 4. Analysis of the Relationship Between Bacterial Type and Antibiotic Resistance Pattern

	Chi-Square Tests	
	df	***p***
Bacterial Culture Secretion		
Antibiotix Resistance	22	0.00*

Based on the results of the Chi-Square test conducted to analyze the relationship between bacterial type and antibiotic resistance pattern in patients with ventilator-associated pneumonia (VAP), a Pearson Chi-Square value of 112.900 was obtained with 22 degrees of freedom (df) and a significance value (Asymp. Sig.) of 0.000. The significance value smaller than 0.05 indicates a highly significant relationship between the detected bacterial type and antibiotic resistance pattern in VAP patients at the Intensive Care Unit (ICU) of Adam Malik Hospital. The results of this study show a significant relationship between bacterial type and antibiotic resistance pattern in VAP patients, which can provide important insights for determining more accurate antibiotic therapy and infection control in the hospital.

Discussion

The findings of this study reveal that *Acinetobacter baumannii* and *Pseudomonas aeruginosa* are the predominant pathogens in pneumonia patients receiving invasive mechanical ventilation (Kasanga et al., 2023). This is consistent with previous research, which has shown that *Acinetobacter baumannii* is frequently isolated in critically ill patients and exhibits high antibiotic resistance, particularly in hospital environments with extensive antibiotic usage (Taslim & Maskoen, 2023). The high prevalence of Gram-negative bacteria in tracheal secretion cultures further supports the significant role of these pathogens in lower respiratory tract infections among ventilated patients (Kohbodi et al., 2022).

The variability in microbial colonization among critically ill patients is indicated by the presence of various bacterial species with differing prevalence rates. Factors such as the length of stay in the ICU, ventilator use, and prior antibiotic therapy can all influence the respiratory tract microbiota composition (Spalding et al., 2017). In this study, approximately 15.8% of the samples showed no bacterial growth, which may be attributed to prior antibiotic use before sampling or limitations in culture techniques that fail to detect certain pathogens. Other studies have also suggested that even in the absence of bacterial growth in cultures, pneumonia could still be caused by pathogens that are difficult to culture or by viral infections (Timsit et al., 2017).

Antibiotic resistance patterns revealed that many bacterial isolates were resistant to β-lactam antibiotics, fluoroquinolones, and third-generation cephalosporins. The high resistance to Ciprofloxacin, Ceftriaxone, and Ceftazidime highlights the need for careful consideration of these antibiotics in empirical therapy (Papazian et al., 2020). On the other hand, some antibiotics, such as Amikacin, Meropenem, and Piperacillin-Tazobactam, continue to show effectiveness, although resistance remains a concern (Kollef et al., 2021). These findings align with studies reporting that *Acinetobacter baumannii* and *Pseudomonas aeruginosa* frequently exhibit multidrug-resistant (MDR) and extensively drug-resistant (XDR) profiles, complicating clinical management (Póvoa et al., 2022).

An analysis of the relationship between bacterial species and antibiotic resistance patterns revealed a significant correlation (Zilberberg et al., 2022), indicating that different bacterial species exhibit varying resistance profiles to antibiotics (Nair & Niederman, 2015). This emphasizes the importance of a culture-based approach to guide appropriate antibiotic therapy for ventilator-associated pneumonia (VAP) patients (Righi et al., 2019). Given the significant correlation observed, it is crucial to monitor resistance patterns regularly to update hospital antibiotic therapy protocols and address the growing challenge of antibiotic resistance (Delle Rose et al., 2023; Restrepo et al., 2020).

Overall, this study underscores the importance of microbiological surveillance and understanding antibiotic resistance patterns in the management of pneumonia in patients undergoing invasive mechanical ventilation (Welte et al., 2021; Rodriguez et al., 2020). The high prevalence of resistant bacteria calls for stricter antibiotic management strategies, including antimicrobial stewardship programs, to curb the spread of resistant bacteria in hospital settings (Vincent et al., 2022). Moreover, the findings highlight the need for the development of alternative therapeutic strategies, such as combination therapies or novel antimicrobial agents, to address infections caused by highly resistant bacteria (Kalil et al., 2016).

Conclusion

This study reveals that *Acinetobacter baumannii* and *Pseudomonas aeruginosa* are the most frequently identified bacteria in patients with pneumonia related to mechanical ventilation in intensive care units, with the majority of isolates being Gram-negative and exhibiting high resistance rates to various antibiotics, particularly β-lactams and fluoroquinolones. This high resistance underscores the challenge of selecting appropriate antibiotic therapy for these infections and highlights the significant relationship between bacterial type and resistance patterns, emphasizing the urgent need for strict surveillance of antibiotic use to prevent further resistance. As a recommendation, antimicrobial stewardship programs should be strengthened to ensure rational and effective antibiotic use, while increased awareness and adherence to infection control protocols are necessary to reduce the spread of resistant bacteria in hospital settings. Future research with larger sample sizes and advanced molecular methods is essential to gain deeper insights into bacterial resistance mechanisms and microbial colonization patterns in patients undergoing mechanical ventilation.

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