International Journal of Medical and Pharmaceutical Research

Online ISSN-2958-3683 | Print ISSN-2958-3675
Frequency: Bi-Monthly
Available online on: https://ijmpr.in/

Original Article

Bacteriological Profile and their Antibiogram of Ventilator-Associated Pneumonia in a Tertiary Care Teaching Hospital from Eastern Gujarat

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Received: 13-02-2026
Accepted: 09-03-2026
Available online: 26-03-2026

ABSTRACT

Background: Ventilator-associated pneumonia (VAP) is an important Intensive Care Unit infection and a frequent cause of broad-spectrum antibiotic use. Local microbiological data are needed to guide empirical therapy.
Methods: This prospective observational study was conducted in the Department of Microbiology, Zydus Medical College and Hospital, Dahod, from December 2023 to October 2025. Respiratory specimens from adults with clinically suspected VAP were examined by Gram stain, culture, biochemical identification, and antimicrobial susceptibility testing according to CLSI 2022 criteria.
Results: Of 309 respiratory specimens, 218 (70.6%) were culture-positive. Positivity was higher among men, and most positive specimens were from the 30-59 year age range. Endotracheal aspirate (ETA) yielded the largest number of positive cultures (175/248, 70.6%), Tracheostomy Tube aspirate (TTA) had the highest positivity proportion (37/47, 78.7%), and Bronchoalveolar lavage (BAL) had the lowest yield (6/14, 42.9%). Klebsiella spp. (26.1%), Pseudomonas spp. (23.9%), Acinetobacter spp. (21.1%), Staphylococcus spp. (18.3%), and Escherichia coli (8.7%) were the predominant isolates. Resistance was frequent among third-generation cephalosporins and fluoroquinolones, whereas some aminoglycosides and carbapenems retained activity against selected isolates.
Conclusion: VAP in this setting was dominated by Gram-negative bacilli. Ongoing local surveillance and antibiotic stewardship are essential to guide empirical therapy.

Keywords: *VAP; pneumonia; antimicrobial resistance; respiratory specimen; antibiogram.*

INTRODUCTION

Ventilator-associated pneumonia (VAP) is one of the most common and serious healthcare-associated infections in intensive care units (ICUs), contributing significantly to patient morbidity, mortality, prolonged hospital stay, and increased healthcare costs [1]. Despite advances in critical care, the burden of VAP remains substantial, particularly in low and middle-income countries where infection control practices and antimicrobial stewardship may be inconsistent [1,2].

The pathogenesis of VAP is complex and involves microaspiration of colonized secretions, biofilm formation on endotracheal tubes, and impaired host defences [3]. Furthermore, VAP is increasingly recognized as a heterogeneous syndrome with variable host responses and microbial profiles, which complicates both diagnosis and management [1]. Clinical diagnosis remains challenging due to the lack of highly specific criteria, and microbiological confirmation is often necessary to guide appropriate therapy [3].

The microbial etiology of VAP is predominantly composed of Gram-negative bacilli, particularly Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter species, although the distribution varies depending on geographical location, ICU practices, and patient population [3,4]. The emergence of multidrug-resistant (MDR) organisms, especially among

Enterobacterales and non-fermenters, has further complicated treatment, limiting therapeutic options and worsening clinical outcomes [5,6].

Antimicrobial resistance in VAP pathogens is driven by multiple mechanisms, including β-lactamase production, efflux pumps, porin loss, and biofilm-associated resistance [5]. Resistance to third-generation cephalosporins and carbapenems among Enterobacterales has become a major concern and is often associated with prior antibiotic exposure and healthcare-related risk factors [6]. However, the relationship between antibiotic consumption and VAP incidence is not always linear, highlighting the complexity of antimicrobial stewardship in ICU settings [2].

Several risk factors for VAP have been identified, including prolonged mechanical ventilation, severity of illness, prior antibiotic use, and underlying comorbidities [7]. While these factors influence both incidence and outcomes, local microbiological profiles and antimicrobial susceptibility patterns remain crucial for guiding empiric therapy and improving patient management [3]. Given the substantial global burden of lower respiratory tract infections and the increasing threat of antimicrobial resistance, there is a need for region-specific data on the microbiological spectrum and resistance patterns of VAP pathogens [8]. Such data are essential for developing effective empirical treatment strategies and infection control policies tailored to local settings.

