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Original Article

Microbiology Section

Comparative Clinicomicrobiological Profile, Risk Factors, and Outcomes of Patients with and without Ventilator Associated Pneumonia: A Retrospective Observational Study from a Tertiary Care Hospital in Northern India

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ABSTRACT

Introduction: Ventilator Associated Pneumonia (VAP) is a common Healthcare Associated Infection (HAI) in mechanically ventilated patients, leading to increased morbidity, mortality, Intensive Care Unit (ICU) stays, and healthcare costs. VAP is most commonly caused by Gram negative, non fermenting bacteria notably *Acinetobacter baumannii, Pseudomonas aeruginosa,* and Enterobacterales such as *Klebsiella pneumoniae* all of which frequently exhibit Multidrug Resistance (MDR), making treatment challenging. Timely diagnosis followed by appropriate, targeted antibiotic therapy is critical in improving patient outcomes.

Aim: To evaluate and compare the clinicomicrobiological profile, risk factors, and clinical outcomes of VAP and Non VAP patients admitted to a tertiary care hospital in Northern India.

Materials and Methods: This retrospective, laboratory-based observational study was conducted in the Department of Microbiology, Sanjay Gandhi Postgraduate Institute of Medical Sciences (SGPGIMS), Lucknow, Uttar Pradesh, India from March 2024 to August 2024. The study included adult patients admitted to ICU and managed on mechanical ventilation, who fulfilled the predefined inclusion criteria for VAP. A total of 243 respiratory samples were analysed during the study period. The methodology involved collection and microbiological processing of Endotracheal (ET) aspirates and bronchoalveolar lavage samples, followed by organism identification and antimicrobial susceptibility testing as per standard guidelines. Demographic parameters such as age and sex were recorded. Statistical analysis was performed using appropriate tests, including the Chi-square test or Fisher's exact test for categorical variables and the Student's t-test or Mann-Whitney U test for continuous variables, with a p-value of <0.05 considered statistically significant.

Results: Of the 243 respiratory samples, 197 (81.07%) samples were obtained through ET aspirates, while remaining 46 (18.93%) were BAL fluid. VAP was diagnosed in 68 (27.98%) patients, while 175 (72.02%) patients were identified as not having VAP. The incidence of VAP was 36.28 per 1000 ventilator days. Among risk factors, supine head position, tracheostomy, total days on MV, length of stay in hospital, re-intubation were significantly higher in VAP group. Among the 68 patients diagnosed with VAP, only 65 had culture-positive samples. Of these 65 isolates, 53 (81.53%) were caused by Gram-negative bacilli (GNB). Of them *A. baumannii* 13 (20%) was the commonest, followed by *P. aeruginosa* 11 (16.92%) and *K. pneumoniae* 10 (15.38%). Among, Gram-positive cocci (GPC) 12 (18.46%), Methicillin-resistant Staphylococcus aureus (MRSA) 9 (13.84%) was the commonest followed by *E. faecium 3* (4.61%).

Conclusion: The incidence of VAP was high in the present study. Mortality rate was slightly higher in VAP group, it was not statistically significant. *A. baumannii* and *P. aeruginosa* are emerging MDR nosocomial pathogens. Therefore, accurate species identification and AST are essential for improving patient outcomes.

Keywords: Antibacterial agents, Bacterial infections, Drug resistance, Intensive care unit, Pneumonia

INTRODUCTION

The VAP is a significant HAI that predominantly affects patients in ICUs who are receiving MV. It is linked to increased rates of morbidity and mortality, extended durations of MV, ICU stays and cost of treatment and adverse outcome of patients [1]. The VAP is defined as pneumonia that develops more than 48 hours after ET intubation or MV, or pneumonia developing even after extubation [2]. It is one of the commonest nosocomial infection with incidence rate ranging from 13 to 51 per 1000 ventilator days [3,4]. VAP increases the length of ICU stay by 4-6 days, furthermore increasing the cost of patient management [5].

