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To Study the Bacteriological Profile and Antimicrobial Susceptibility Patterns of Pathogens Isolated from Urine Samples in Icu Patients at a Tertiary Care Hospital in North India

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ABSTRACT

Background: Intensive care units (ICUs) are hotspots for multidrug-resistant (MDR) bacterial infections, which significantly contribute to patient morbidity and mortality. Prompt identification of pathogens and knowledge of their resistance profiles is essential for empirical therapy and infection control.

Aim and Objective: To evaluate the distribution of pathogens from various clinical specimens in ICU patients and to analyze their antibiotic susceptibility patterns.

Material and Methods: A retrospective study was conducted in the Department of Microbiology, Sharda Hospital, Greater Noida, over a defined period. A total of 2,125 clinical samples from ICU patients were processed according to standard microbiological protocols. Identification of isolates was done by biochemical testing, and antimicrobial susceptibility was determined by the Kirby-Bauer disk diffusion method as per CLSI guidelines (2023) [1].

Results: In the present study out of the 2,125 samples, blood constituted 46%, urine 30%, respiratory 20%, and pus 4%. A total of 285 pathogens were isolated, with respiratory samples showing the highest positivity (46%). The most common organisms were E. coli (24%), Acinetobacter spp. (23%), Klebsiella spp. (13%), and Staphylococcus aureus (10%). Among Enterobacteriaceae, carbapenems (43%), tigecycline (43%), and aminoglycosides (41–42%) were the most effective drugs. Acinetobacter spp. showed high sensitivity to minocycline (68%) and tigecycline (45%) but complete resistance to nitrofurantoin and norfloxacin. Pseudomonas aeruginosa responded well to amikacin (79%) and carbapenems (75%). Gram-positive isolates like S. aureus and Enterococcus spp. were highly susceptible to linezolid (95–100%) and vancomycin (50–78%).

Conclusion: The findings highlight a high burden of multidrug-resistant pathogens in ICU settings, with varying resistance patterns requiring continuous surveillance and rational antimicrobial stewardship.

Keywords: *Bacteriological, Profile, Antimicrobial Susceptibility Patterns, Icu, Blood, Clsi*

1. INTRODUCTION

Intensive Care Units (ICUs) are considered critical care environments where patients are at heightened risk of acquiring healthcare-associated infections (HAIs), primarily due to invasive procedures, prolonged hospital stays, and immunocompromised conditions. These settings often harbor multidrug-resistant (MDR) organisms, making infection control and effective antimicrobial therapy essential components of ICU management [1]. The growing threat of antimicrobial resistance (AMR) in ICUs is a global public health concern, as it leads to increased morbidity, mortality, and economic burden [2,3].

The bacteriological profile in ICUs is typically dominated by Gram-negative organisms such as Acinetobacter spp., Klebsiella spp., Pseudomonas aeruginosa, and Escherichia coli, along with Gram-positive pathogens like Staphylococcus aureus and Enterococcus spp. [4-6]. These organisms are notorious for exhibiting resistance to multiple classes of antibiotics, including carbapenems, cephalosporins, aminoglycosides, and fluoroquinolones [7]. Moreover, the increasing incidence of extended-spectrum β-lactamases (ESBLs) and carbapenem-resistant Enterobacteriaceae (CRE) has further complicated the management of ICU infections [8].

Recent studies in India and globally have shown that antibiotic resistance patterns vary with geography, hospital policies, and antibiotic stewardship practices [9]. The World Health Organization (WHO) has identified priority pathogens that require urgent research and development of new antimicrobials, with many ICU pathogens making the list . Surveillance studies help in formulating local antibiograms, guiding empirical therapy, and minimizing therapeutic failures [10].

In India, studies have reported a rising trend in resistance to first-line antibiotics, with some centers noting up to 70–80% resistance in ICU isolates, particularly among Acinetobacter and Klebsiella species [11]. The Clinical and Laboratory Standards Institute (CLSI) guidelines provide standardized methods for antimicrobial susceptibility testing, enabling laboratories to detect resistance trends and contribute to national and global surveillance efforts.

Understanding the local bacteriological profile and antibiotic susceptibility patterns is critical for implementing targeted therapy and infection control strategies. This is especially relevant in tertiary care hospitals where ICUs manage a diverse range of critically ill patients, including those with ventilator-associated pneumonia, bloodstream infections, urinary tract infections, and surgical site infections [12].

Therefore, this study was undertaken to identify the distribution of bacterial pathogens isolated from ICU patients and analyze their antimicrobial susceptibility patterns. The results will help in guiding clinicians for appropriate empiric therapy and contribute to improved antimicrobial stewardship and infection prevention policies in the ICU setting.

2. MATERIAL AND METHODS

This retrospective study was conducted in the Bacteriology Division of the Department of Microbiology at Sharda Hospital, Greater Noida, a tertiary care center in North India. During the study period, 2,125 clinical samples were collected from ICU patients, including blood (988), urine (627), respiratory samples (420), and pus (90).

All specimens were processed using standard microbiological techniques. Culture was performed on appropriate media, and bacterial isolates were identified based on colony morphology, Gram staining, and standard biochemical tests.

Type of Sample - Blood, Central line tips, Broncho-alveolar lavage (BAL), Pleural fluid, Cerebrospinal Fluid (CSF), Asciticfluid, Endotrachealaspirate, PusorTissue, sputum, throat swab, Urine samples received for culture and sensitivity.

Antimicrobial susceptibility testing (AST) was performed using the Kirby-Bauer disk diffusion method in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines (2023) [13]. The antibiotics tested included beta-lactams, aminoglycosides, fluoroquinolones, carbapenems, and others relevant to Gram-negative and Gram-positive pathogens. Data were recorded and analyzed to assess the prevalence of organisms and their resistance profiles.