Therefore, the present study was undertaken to determine the bacterial profile and antimicrobial susceptibility patterns of pathogens isolated from suspected VAP cases in a tertiary care hospital in Gujarat, India, and to contribute to the existing evidence base for optimizing antimicrobial therapy in ICU patients.

MATERIALS AND METHODS

Study design and setting: This prospective observational study was conducted in the Department of Microbiology at Zydus Medical College and Hospital, Dahod, from December 2023 to October 2025.

Study population: Adults (18 years and older) receiving mechanical ventilation for 48 hours or more were evaluated. VAP was diagnosed using Centers for Disease Control and Prevention/National Healthcare Safety Network (CDC/NHSN) surveillance criteria [9], including radiological evidence of a new or progressive infiltrate, consolidation, or cavitation together with at least two compatible clinical features such as fever or hypothermia, leucocytosis or leukopenia, purulent respiratory secretions, or worsening gas exchange.

Exclusion criteria: Patients with pneumonia present at admission, those developing infection within the first 48 hours of ventilation, severe immunocompromised states such as AIDS or terminal cancer, and pre-existing chronic respiratory diseases such as COPD or bronchial asthma were excluded.

Specimen collection and microbiology: A total of 309 respiratory specimens were collected under aseptic conditions. The specimen types included endotracheal aspirate (ETA), tracheostomy tube aspirate (TTA), and bronchoalveolar lavage (BAL). Samples were examined by direct Gram stain and cultured on MacConkey agar, blood agar, and chocolate agar. Isolates were identified by colony morphology, Gram staining, and standard biochemical tests including indole, urea hydrolysis, triple sugar iron, citrate utilization, catalase, coagulase, and bile esculin reactions.

Antimicrobial susceptibility testing: Antimicrobial susceptibility testing was performed by the Kirby-Bauer disk diffusion method and interpreted according to Clinical and Laboratory Standards Institute (CLSI) M100 2022 guidelines [10]. Organism-antibiotic combinations not recommended for testing or considered intrinsically inactive were reported as not applicable (NA).

Definitions and statistics: Multidrug resistance (MDR) was defined as non-susceptibility to at least one agent in three or more antimicrobial categories. Categorical variables were summarized as counts and percentages. Association between gender and culture positivity was assessed using the chi-square test, and a p value < 0.05 was considered statistically significant. Because specimen types were not uniformly paired across patients, comparisons among ETA, TTA, and BAL were descriptive rather than paired inferential comparisons.

Ethics: The study was approved by the Institutional Ethics Committee (IEC no. ZMCH/IEC/010(04)-2024). Written informed consent was obtained from participants or their legally authorized representatives.

RESULTS

Demographic distribution

As shown in Table 1, of the 309 respiratory specimens processed, 218 (70.6%) were culture-positive and 91 (29.4%) were culture-negative. As shown in Table *1*, the largest number of positive specimens occurred in the 40-49 year age group, and overall positivity was concentrated in the 30-59 year range. Male patients accounted for 160 of the 218 positive cases

(73.4%), whereas female patients accounted for 58 (26.6%). The association between gender and culture positivity was statistically significant (chi-square = 4.5458, p = 0.0330).

Table 1. Age and gender-wise distribution of culture-positive and culture-negative specimens.

Age group	Positive male	Positive female	Negative male	Negative female	Total
18-19	8	3	1	3	15
20-29	22	16	10	10	58
30-39	26	7	10	7	50
40-49	34	14	8	10	66
50-59	30	6	8	1	45
60-69	30	8	9	3	50
70-79	6	4	6	2	18
80-89	4	0	2	1	7

Note: The table shows the number of specimens in each age and gender subgroup. It is descriptive and should not be interpreted as a paired longitudinal analysis.

Diagnostic yield of respiratory specimen types

As shown in Table 2, Endotracheal aspirate (ETA) accounted for the largest number of positive cultures (175/248, 70.6%). Tracheostomy tube aspirate (TTA) had the highest positivity proportion (37/47, 78.7%), while BAL had the lowest yield (6/14, 42.9%). Because these specimen categories were not paired in the same patients, the observed differences are descriptive and should not be used to claim formal diagnostic superiority of one method over another.

Table 2. Culture positivity by respiratory specimen type.