The VAP developed during the first four days of mechanical ventilation is early-onset, usually less severe, mostly caused by antibiotic sensitive bacteria and with a better prognosis, whereas late-onset VAP develops five or more days after the initiation of MV and is due to MDR pathogens and is usually associated with increased morbidity and mortality [6]. When assessing the microbial aetiology of VAP aerobic GNB are the most common, accounting for over 60% of cases, and management becomes particularly challenging due to high levels of antibiotic resistance. Among these, non fermentative species such as Acinetobacter baumannii and Pseudomonas aeruginosa have emerged as the most important pathogen. Their treatment is complicated because they are often MDR, frequently harboring mechanisms like efflux pumps, porin loss, and β-lactamase enzymes [7]. Also, Escherichia coli, Klebsiella pneumoniae, Acinetobacter spp., and Gram positive bacteria such as Staphylococcus aureus are the common causative pathogens of VAP [8,9]. VAP results in significant mortality rate of 25-50% [10]. Delay in starting appropriate antibiotic therapy can increase the mortality associated with VAP, and thus, therapy should be started immediately.

Diagnosis of VAP involves clinical, radiological, and microbiological assessments, using samples from bronchoscopic (e.g., BAL) or non bronchoscopic techniques (e.g., ET aspirates [11]. Whereas, ET aspirates might have lower sensitivity compared to bronchoscopic methods [12]. Pugin J et al., developed a scoring system which comprises of seven clinical parameters and was named as Clinical Pulmonary Infection Score (CPIS). A total score of 6 or more suggests VAP. They found that CPIS had a sensitivity and specificity of 93% and 100%, respectively [13].

The novelty of this study lies in its integrated evaluation of VAP by combining clinical characteristics, risk factors, microbiological spectrum, and antimicrobial resistance patterns in a tertiary-care hospital ICU in Northern India. The study provides recent, region-specific data (2024) using advanced diagnostic techniques such as Matrix-Assisted Laser Desorption/Ionization Time-of-Flight (MALDI-TOF), and includes a comparative analysis of VAP and non VAP patients. Additionally, the assessment of diagnostic markers such as CPIS, Total Leukocyte Count (TLC), and procalcitonin alongside microbiological findings offers practical insights into early diagnosis and outcome prediction of VAP.

The aim of this study was to assess the clinicomicrobiological characteristics and clinical outcomes of patients with VAP and non VAP, admitted to a tertiary care hospital in Northern India. The primary objective was to evaluate the antimicrobial susceptibility patterns and MDR profiles of bacterial isolates recovered from VAP patients. The secondary objectives were to identify risk factors and associated co-morbidities contributing to the development of VAP, and to examine the relationship between key diagnostic parameters such as CPIS, TLC, and procalcitonin levels and the occurrence of VAP.

MATERIALS AND METHODS

This was a retrospective, laboratory-based observational study conducted in the Department of Microbiology, Sanjay Gandhi Postgraduate Institute of Medical Sciences (SGPGIMS), Lucknow, Uttar Pradesh, India. The study was carried out over a period of six months, from March 2024 to August 2024, and included respiratory samples received from ICU patients clinically suspected of having VAP. The study was approved by the Institutional Ethics Committee of SGPGIMS (IEC No: 2021-48-EMP-EXP; dated November 29, 2021). The study was conducted in compliance with the Helsinki Declaration of 1964 and all of its amendments. All patient data was kept confidential and secured. The collected patient information was used only for research purposes. As this was a retrospective analysis of routine clinical specimens collected for diagnostic purposes, the requirement for informed consent was waived by the Ethics Committee in accordance with national guidelines.

Sample size and study population: Since this was a time-bound retrospective study, all eligible samples received within the study period were included. A total of 243 respiratory samples were processed, of which 197 (81.07%) were ET aspirates and 46 (18.93%) were BAL samples. Based on clinical, radiological, and microbiological assessment, patients were grouped into VAP and non VAP categories. Patients who were on mechanical ventilation but did not meet the CDC-NHSN diagnostic criteria for VAP and had culture-positive respiratory samples were classified as the non VAP group.

Inclusion criteria: Adult patients aged 18 years or older who were admitted to the ICU and managed on MV. Patients were eligible if they developed pneumonia 48 hours or more after ET intubation, initiation of MV, or extubation, and met the CDC-NHSN diagnostic criteria for VAP. Only cases with complete clinical and microbiological data were included in the study.

Exclusion criteria: Patients were excluded if pneumonia was diagnosed within 48 hours of intubation or initiation of ventilation, if they had been diagnosed with pneumonia prior to ICU admission, if they died within 48 hours of intubation, or if they had Acute Respiratory Distress Syndrome (ARDS) before the suspicion of VAP were excluded from the study.