Inclusion Criteria- Blood, Central line tips, Broncho-alveolar lavage (BAL), Pleural fluid, CerebrospinalFluid(CSF), Asciticfluid, Endotrachealaspirate, PusorTissue, sputum, throat swab, Urine received in Microbiology Section, Bacteriology Laboratory.

Exclusion Criteria-

1.Sputum showing 10 or more squamous epithelial cells per low power field on gram stain.

2. Bacterial isolates identified as commensals or contaminants.

3. Mixed bacterial growth.

4. Excessive delay between specimen collection and arrival in laboratory.

The experimental group includes the patients undergo treatment by Driftodontics based upon the philosophy of Alexander Discipline and control group includes the patient undergo by conventional MBT treatment.

3. RESULTS

During the study period, a total of 2,125 samples were received from various ICUs and analyzed in the Bacteriology Lab at Sharda Hospital,Greater Noida. Out of the 2,125 ICU samples analyzed, blood was the most common specimen (46%), followed by urine (30%), respiratory samples (20%), and pus (4%). From these, 285 bacterial isolates were obtained, with respiratory samples yielding the highest number (131, 46%), followed by blood (64, 23%), urine (58, 20%), and pus (32, 11%). The most common organisms across all samples were Escherichia coli (69, 24%), Acinetobacter spp. (65, 23%), Klebsiella spp. (38, 13%), Pseudomonas aeruginosa (28, 10%), Staphylococcus aureus (28, 10%), Enterococcus spp. (28, 10%), coagulase-negative Staphylococci (17, 6%), and Citrobacter spp. (10, 3%).Among Enterobacteriaceae, carbapenems (meropenem and imipenem) and tigecycline were the most effective agents (43%), followed by gentamicin (42%) and amikacin (41%). Nitrofurantoin showed high efficacy (70%) in urinary tract infections, while norfloxacin was the least effective (10%). Acinetobacter spp. displayed alarming resistance, with only minocycline (68%) and tigecycline (45%) showing moderate activity. Carbapenems, cephalosporins, and fluoroquinolones had <5% sensitivity. Pseudomonas aeruginosa showed good susceptibility to amikacin (79%), gentamicin, and carbapenems (75%).

The distribution of these samples were as follows- 988 blood samples (46%), 627 urine samples (30%), 420 respiratory samples (20%), and 90 pus samples (4%).(Table1).

Sample Type	No.of samples (Percentage)
Blood	988 (46%)
Urine	627 (30%)
Respiratory samples	420 (20%)
Pus	90 (4%)

Table 1: Total Samples Collected from ICUs (n=2125)

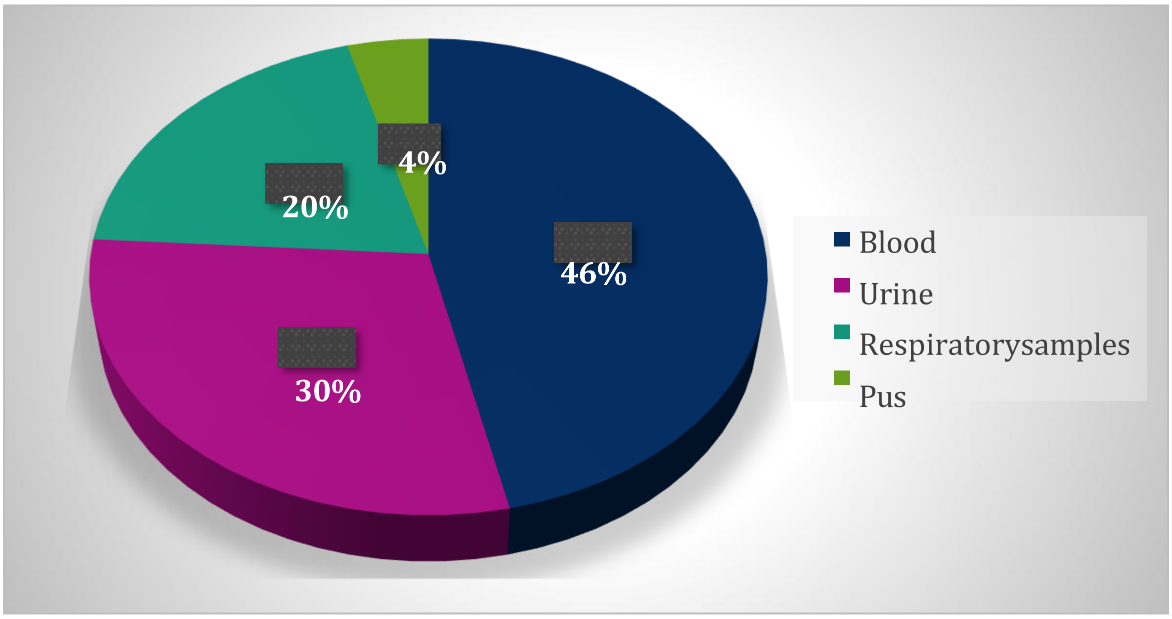


Fig1-Total Samples Collected from ICUs

A total of 285 clinical isolates have been obtained from various samples collected across different ICUs. Respiratory samples showed the highest isolation rate, with 131 isolates (46%),followed by blood samples with 64 isolates (23%), urine samples with 58 isolates (20%), and pus samples with 32 isolates (11%). (Table 2)

Sample Type	No.of isolates (Percentage)
Blood	64 (23%)
Urine	58 (20%)
Respiratory samples	131 (46%)
Pus	32 (11%)

Table 2: Sample wise distribution of isolates (n=285)