Specimen type	Positive	Negative	Total	Positivity %
Endotracheal aspirate (ETA)	175	73	248	70.6
Tracheostomy tube aspirate (TTA)	37	10	47	78.7
Bronchoalveolar lavage (BAL)	6	8	14	42.9

Bacteriological profile of isolates

As shown in Table 3, among the 218 culture-positive specimens, Gram-negative bacilli predominated. Klebsiella spp. was the most frequent isolate (57/218, 26.1%), followed by Pseudomonas spp. (52/218, 23.9%), Acinetobacter spp. (46/218, 21.1%), Staphylococcus spp. (40/218, 18.3%), and Escherichia coli (19/218, 8.7%). Citrobacter spp. (2 isolates), Proteus spp. (1 isolate), and Enterococcus spp. (1 isolate) were recovered only occasionally.

Table 3. Distribution of bacterial isolates recovered from culture-positive VAP specimens

Organism	Isolates (n)	Percentage of positive isolates (%)
Klebsiella	57	26.1
Pseudomonas	52	23.9
Acinetobacter	46	21.1
Staphylococcus	40	18.3
E. coli	19	8.7
Citrobacter	2	0.9
Proteus	1	0.5
Enterococcus	1	0.5

As shown in Figure 1, Antimicrobial susceptibility patterns showed frequent resistance to third-generation cephalosporins and fluoroquinolones among the common Gram-negative isolates. Some aminoglycosides and carbapenems retained better activity against selected isolates, but susceptibility varied by organism and by antibiotic. The heat map therefore supports local stewardship decisions, but it should not be used to infer uniform susceptibility across all species or to extrapolate resistance mechanisms without confirmatory testing.

Figure 1: Antibiotic susceptibility pattern of isolates.

	Staphylococcus spp.	Klebsiella spp.	E. coli	Proteus species	Citrobacter spp.	Pseudomonas spp.	Acinatobacter species	Enterococcus species
Amikacin	NA	47.37 %	63.16 %	100.00 %	0.00 %	75.00 %	34.78 %	0.00 %
Gentamicin	57.50 %	75.44 %	84.21 %	100.00 %	0.00 %	90.38 %	58.70 %	100.00 %
Ciprofloxacin	67.50 %	71.93 %	73.68 %	100.00 %	0.00 %	86.54 %	65.22 %	0.00 %
Levofloxacin	52.50 %	92.98 %	84.21 %	0.00 %	0.00 %	92.31 %	78.26 %	0.00 %
Tetracycline	85.00 %	68.42 %	73.68 %	NA	100.00 %	61.54 %	60.87 %	100.00 %
Imipenem	NA	35.09 %	47.37 %	100.00 %	50.00 %	53.85 %	60.87 %	NA
Meropenem	NA	49.12 %	63.16 %	0.00 %	50.00 %	75.00 %	58.70 %	NA
Ertapenem	NA	40.35 %	47.37 %	0.00 %	0.00 %	NA	NA	0.00 %
Piperacillin Tazobactam	NA	70.18 %	73.68 %	0.00 %	100.00 %	88.46 %	80.43 %	0.00 %
Cefotaxime	NA	3.51 %	63.16 %	0.00 %	0.00 %	NA	0.00 %	NA
Cefepime	NA	64.91 %	63.16 %	100.00 %	100.00 %	82.69 %	73.91 %	NA
Ceftazidime	NA	96.49 %	84.21 %	0.00 %	0.00 %	96.15 %	89.13 %	NA
Cefuroxime	NA	1.75 %	36.84 %	0.00 %	50.00 %	NA	NA	NA
Ceftriaxone	NA	8.77 %	73.68 %	100.00 %	0.00 %	NA	NA	NA
Cefpodoxime	NA	0.00 %	57.89 %	0.00 %	0.00 %	NA	0.00 %	NA
Aztreonam	NA	3.51 %	0.00 %	100.00 %	0.00 %	7.69 %	6.52 %	NA
Chloramphenicol	65.00 %	73.68 %	78.95 %	100.00 %	50.00 %	NA	71.74 %	100.00 %
Cotrimoxazole	37.50 %	3.51 %	84.21 %	0.00 %	0.00 %	NA	73.91 %	NA
Ampicillin	NA	NA	10.53 %	0.00 %	NA	NA	0.00 %	0.00 %
Amox-Clav	65.00 %	NA	0.00 %	0.00 %	100.00 %	NA	8.70 %	0.00 %
Ampicillin-Sulbactam	100.00 %	NA	15.79 %	100.00 %	100.00 %	5.77 %	10.87 %	100.00 %
Cefoxitin	35.00 %	NA	NA	NA	NA	0.00 %	NA	NA

Note: Values in the heat map represent organism-specific susceptibility percentages for antibiotics that were tested. NA indicates intrinsic resistance, non-reportable combinations, or agents not recommended for testing against that organism. Because denominators vary by organism and some rows contain very small isolate counts, the figure should be interpreted as a descriptive antibiogram rather than a direct cross-organism ranking.