Study Procedure

The ET aspirate and BAL fluid samples were first subjected to Gram staining. Each specimen was then cultured on blood agar, MacConkey agar, and chocolate agar plates. These plates were incubated at 35°C for 18-24 hours as per standard laboratory protocol. For semiquantitative culture, a calibrated loop was used to inoculate the samples. If bacterial growth extended beyond the tertiary streak on the plate, it was interpreted as $\geq 10^5$ colony forming units per milliliter (cfu/mL). A colony count of $\geq 10^5$ cfu/mL for ET aspirate, and $\geq 10^4$ cfu/mL for BAL fluid, was considered significant [14]. Also, counts below these levels were considered as colonisation or contamination.

Identification of microorganism: All bacterial isolates were identified using Gram staining, colony morphology, routine standard biochemicals (indole, methyl red, Voges-Proskauer, citrate utilisation, urease, motility, oxidase and triple sugar iron agar reactions), followed by automated identification using VITEK-2 system and confirmation by matrix-assisted laser desorption/ionisation time-of-flight mass spectrometry method (VITEK MS, bioMerieux).

Antibiotic susceptibility tests (AST): Routine AST were performed by Kirby Bauer disk diffusion method and evaluated by recommendations of Clinical Laboratory Standards Institute (CLSI) guideline (CLSI, 32nd ed., M100., 2022), using commercially available antibiotic discs procured from HiMedia (Mumbai, India) [15]. Susceptibility testing for colistin and vancomycin was carried out using Minimum Inhibitory Concentration (MIC) values obtained from the VITEK-2 automated system. In accordance with CLSI guidelines, colistin MIC values of ≤2 µg/mL were categorised as susceptible, while values ≥4 µg/mL were considered resistant. For vancomycin, susceptibility was interpreted according to CLSI MIC criteria, with *Staphylococcus* spp. categorised as susceptible at MIC ≤2 µg/mL, intermediate at 4-8 µg/mL, and resistant at ≥16 µg/mL, while *Enterococcus* spp. were considered susceptible at MIC ≤4 µg/mL, intermediate at 8-16 µg/mL, and resistant at ≥32 µg/mL [15].

MDR was recognised in an isolate when it requires resistance to at least one agent in three or more antimicrobial categories. Isolates not found susceptible to at least one agent in two or fewer antimicrobial categories were deemed extremely drug-resistant [16].

Case definition of VAP: VAP was defined, according to Centers for Disease Control and Prevention (CDC)'s National Healthcare Safety Network (NHSN) definitions [3,17]. Patient data within the ICU were collected daily using specially designed data collection forms. Infection control nurses were dedicated exclusively to gathering this information. At the end of each month, clinicians and microbiologists reviewed and validated all forms to ensure strict adherence to CDC-NHSN criteria for HAIs. Additionally, daily clinical monitoring of these patients was performed using the CPIS [18].

Data collection: The data on demographic characteristics, risk factors, associated co-morbidities, pathogen isolated, antimicrobial susceptibility profile, antibiotic prescription and outcome of the patients were collected from HIS and laboratory record registers. Also, data was extracted from case sheets of admitted patients included duration of hospital stay, length of MV, length of pre-ICU admission and diagnostic parameters specifically TLC and procalcitonin assay. The risk factors evaluated in this study- such as prolonged MV, prior antibiotic exposure, supine positioning, impaired consciousness, tracheostomy, and underlying chronic illnesses- were selected based on established evidence and standard guidelines [19].

Diagnostic parameters: Diagnostic laboratory parameters, including TLC and procalcitonin levels, were recorded at the time of clinical suspicion of VAP. TLC is a routinely used inflammatory

marker in the diagnosis of VAP, as outlined in standard guidelines [19]. Procalcitonin is a validated biomarker for bacterial pneumonia and ventilator-associated infections, and its diagnostic utility is supported by published evidence [20].

STATISTICAL ANALYSIS

All data were entered in Microsoft Excel (Microsoft Office 2019) and analysed using IBM Statistical Package for the Social Sciences (SPSS) Statistics version 26.0 and GraphPad Prism Version 9. Categorical variables were summarised as frequencies and percentages, while continuous variables were expressed as mean±Standard Deviation (SD) or median, depending on the distribution of data. Comparisons between VAP and non VAP groups were performed using Chi-square test or Fisher's exact test for categorical variables. Continuous variables were compared using independent Student's t-test for normally distributed data and Mann-Whitney U test for non normally distributed data. Diagnostic parameters including CPIS score, TLC, and procalcitonin levels were evaluated for their association with VAP. A p-value of <0.05 was considered statistically significant for all analyses.