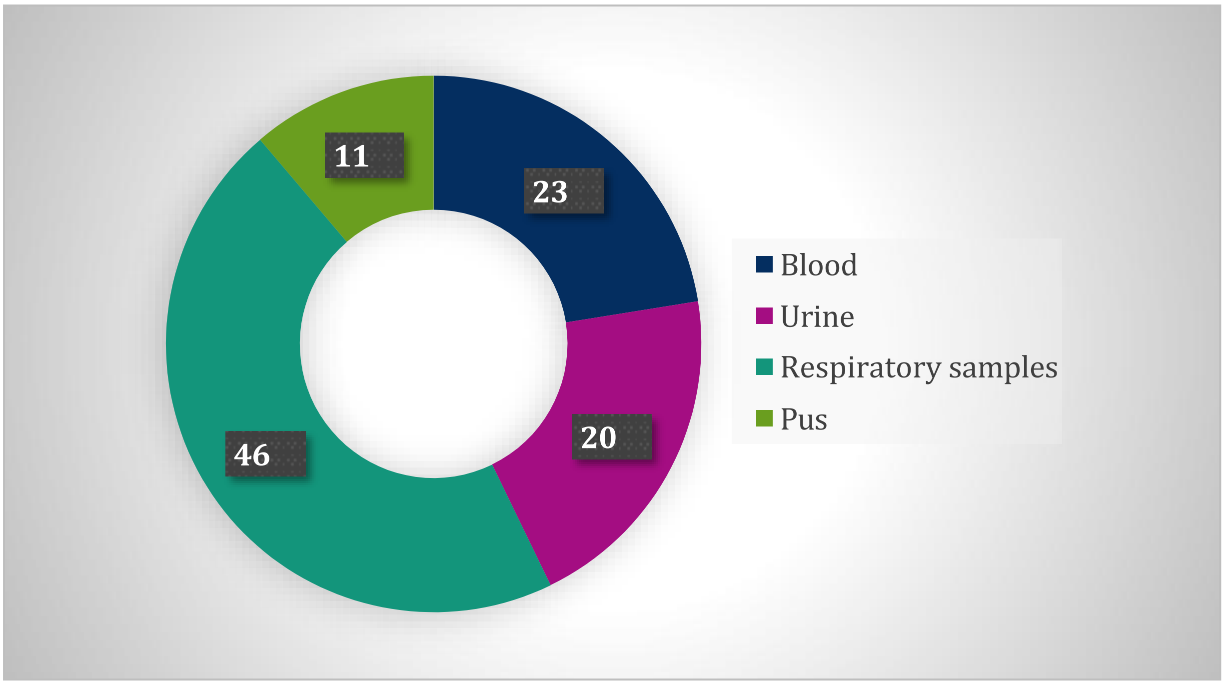


Fig2-Sample wise distribution of isolates

The most frequently isolated organisms were *Staphylococcus aureus* (including both *MRSA* and *MSSA)* and *Coagulase-negativestaphylococci (CONS)* with17isolates (27%), followed by *Klebsiella spp.* with 10 isolates (16%), *E. coli* with 8 isolates (12%), *Acinetobacter spp.* With 6 isolates (9%), and *Enterococcusspp.*with4 isolates (6%). *Pseudomonasspp.* was the least isolated organism, with only 2 isolates (3%) in bloodstream infections. (Table 3.1)

Urine samples(n=58)

Causative Organisms	Numbers(Percentage)
E.coli	23 (40%)
Enterococcusspp.	23 (40%)
Klebsiellaspp.	6 (9%)
Pseudomonasspp.	3 (5%)
Acinetobacterspp.	1 (2%)
Citrobacterspp.	1 (2%)
Staphylococcusspp. (MSSA)	1 (2%)