DISCUSSION

The present study adds local microbiological evidence from Eastern Gujarat. In our cohort, culture positivity was 70.6% and Gram-negative bacilli predominated, with Klebsiella spp. the leading isolate, followed by Pseudomonas spp. and Acinetobacter spp. These findings support the central message of Howroyd et al. and Papazian et al. that VAP is diagnostically challenging, heterogeneous, and best interpreted with microbiological confirmation rather than clinical criteria alone [1,3].

The organism distribution in our study is broadly consistent with the ICU VAP literature, but it differs from the pattern reported by Karakuzu et al., who found Acinetobacter baumannii, Pseudomonas aeruginosa, and MRSA to be most frequent [4]. This difference likely reflects local ICU ecology, antibiotic pressure, and patient mix. Our data therefore reinforce that VAP microbiology is hospital-specific and that empiric therapy should be guided by local surveillance rather than by findings from other centers [1,3,4,7].

The resistance profile in our isolates is clinically important because resistance was frequent to third-generation cephalosporins and fluoroquinolones, while some aminoglycosides and carbapenems retained activity against selected organisms. This pattern is compatible with the stewardship concerns raised by Nora and Póvoa, who noted that antibiotic consumption and VAP rates do not always move in parallel [2]. It also fits with the broader problem of Klebsiella pneumoniae resistance mechanisms described by Li et al. and with the risk of carbapenem resistance among third-generation cephalosporin-resistant Enterobacterales highlighted by Moghnieh et al. [5,6].

However, the present study did not perform molecular resistance testing, and the heat map should therefore be interpreted only as a descriptive antibiogram. Reduced susceptibility does not by itself prove ESBL or carbapenemase production. Likewise, the observed organism-specific differences should not be extrapolated across all isolates because several species were represented by small numbers. These limitations are particularly important when comparing our findings with epidemiologic reviews such as Weinstein et al., which emphasize patient management and risk-factor assessment rather than culture counts alone [7].

Finally, the global burden of lower respiratory infection remains substantial, which gives practical value to even a single-center VAP antibiogram [8]. Although our study was not designed to measure incidence, mortality, or independent risk

factors, it shows that VAP in this ICU is dominated by Gram-negative bacilli and that empiric treatment policies should be periodically updated using local microbiology data. In that sense, the study contributes directly to antimicrobial stewardship and ICU infection-control planning.

Limitations

This was a single-center study, which limits generalizability. The analysis was based on culture positivity among clinically suspected cases rather than true incidence of VAP. Some organisms were represented by very small numbers, which limits the robustness of their susceptibility percentages. Molecular mechanisms of resistance were not evaluated, and specimen types were not uniformly paired across patients.

CONCLUSION

VAP in this tertiary care setting was predominantly caused by Gram-negative bacilli. Klebsiella spp., Pseudomonas spp., and Acinetobacter spp. were the leading isolates, and resistance to several commonly used antibiotics was frequent. ETA produced the greatest number of positive cultures, whereas TTA had the highest positivity proportion; however, these specimen categories were not paired, so direct diagnostic superiority cannot be claimed. Local microbiological surveillance and stewardship remain essential for rational empirical therapy and for updating ICU antibiotic policy.

Acknowledgements

The authors thank the microbiology departmental and laboratory staff.

Authorship Statement

Dr. Darpan B. Katira: Conceptualization and design of the study; primary responsibility for data collection and laboratory procedures; drafting the initial manuscript; and statistical analysis.
Dr. Deepak W. Deshkar: Administrative and technical support; critical revision of the study design; oversight of the methodology; and final critical review of the manuscript.
Dr. Tabrez Y. Chauhan: Assistance with experiments and data acquisition; literature review; and drafting and revision of the manuscript.
Dr. Heena R. Nihalani: Assistance with data interpretation and clinical/laboratory investigation; contribution to drafting specific sections; and technical support during the experimental phase.

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