RESULTS

Of the 243 respiratory samples received from 222 patients, 81.07% (n=197/243) samples were obtained through ET aspirates, while the remaining 18.93% (n=46/243) were collected via BAL fluid. Out of total samples received, 66.26% (n=161/243) samples were from MICU, while 33.74% (n=82/243) were from SICU. All the patients admitted to MICU and SICU were managed on MV. VAP was diagnosed in 27.98% (n=68/243) patients, out of them 55.89% (n=38/68) were from MICU and 44.11% (n=30/68) were from SICU while 72.02% (n=175/243) patients were identified as not having VAP. The total duration of MV was 1874 days. The incidence of VAP was 36.28 per 1000 ventilator days.

Demographic and clinical characteristics/Co-morbidities of patients were recorded and analysed as shown in [Table/Fig-1]. The mean age of the patients was 45.2±12.4 with a male predominance of 60.49% (n=147/243). Neither age nor sex was significantly associated with development of VAP in study group. Also, mean CPIS. was 5.3±2.8. Among the clinical characteristics and co-morbidities observed, anemia, diabetes, hypertension, malignancy, and solid organ transplantation were significantly associated with VAP patients.

Among the risk factors identified supine head position, tracheostomy, total days on MV, length of stay in hospital, re-intubation were all significantly higher in VAP group in comparision to non VAP group as illustrated in [Table/Fig-2]. Among diagnostic parameters, TLC and procalcitonin levels were statistically significantly in patients belonging to VAP group .The mortality rate between VAP and non VAP groups was not statistically significant (p-value=0.26) as shown in [Table/Fig-2].

Of the 68 patients who had VAP, bacterial growth was observed in 65 samples. Among VAP group, 52.94% (n=36/68) were BAL samples, while 47.05% (n=32/68) were ET aspirates. Out of which, bacterial growth was detected in all 36 BAL samples. In contrast, only 29 ET aspirate samples showed bacterial growth. Three samples were culture-negative; however, these patients were diagnosed with VAP based on clinical and radiological evidence. These cases had a CPIS of 6. The CPIS scoring system was utilised in this study to diagnose VAP.

The most common organism identified in VAP group was *A. baumannii* 18% (n=12/65) followed by *P. aeruginosa* 14% (n=9/65), *K. pneumonie* 15% (n=10/65), *E. coli* 6% (n=4/65), MRSA 14% (n=9/65), *E. faecium* 5% (n=3/68) as shown in [Table/Fig-3]. All the isolates were monomicrobial in origin. The distribution of isolates among BAL and ET aspirate samples are illustrated in [Table/Fig-4,5].

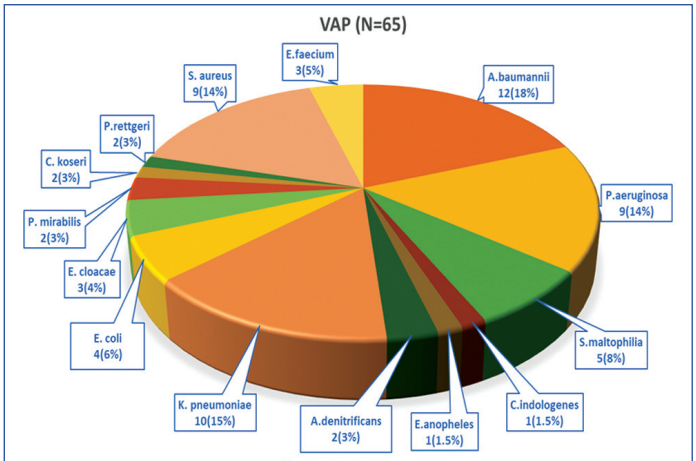
Parameters	Total (n=243)	VAP (n=68) 27.98%	Non VAP (n=175) 72.02%	p-value	χ^2 value
Age (yrs) mean±SD	45.2±12.4	42.5±15.4	46±13.4	0.10	NA#
Male	147 (60.49%)	40 (58.82%)	107 (61.14%)	0.72	0.11
Female	96 (39.51%)	28 (41.18%)	68 (38.86%)	0.74	0.11
CPIS mean±SD	5.3±2.8	5.2±2.7	3.1±1.2	<0.001*	NA#
Clinical characteristics/co-morbidities					
Diabetes	127 (52.26%)	36 (52.94%)	91 (52%)	0.018*	0.52
Hypertension	121 (49.79%)	34 (50%)	87 (49.71%)	0.0016*	0.97
CKD	35 (14.40%)	11 (16.17%)	24 (13.71%)	0.24	0.62
CLD	31 (12.75%)	10 (14.70%)	21 (12%)	0.07	0.33
COPD	37 (15.22%)	11 (16.17%)	26 (14.9%)	0.07	0.79
Coronary artery disease	29 (11.93%)	12 (17.64%)	17 (9.71%)	2.92	0.09
Anaemia	151 (62.13%)	42 (61.76%)	109 (62.28%)	0.006*	0.94
Malignancy	22 (9.05%)	6 (8.82%)	16 (9.14%)	0.0066*	0.93
Solid organ transplant	11 (4.52%)	3 (4.41%)	8 (4.57%)	0.003*	0.95