Table 3: Etiological distribution of Urinary tract infections

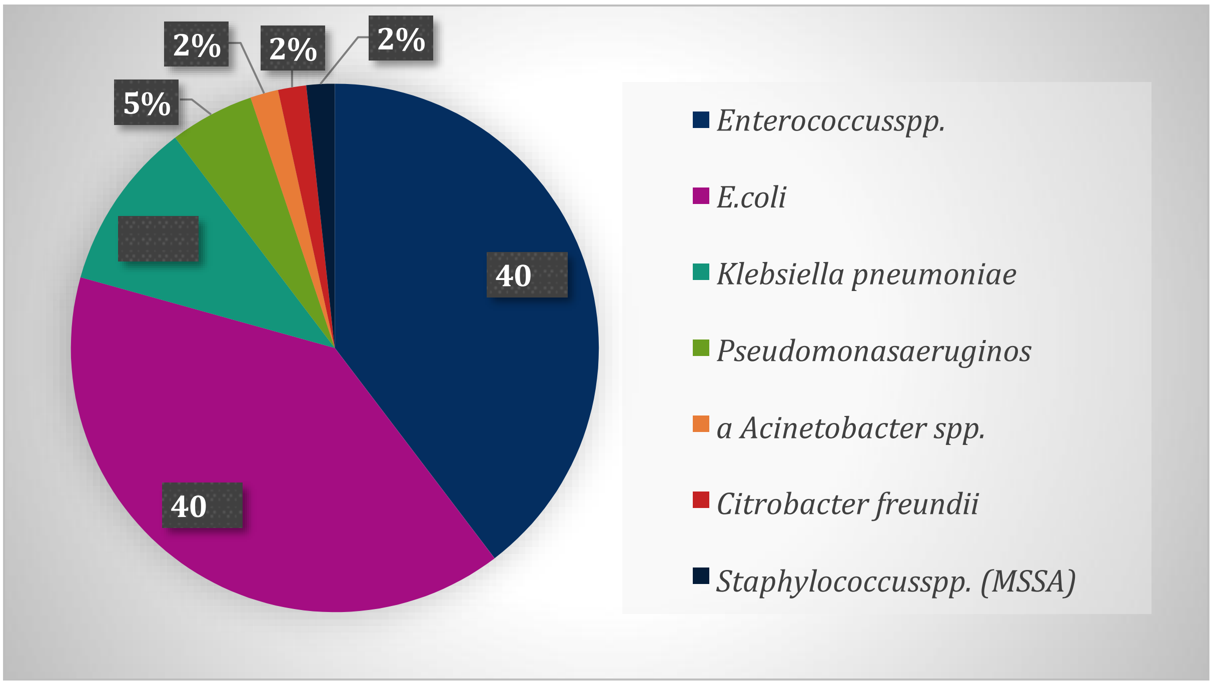


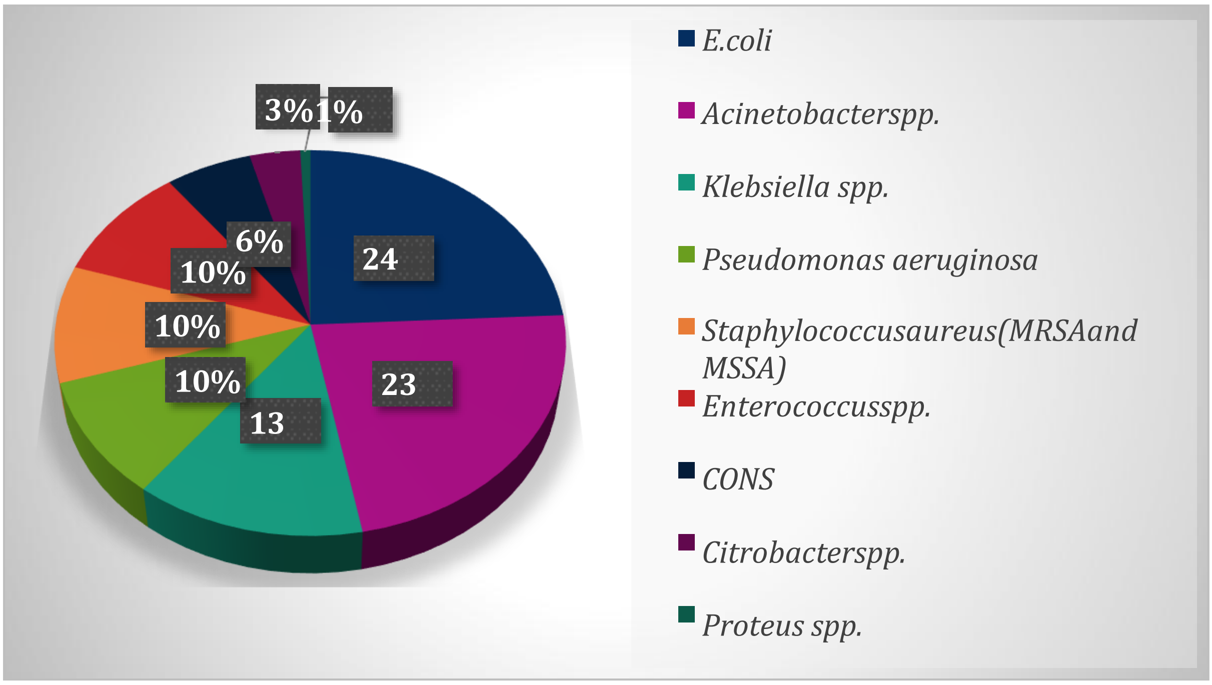
Fig 3 Etiological distribution of Urinary tract infections

In respiratory tract infections, *Acinetobacter spp.* was the most frequently isolated organism, with54isolates (41%) followed by *E.coli* with27 isolates (21%), *Pseudomonasspp.* with21 isolates (16%), *Klebsiella spp.* with 17 isolates (13%), and *Staphylococcus aureus* (both MRSAand MSSA) with 8 isolates (6%). *Citrobacter spp.* was the least isolated organism, with only 4 isolates (3%). (Table3.3)

InTotal samples(n=285)

Causative organisms	Numbers(Percentage)
E.coli	69 (24%)
Acinetobacterspp.	65 (23%)
Klebsiellaspp.	38 (13%)
Pseudomonasspp.	28 (10%)
Staphylococcusaureus(MRSAandMSSA)	28 (10%)
Enterococcusspp.	28 (10%)
CONS	17 (6%)
Citrobacterspp.	10 (3%)
Proteus spp.	2 (1%)

Table 4: Overall distribution of microorganisms causing infections in ICUs



Ward wise distribution	**No. of cases**
EICU-	2
ICCU-	13
MICU-	14
NeuroICU-	1
PICU-	4
RICU-	9
SICU-	13
NICU-	2

Table 5: Wardwise distribution of cases

The antimicrobial susceptibility profiles of all Gram-negative and Gram-positive bacteria (GNB and GPC) isolates (n = 285) were determined using the Clinical and Laboratory Standards Institute (CLSI) disk diffusion method.

Enterobacteriaceae

- Carbapenems (meropenem, imipenem) and tigecycline were the most effective antibiotics, showinga43%efficacy, followed by gentamicin (42%), amikacin (41%), minocycline (39%), cotrimoxazole (35%), andtobramycin (31%). Ampicillinwasthe least effective, with an efficacy of only 8%.
- In urinary tract infections, nitrofurantoin showed the highest efficacy (70%), while norfloxacin was the least effective (10%).
- Fosfomycin demonstrated high effectiveness, with 66% efficacy in both urinary and respiratory tract infections.

