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Research Article

One-Year Retrospective Study of ICU Isolates: Epidemiology and Antibiotic Resistance Patterns

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A B S T R A C T

Background: Intensive Care Units (ICUs) are environments with high risk for nosocomial infections due to invasive procedures and critically ill patient populations. Understanding the distribution of pathogens and their antibiotic susceptibility patterns is vital for effective infection control and therapeutic strategies.

Aim: This study aimed to analyze the distribution of bacterial isolates across various ICUs and assess their antimicrobial resistance and susceptibility patterns.

Methods: This retrospective study was performed on 496 culture-positive clinical samples collected from six ICUs within the tertiary care hospital. The isolates were characterized and tested for antimicrobial susceptibility using standard conventional methods.

Results: The majority of culture-positive samples originated from the general ICU (83%), followed by the Cardio Thoracic ICU (8%) and CATH ICU (7%). Gram-negative bacilli (70%) were predominant, with *Klebsiella spp.* (22%) and *Escherichia coli* (18.5%) being the frequently isolated organisms. Among Gram-positives, Staphylococcus(13.3%) and *Enterococcus spp.* (8.1%) were common. Meropenem, imipenem, and piperacillin-tazobactam showed higher efficacy against Gram-negative bacterial isolates. *Vancomycin, linezolid,* and Teicoplanin demonstrated high efficacy against Gram-positive isolates. Alarmingly, high resistance was noted to ampicillin, polymyxins, and certain cephalosporins. *Acinetobacter spp*. in ET aspirates exhibited pan-resistance.

Conclusion: The predominance of multidrug-resistant Gram-negative organisms, particularly in the general ICU, underscores the need for stringent infection control measures and periodic surveillance of antimicrobial resistance. Tailored antibiotic policies and effective stewardship programs are crucial for curbing ICU-acquired infections.

Keywords: ICU Infections, Antimicrobial Resistance, Retrospective Analysis, General ICU, Antibiotic Susceptibility.

Introduction

Antibiotics have long been the foundation of contemporary medical practice. However, the emergence of antibiotic resistance in close pursuit has become a significant global public health concern, posing a serious threat to humanity.[1] Bacterial infections frequently lead to hospital admissions, with nosocomial infections being particularly prevalent in critical care units. The growing resistance to antibiotics, coupled with limited therapeutic alternatives, has created substantial challenges in managing bacterial infections worldwide.[2] Infections contracted within intensive care units (ICUs) are often linked to high rates of morbidity and mortality. The distribution of common pathogens in ICU settings varies across different regions, with international reports indicating that up to 36% of isolates from certain ICUs exhibit multidrug resistance.[3] This variation is crucial when considering empirical antibiotic therapy in these settings. Nosocomial infection rates among ICU patients range from 5% to 30%, with the likelihood of infection increasing due to factors such as the severity of illness, prolonged use of invasive medical devices and procedures, frequent interactions with healthcare personnel, and extended hospital stays.[4] Over the past 15 to 20 years, infection control strategies and advancements in antimicrobial therapy have primarily focused on combating gram-positive bacterial infections. However, there has been a recent surge in ICU-associated infections caused by GNB.[5] Many ICUs face a heightened risk from ESBL (extended-spectrum beta-lactamase)-producing Enterobacterales and MRSA (methicillin-resistant *Staphylococcus aureus*), while VRE (vancomycin-resistant enterococci) are classified as a medium-level concern.[6,7] Given these challenges, our study aims to analyze the distribution of bacterial pathogens in ICU settings, evaluate their antibiotic resistance patterns, and identify key trends in antimicrobial susceptibility. By understanding these resistance profiles, we seek to provide valuable insights that can aid in the development of more effective infection control strategies and empirical treatment protocols for critically ill patients.

Materials and Methods

Study Design and Setting: This retrospective observational study analyzed all the ICU samples showing positive growth, over one year, from January to December 2024, at Chettinad Hospital and Research Institute, Kelambakkam. This study specifically included only culture-positive bacterial isolates (n=496) obtained from ICU patients during the study period. As the objective was to analyze pathogen distribution and antimicrobial susceptibility patterns, culture-negative samples were not included in the analysis. IHEC clearance was obtained before commencing this retrospective analysis. The overall workflow of positive bacterial isolate details, their distribution, and microbiological analysis is illustrated in Figure 1.