[Table/Fig-1]: Showing demographic and clinical characteristics/Co-morbidities of patients with VAP and without VAP (Non VAP) n=243.
*Statistically significant. Values expressed as mean±SD or frequency (%). p-value of <0.05 was considered statistically significant. Abbreviations: SD: Standard deviation; VAP: Ventilator associated pneumonia; MV: Mechanical ventilation; CPIS: Clinical Pulmonary Infection Score; CKD: Chronic kidney disease; COPD: Chronic obstructive pulmonary disease; CLD: Chronic liver disease. p-values for categorical variables were calculated using Chi-square (χ^2) test, while continuous variables were analysed using independent Student's t-test. NA# = Not applicable; Chi-square test is applicable only for categorical variables. Continuous variables are expressed as mean±standard deviation and were compared using independent sample Student's t-test

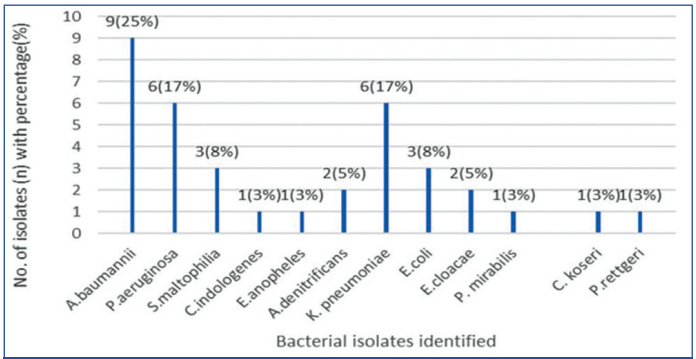
Parameters	Total (n=243)	VAP (n=68) 27.98%	Non VAP (n=175) 72.02%	p-value	χ^2 value
Risk factors					
Duration of MV >5 days	203 (83.53%)	59 (86.76%)	144 (82.28%)	0.514	0.424
Supine head position	8 (3.29%)	6 (8.82%)	2 (1.14%)	0.0026*	9.07
Steriod therapy	66 (27.16%)	15 (22.05%)	51 (29.14%)	0.265	1.24
Stress ulcer prophylaxis	243 (100%)	68 (100%)	175 (100%)	NA	NA
Surgery	42 (17.28%)	11 (16.17%)	31 (17.71%)	0.78	0.08
Tracheostomy	48 (19.75%)	19 (27.94%)	29 (16.57%)	0.045*	4
Trauma	26 (10.69%)	7 (10.29%)	19 (10.85%)	0.90	0.017
Coma or impaired consciousness	118 (48.55%)	39 (57.35%)	79 (45.14%)	0.087	2.93
Total days on MV (mean ±SD)	27.5±23.3	30.8±24.1	20.8±19.8	0.003*	NA#
Length of stay in hospital (mean ±SD)	39.2±35.5	44.5±38.6	29.7±26.4	0.005*	NA#
Re-intubation	76 (31.27%)	31 (45.58%)	45 (25.71%)	0.003*	8.99
Diagnostic parameters					
Total Leukocyte Count (TLC) (cells/mm^3)	20201.3± 11933.8	21657.3± 12393.4	17562.6± 10592.8	0.018*	NA#
Procalcitonin (IU/mL)	8.6±15.5	10.35±17.7	5.16±9.9	0.025*	NA#

Outcome					
Recovered	177 (72.84%)	46 (67.65%)	131 (74.86%)	0.26	1.28
Died	66 (27.16%)	22 (32.35%)	44 (25.14%)		

[Table/Fig-2]: Showing distribution of risk factors, diagnostic parameters and outcome among patients with VAP and without VAP.
Abbreviations: MV: Mechanical Ventilation; NA: Not applicable; Chi-square test and p-value are not applicable as all patients received stress ulcer prophylaxis. NA#= Not applicable; Chi-square test is applicable only for categorical variables. Continuous variables are expressed as mean±standard deviation and were compared using independent sample Student's t-test



[Table/Fig-3]: Showing distribution of isolates among VAP group (n=65); Bacterial growth was detected in 65 respiratory samples.