Antibiotics	Sensitivity (%)	Resistance (%)
Ampicillin	8%	92%
Gentamicin	42%	58%
Tobramycin	31%	69%
Amoxyclav	22%	78%
Ceftriaxone	26%	74%
Cefotaxime	26%	74%
Cefuroxime	12%	88%
Cefepime	22%	78%
Ciprofloxacin	26%	74%
Levofloxacin	26%	74%
Amikacin	41%	59%
Imipenem	43%	57%
Meropenem	43%	57%
Piperacillin/tazobactum	27%	73%
Cotrimoxazole	35%	65%
Ceftazidime	13%	87%
Aztreonem	19%	81%
Tetracycline	26%	74%
Minocycline	39%	61%
Tigecycline	43%	57%
Nitrofurantoin	70%	30%
Fosfomycin	66%	34%
Norfloxacin	10%	90%

Table 6: Antibiotic susceptibility profile of *Enterobacteriaceae*(n=119)

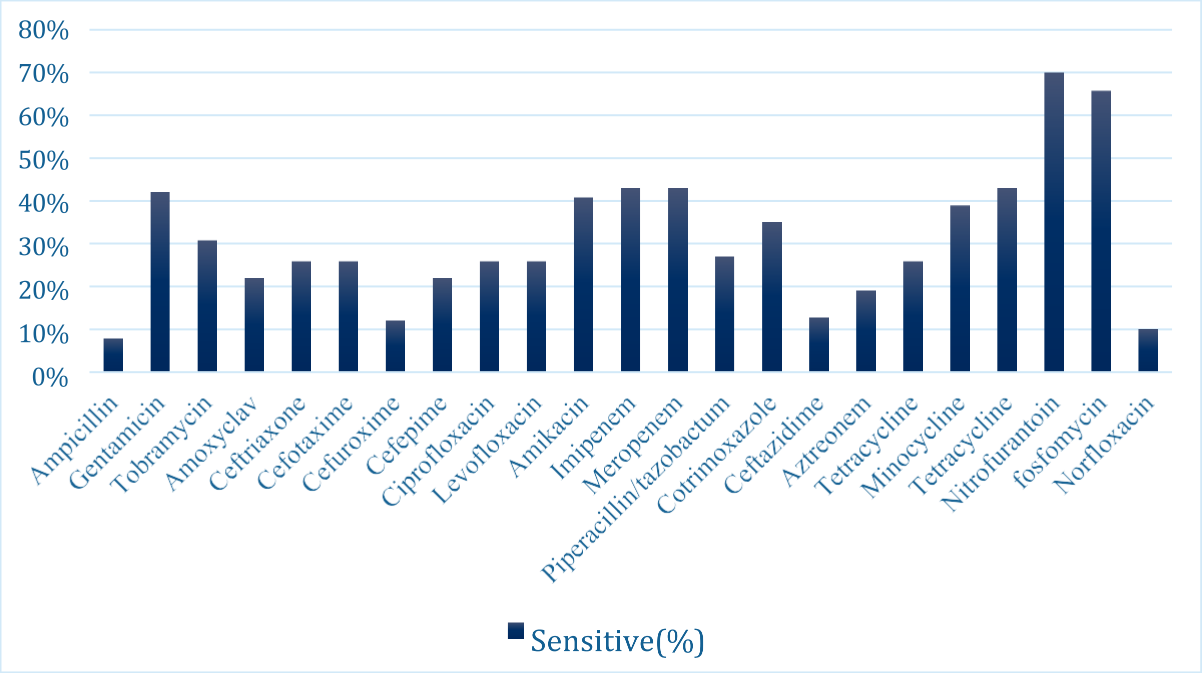


Fig 5-Antibiotic sensitive profile of *Enterobacteriaceae*(n=119)

Non-Enterobacteriaceae-Among the 285isolates, 65 were as *Acinetobacterspp,* and 28 as *Pseudomonasspp.*

1-*Acinetobacter spp.*

A total of 65 *Acinetobacter species* were isolated from 285 isolates. *Acinetobacter spp.* were found to be highly effective for Minocycline (68%) followed by Tigecycline (45%), Cotrimoxazole (15%), Ceftriaxone and Cefotaxime (14%) whereas, Meropenem, Imipenem, Cefepimeand Cefuroxime were least effective (1%) among all the antibiotic agents tested.

Nitrofurantoin and Norfloxacin showed resistant to all the isolates of *Acinetobacter spp*. in urinary tract infection.

Antibiotics	Sensitivity(%)	Resistance(%)
Ceftazidime	4%	96%
Ciprofloxacin	4%	96%
Levofloxacin	4%	96%
Gentamicin	4%	96%
Tobramycin	5%	95%
Imipenem	1%	99%
Meropenem	1%	99%
Ceftriaxone	14%	86%
Cefotaxime	14%	86%
Cefepime	1%	99%
Amikacin	7%	93%
Piperacillin/tazobactam	7%	93%
Minocycline	68%	32%

Cotrimoxazole	15%	85%
Tigecycline	45%	55%
Cefuroxime	1%	99%
Tetracycline	6%	94%
Nitrofurantoin	0%	100%
Norfloxacin	0%	100%

Table 7: Antibiotic susceptibility pattern of *Acinetobacterspp.*(n=65)