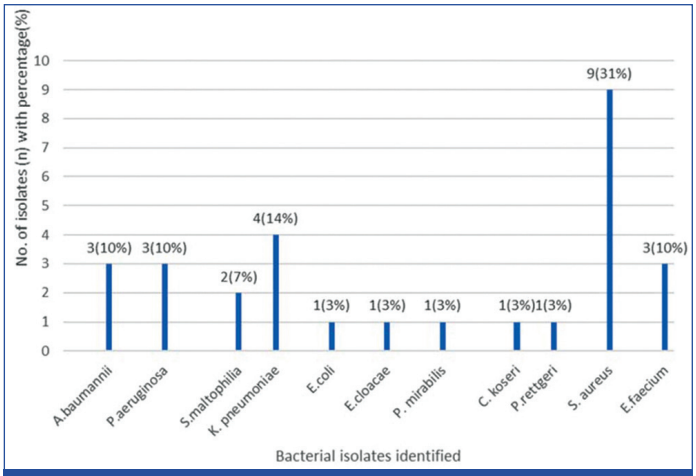


[Table/Fig-4]: Showing distribution of microorganisms in BAL samples (n=36) among VAP group; x-axis shows the number of isolates; y-axis shows the isolates identified.

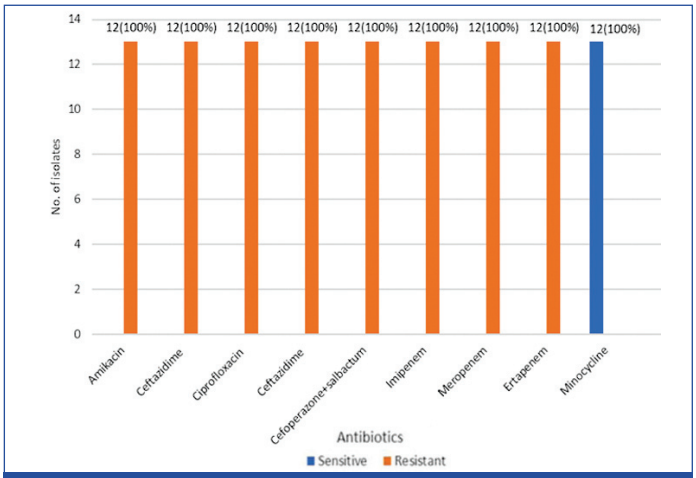
In terms of antimicrobial susceptibility pattern of isolates, all the isolates of *A. baumannii* 12(18%) [Table/Fig-6], *P. aeruginosa* 9 (14%), *K. pneumoniae* 10 (15%), *E.coli* 4 (6%), *E. cloacae* 3 (5%), all were resistant to amikacin, ceftazidime, ceftriaxone, ciprofloxacin, cefoperazone+salbactum, imipenem, meropenem. They were sensitive only to colistin and minocycline. There was only one isolate of *K. pneumonie* which was resistant to colistin and minocycline. Colistin susceptibility was interpreted based on MIC values obtained by VITEK-2 system, with all isolates demonstrating MIC ≤ 2 µg/mL; except one of *K. pneumoniae*, demonstrated an MIC > 32 µg/mL.

Among Gram positive isolates, all MRSA were sensitive to vancomycin, teicoplanin and linezolid as shown in [Table/Fig-7]. Vancomycin susceptibility among Gram-positive isolates was interpreted based on MIC values obtained using VITEK-2 system. All MRSA isolates demonstrated vancomycin MIC values ≤2 µg/mL, while all Vancomycin-Resistant *Enterococcus* (VRE) isolates exhibited MIC values ≥ 32 µg/mL. All three VRE isolates were sensitive only to linezolid. As all isolates were found resistant to at least one antibiotic from three different classes and, hence, considered as MDR.