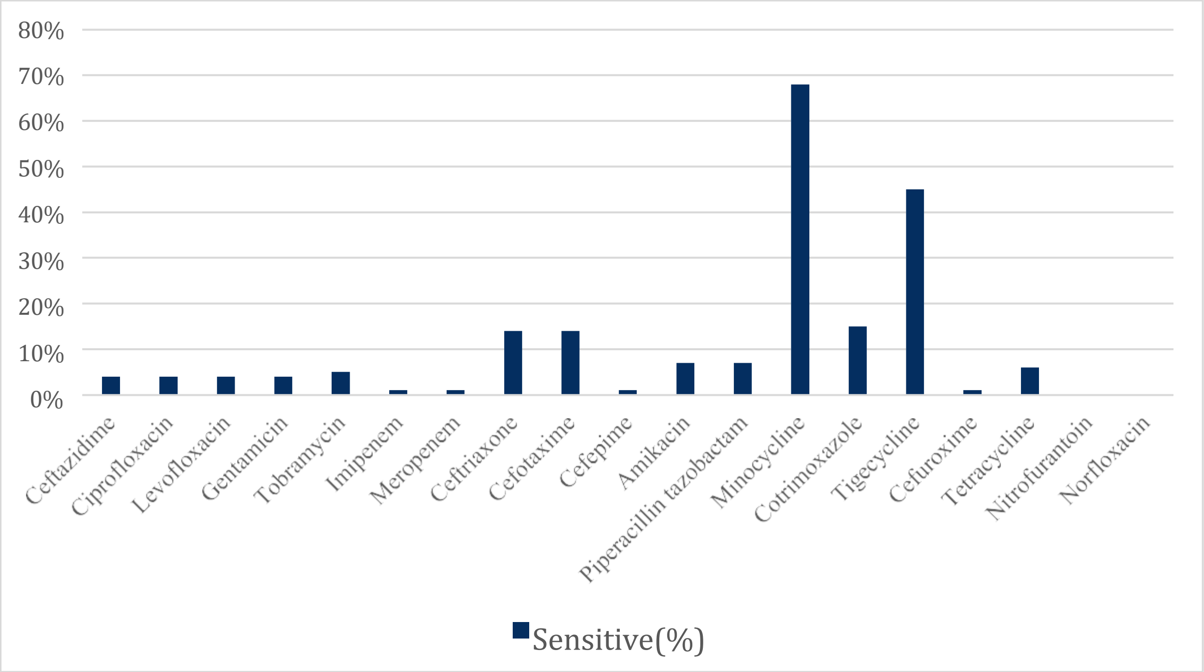


Fig6-Antibiotic sensitive pattern of *Acinetobacterspp.*(n=65)

2-*Pseudomonas aeruginosa* Aminoglycosides (Amikacin, Gentamicin, Tobramycin) were found to be highly effective(79%,75%,75%) followed by Carbapenems (meropenem, imipenem) (75%) Cefepime (75%) and flouroquinolones (Ciprofloxacin, Levofloxacin) (60%) respectively. whereas, Piperacillin-tazobactum was least effective (53%).

Nitrofurantoin and Norfloxacin showed resistant to all the isolates of *Pseudomonas aeruginosa* in urinary tract infection.

Antibiotics	Sensitivity(%)	Resistance(%)
Ceftazidime	58%	42%
Gentamicin	75%	25%
Tobramycin	75%	25%
Piperacillin-tazobactum	53%	47%
Cefepime	75%	25%
Ciprofloxacin	60%	40%

Levofloxacin	60%	40%
Amikacin	79%	21%
Imipenem	75%	25%
Meropenem	75%	25%
Aztreonem	67%	33%
Nitrofurantoin	0%	100%
Norfloxacin	0%	100%

Table 8: Antibiotic susceptibility pattern of *Pseudomonas aeruginosa*(n=28)

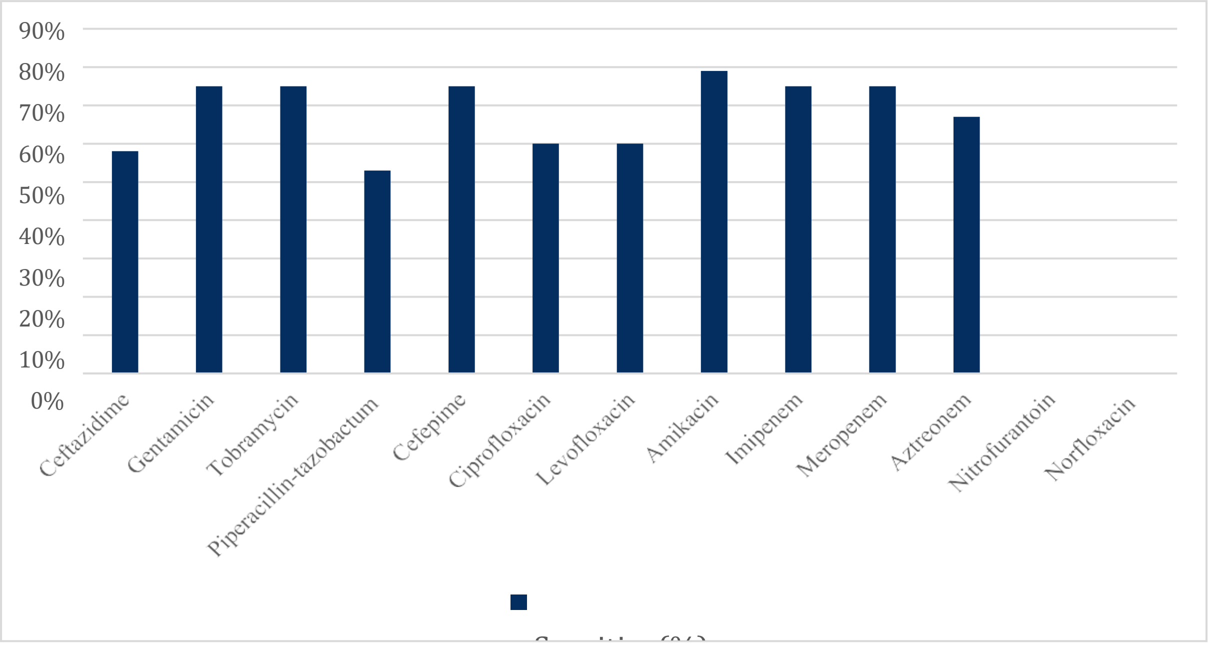


Fig7-Antibiotic sensitive pattern of *Pseudomonas aeruginosa* (n=28)

Among the 285isolates,28 were as *Staphylococcusaureus*,28 as *Enterococcusspp.*and17 as *Coagulase negative Staphylococci (CoNS).*

1-*StaphylococcusaureusandCoNS*

Linezolid was found to be highly effective (95%) followed by Vancomycin (86%), Tetracycline (81%), Cotrimaxazole (68%), Gentamicin (63%) and Teicoplanin (46%) whereas, Penicillin was least effective (15%) respectively.