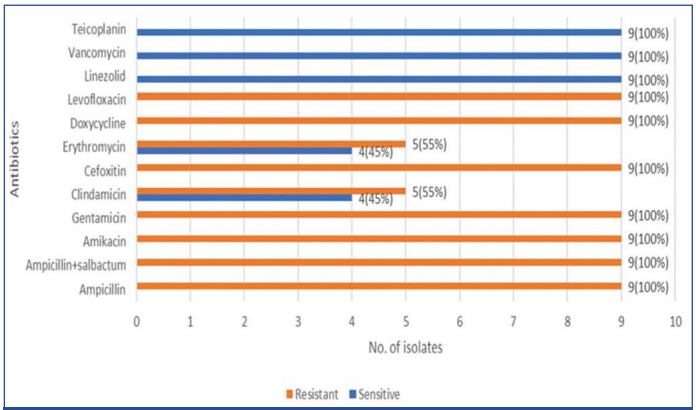
There were 5 (8%) isolates of *Stenotrophomonas maltophilia* that showed resistance to chloramphenicol, ceftazidime, and levofloxacin, but were sensitive to ticarcillin-clavulanic acid and minocycline. Additionally, one isolate each of *Chryseobacterium indologenes* (1.53%) and *Elizabethkingia anophelis* (1.53%) were



[Table/Fig-5]: Showing distribution of microorganisms in ET aspirate (n=29) among VAP group; x-axis shows the number of isolates; y-axis shows the isolates identified.



[Table/Fig-6]: Shows sensitivity profile of *Acinetobacter baumannii* (n=12).
As per CLSI the number of isolates less than 30 are not significant. However, this data has been presented here for epidemiological reasons, so that it can be later on pooled in a different meta-analysis. Colistin susceptibility was interpreted based on MIC values obtained by VITEK-2 system, with all *Acinetobacter baumannii* isolates demonstrating MIC ≤2 µg/mL.



[Table/Fig-7]: Shows sensitivity profile of *S. aureus* (n=9).
As per CLSI the number of isolates less than 30 are not significant. However, this data has been presented here for epidemiological reasons, so that it can be later on pooled in a different meta-analysis. Vancomycin susceptibility was interpreted based on MIC values using VITEK-2 system. All MRSA isolates demonstrated vancomycin MIC values ≤2 µg/mL

identified, both of which were only sensitive to ticarcillin-clavulanic acid and minocycline.

Also, two isolates of *Citrobacter koseri* 2 (3.07%) sensitive only to tigecycline with MIC of colistin ≤2 µg/mL. Two isolates of *Achromobacter denitrificans* 2 (3.07%) were found to be resistant to ceftazidime, piperacillin-tazobactam, imipenem, meropenem, cotrimoxazole, and levofloxacin, but were sensitive to doxycycline, chloramphenicol, and tigecycline. Furthermore, there were two isolates of *Proteus mirabilis* 2 (3.07%), and two isolates of *Providencia rettgeri* 2 (3.07%) all of which were resistant to all first line antibiotics tested.

DISCUSSION

The incidence of VAP in the present study (36.28 per 1000 ventilator days) falls within the range reported by earlier Indian studies, where rates have varied between 8.9 and 46 episodes per 1000 ventilator days [21]. Such elevated incidence is frequently attributed to factors such as staffing constraints in ICUs, particularly inadequate nurse-to-patient ratios, which may indirectly influence adherence to ventilator care bundles and infection-prevention practices.

In the present study, a slight male predominance in VAP occurrence (58.82%) was observed, although the difference was not statistically significant. Similar gender distributions have been documented by Sharpe JP et al., and Goel V et al., who also reported higher- but not significantly different- rates among males, though the underlying reasons remain unclear [22,23]. The mean age of patients developing VAP was 42.5±15.4 years. In the study by Rodrigues PM et al., the median age of the study population was 79 years, indicating a predominance of elderly patients. However, the present findings did not reveal a significant age difference between VAP and non-VAP groups [24].

Several risk factors demonstrated statistically significant associations with VAP, including, supine positioning, tracheostomy, extended duration of mechanical ventilation, longer hospital stay, and re-intubation. These determinants are well-recognised contributors to VAP pathogenesis and are consistent with findings from prior studies [25-27]. Because stress-ulcer prophylaxis was universally administered in both groups, its association could not be evaluated. A clear understanding of these risk factors is essential for early risk stratification and for guiding preventive strategies in mechanically ventilated patients.

Among co-morbidities, anaemia, diabetes, hypertension, malignancy, and solid organ transplantation were significantly more common in patients with VAP. The increased susceptibility in these patients may be attributed to impaired host immunity, frequent invasive interventions, and prolonged hospitalisation. These findings partially align with those of Shah H et al., who reported a significant association of anaemia and hypertension with VAP [28].