Nitrofurantoin and Norfloxacin was found to be highly effective (100%) in urinary tract infections.

Fosfomycin was found to be highly effective (66%) in urinary tract infections and respiratory tract infections.

Antibiotics	Sensitivity(%)	Resistance(%)
Penicillin	15%	85%
Cefoxitin	37%	63%
Vancomycin	50%	50%
Teicoplanin	46%	54%

Linezolid	95%	5%
Gentamicin	63%	37%
Azithromycin	34%	66%
Erythromycin	28%	72%
Tetracycline	81%	19%
Ciprofloxacin	32%	68%
Levofloxacin	32%	68%
Nitrofurantoin	100%	0%
Clindamycin	28%	72%
Cotrimaxazole	68%	32%
Norflox	100%	0%
Fosfomycin	66%	34%

Table 9: Antibiotic susceptibility pattern of *Staphylococcus aureus*and*CoNS*(n=45)

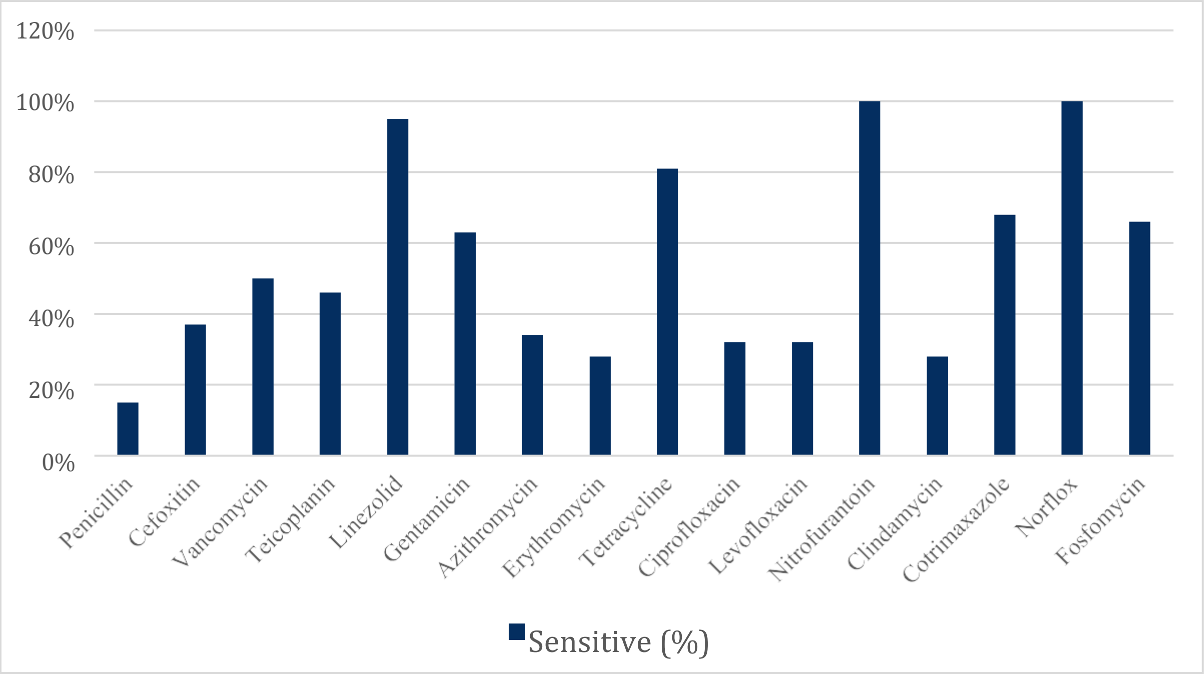


Fig8-Antibiotic sensitive pattern of *Staphylococcus aureus and CoNS*(n=45) 2-*Enterococcus spp.*

Linezolid was found to be highly effective (100%) followed by Teicoplanin (90%), Vancomycin (78%), Ampicillin (33%), High level gentamycin (15%) and High level streptomycin (15%) respectively. Erythromycin showed resistant to all the isolates of *Enterococcus spp.*

Nitrofurantoin was found to be highly effective (60%) whereas Fosfomycin was least effective (18%) respectively and Norfloxacin showed resistant to all the isolates of *Enterococcusspp* .in urinary tract infections.

Antibiotics	Sensitivity(%)	Resistance(%)
Ampicillin	33%	67%
Penicillin	15%	85%
Linezolid	100%	0%
Vancomycin	52%	48%
Highlevel gentamycin	15%	85%
Highlevel streptomycin	15%	85%
Ciprofloxacin	8%	92%
Levofloxacin	8%	92%
Fosfomycin	18%	82%
Nitrofurantoin	60%	40%
Tetracycline	9%	91%
Teicoplanin	90%	10%
Erythromycin	0%	100%
Norflox	0%	100%

Table 10: Antibiotic susceptibility pattern of *Enterococcusspp.*(n=28)