A total of 68 VAP cases were identified, of which 65 were culture-positive and three were culture-negative; therefore, microbiological analyses, organism distribution, and antimicrobial susceptibility patterns were calculated using the 65 culture-positive isolates. All infections were monomicrobial. Monomicrobial patterns in VAP have been documented previously and may be attributed to prior antibiotic exposure, predominance of late-onset VAP, and the presence of co-morbidities that predispose patients to infections caused by multidrug-resistant organisms. Ben Lakhal H et al., reported monomicrobial VAP in 77% of cases, whereas Hejazi ME et al., demonstrated a much higher rate of polymicrobial infections [29,30].

In the present study, Gram-negative bacteria accounted for the majority of isolates (81.54%), a distribution that closely resembles findings of Joseph NM et al., who reported 80.9% Gram-negative pathogens in VAP, including 59.6% non fermenters [31]. Non fermenting Gram-negative bacilli, particularly *Acinetobacter baumannii* (18%), *Pseudomonas aeruginosa* (14%), and *Klebsiella pneumoniae* (15%), were predominant. Among Gram-positive organisms (18.46%), MRSA (14%) was most common, followed by *Enterococcus faecium* (5%).

The susceptibility patterns observed in this study indicate a substantial burden of MDR Gram negative pathogens in the ICU. The dominant organisms demonstrated extensive resistance to multiple antibiotic classes, including aminoglycosides, β-lactams, fluoroquinolones, and carbapenems, leaving only last-line agents effective in most cases. The identification of strains exhibiting resistance even to these reserve drugs reflects the possible emergence of pan drug resistant organisms, a trend increasingly reported in critical-care environments. In contrast, the Gram positive isolates displayed relatively preserved susceptibility to glycopeptides and oxazolidinones. Overall, the antimicrobial profile highlights significant therapeutic limitations and reinforces the necessity for stringent antimicrobial stewardship and robust infection control measures.

Less common pathogens such as *Stenotrophomonas maltophilia*, *Chryseobacterium indologenes*, and *Elizabethkingia anophelis* also demonstrated highly restricted susceptibility patterns, being sensitive mainly to ticarcillin- clavulanate, minocycline, or doxycycline. The presence of such organisms suggests environmental contamination, selective antibiotic pressure, and challenges in infection-control practices within the ICU. Markers of systemic inflammation- including TLC and procalcitonin were significantly elevated in patients with VAP, supporting their utility as adjunctive tools in clinical diagnosis.

The mortality rate among VAP patients (32.35%) was higher than in the non VAP group (25.14%), although the difference was not statistically significant. Mortality was particularly high among patients infected with *A. baumannii*, *K. pneumoniae*, and *S. maltophilia*. This observation was consistent with findings by Zirpe K et al., who also reported increased mortality in infections caused by these organisms, though overall mortality differences between VAP and non VAP patients were not significant [32]. Given the heterogeneous patient population with multiple co-morbidities and varied clinical conditions, it is challenging to attribute mortality to a single factor. Further prospective studies are warranted to better understand determinants of poor outcomes.

The predominance of MDR Gram-negative bacteria, combined with limited therapeutic options, highlights the urgent need for robust antimicrobial-stewardship programs, reinforcement of ventilator care bundles, and enhanced infection-control practices. Future studies should focus on multicentric data, molecular mechanisms of resistance, rapid diagnostic techniques, and targeted preventive interventions to reduce the burden of VAP in resource-limited settings.

Limitation(s)

Since this was a retrospective observational study conducted at a single centre, the findings regarding epidemiology, co-morbidities, and clinical presentation may not be applicable to other settings.

CONCLUSION(S)

This study emphasises that VAP, as a HAI, is increasingly associated with non fermenting Gram negative bacilli such as *A. baumannii* and *P. aeruginosa*, along with *K. pneumoniae* among Enterobacterales. These organisms exhibit MDR, leaving very limited therapeutic options and making management particularly difficult. The presence of MRSA and VRE among Gram positive pathogens further adds to the complexity of treatment. Given the predominance of such difficult-to-treat organisms, accurate species level identification coupled with comprehensive antimicrobial susceptibility testing remains essential to guide appropriate, targeted therapy and optimise clinical outcomes.

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Authors' contribution

NY: Protocol development, Conception and design; NY, CS: Methodology used to collect isolates; KK: Data collection; CS, SSI: Data analysis , Data curation; CS: Supervision; NY, CS: Writing original draft, Interpretation of data; CS, SSP; Writing review and editing. All authors read and approved the final manuscript for submission.

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