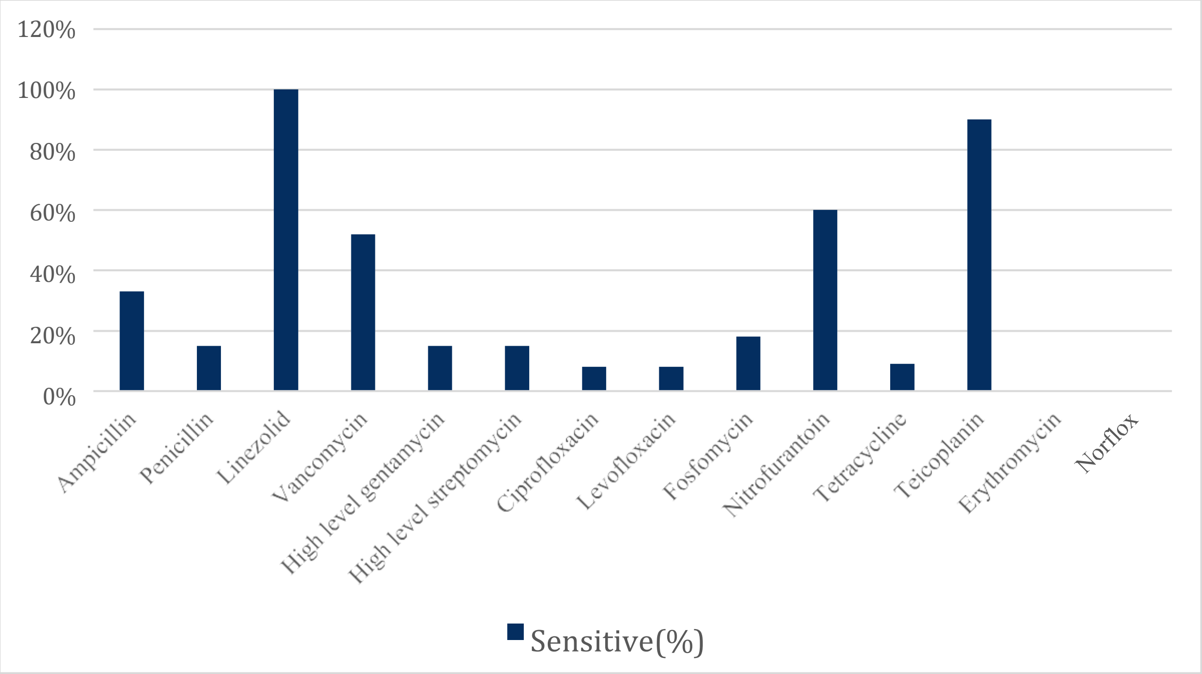


Fig9-Antibiotic sensitive pattern of *Enterococcusspp.*(n=28)

Among Gram-positive bacteria, S. aureus and coagulase-negative Staphylococci were most sensitive to linezolid (95%), vancomycin (86%), and tetracycline (81%). Enterococcus spp. demonstrated 100% susceptibility to linezolid and 90% to teicoplanin, but showed high resistance to erythromycin, ciprofloxacin, and aminoglycosides.

4. DISCUSSION

This study provides valuable insight into the bacteriological spectrum and antimicrobial susceptibility patterns among ICU patients in a tertiary care hospital. Among 2,125 samples, 285 isolates were identified, predominantly from respiratory specimens, reflecting the burden of ventilator-associated infections.

The predominance of Gram-negative organisms such as E. coli (24%), Acinetobacter spp. (23%), and Klebsiella spp. (13%) mirrors findings from other Indian ICUs [14,15]. Acinetobacter spp., in particular, has emerged as a formidable pathogen due to its capacity for biofilm formation and multidrug resistance [16]. In this study, its sensitivity was limited to minocycline (68%) and tigecycline (45%), consistent with reports by Gupta et al. (2021) and Joseph et al. (2020) [18,19].

E. coli and Klebsiella spp., the common Enterobacteriaceae, showed moderate sensitivity to carbapenems (43%) and aminoglycosides (41–42%), which is lower than earlier reports indicating 60–70% susceptibility [20,21]. A study in Tamil Nadu found similar resistance patterns, highlighting the rising incidence of ESBL and carbapenem-resistant strains [22]. Fosfomycin and nitrofurantoin maintained good activity in urinary isolates, confirming findings by Singh et al. (2022) [23].

Pseudomonas aeruginosa showed good susceptibility to amikacin and carbapenems (~75%), in agreement with studies from Kerala and Delhi [24,25]. However, resistance to fluoroquinolones and β-lactams continues to rise due to efflux pumps and β-lactamase production [26].

Among Gram-positive cocci, Staphylococcus aureus (including MRSA) showed high susceptibility to linezolid (95%) and vancomycin (86%), corroborating studies by Dey et al. (2023) and Ahmed et al. (2021) [27,28]. The high sensitivity to linezolid is promising, but vancomycin-intermediate strains necessitate ongoing surveillance [29]. Similarly, Enterococcus spp. displayed 100% sensitivity to linezolid and 90% to teicoplanin, but near-total resistance to erythromycin, reflecting trends observed in multicenter surveillance studies [30,31].

The overall high burden of MDR pathogens in this ICU study aligns with national trends indicating increasing resistance to first-line agents in critical care settings [32]. Antimicrobial stewardship programs, infection control measures, and periodic antibiograms are essential to curtail further resistance [33].

5. CONCLUSION

The study underscores a concerning prevalence of multidrug-resistant organisms in ICU settings, especially Acinetobacter spp., E. coli, and Klebsiella spp. The observed resistance to key antibiotics like carbapenems and aminoglycosides necessitates urgent attention.

Empirical treatment should be tailored based on local antibiogram data, and the use of last-resort antibiotics must be guided strictly by susceptibility testing.

6. LIMITATIONS

1. This was a single-center retrospective study, which may not be generalizable to other settings.
2. Molecular methods for resistance gene detection were not used.
3. 3Clinical outcomes of patients and infection-related mortality were not analyzed.
4. Viral, fungal, and anaerobic pathogens were not included.

7. DECLARATIONS

Conflicts of interest: There is no any conflict of interest associated with this study

Consent to participate: There is consent to participate.

Consent for publication: There is consent for the publication of this paper.

Authors' contributions: Author equally contributed the work

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