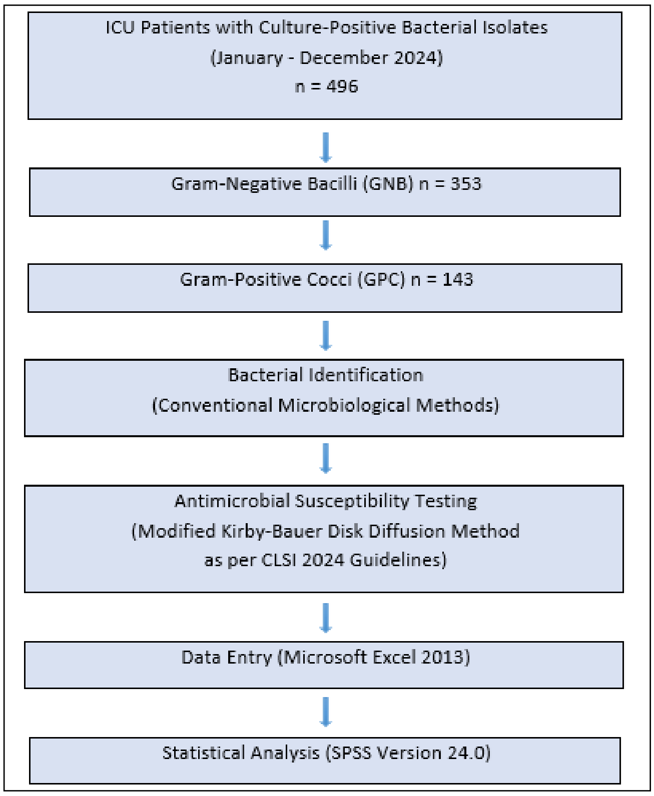

Figure 1.CONSORT Flow Diagram of Culture-Positive ICU Isolates

Inclusion and Exclusion Criteria

All patients who were admitted to the ICU between January and December 2024 with culture-confirmed bacterial infections, provided they had at least one positive microbial culture (from blood, urine, respiratory samples, or other sites) and valid antibiotic susceptibility testing (AST) results. Patients without any cultures sent during their ICU stay were excluded, along with duplicate isolates (only the first episode per patient was considered unless a new infection was suspected). Fungal or viral isolates were not analyzed, and cases with incomplete or missing microbiological data (e.g., unidentified species or unresolved AST reports) were also excluded to maintain data reliability.

Data Collection

Data were retrieved from the Medical Records Department (MRD), including both microbial culture reports (identifying bacterial strains up to the species level) and their antibiotic sensitivity and resistance patterns. In some cases, multiple

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culture samples were obtained from different anatomical sites (e.g., blood, urine, respiratory secretions) based on clinical suspicion of infection.

Microbiological Methods

Bacterial identification was performed using conventional microbiological techniques. The modified Kirby-Bauer disk diffusion method was employed for AST as per the CLSI 2024 guidelines.

Statistical Analysis

This data was analyzed using descriptive and inferential statistics to characterize antibiotic resistance patterns. The collected data for each isolate were entered into an MS Excel spreadsheet (Microsoft Office Professional 2013), and analysis was performed using SPSS software, version 24.0.

Ethical Considerations

Since this was a retrospective study, patient confidentiality was maintained, and ethical approval was obtained from the CARE (IHEC-II/0852/2).

Results

A total of 496 bacterial isolates were obtained from ICU patients, with a clear predominance of GNB (353 isolates) over GPC (143 isolates). The largest number of isolates was observed in patients aged above 61 years (n=248), followed by those in the 46-60 -year age group (n=138). In contrast, very few isolates were recovered from younger age groups, particularly those aged <1 year (n=9) and 1 to 15 years (n=1). GNB were consistently more prevalent than GPC across all age categories. Regarding gender distribution, male patients showed a higher number of isolates (n=328), including 96 GPC and 232 GNB, compared to female patients (n=168), with 55 GPC and 113 GNB. Overall, GNB were the predominant organisms isolated in both age and gender categories. The details are illustrated in Table 1.

Distribution of isolates across ICU wards

Among the 496 culture-positive patients analyzed, the majority had been admitted to the general ICU (83%, n=410) with isolates. The remaining cases were distributed across cardio-thoracic ICU (8%, n=38), CATH ICU (7%, n=34), and NICU Ward (2%, n=9), with minimal representation from CT Step-down ICU (1%, n=4) and ICCU general (0.2%, n=1), which was illustrated in Table 2.

Specimen distribution across ICU wards

Out of the total 496 clinical specimens analyzed, the highest number was collected from the general ICU, accounting for 410 samples (82.6%), indicating a higher infection burden or diagnostic demand in this unit. This was followed by 38 samples (7.7%) from the cardio-thoracic ICU, 34 samples (6.9%) from the CATH ICU, 9 samples (1.8%) from the NICU ward, and the least, 4 samples (0.8%), from the CT Step-down ICU. The details are shown in Table 3.

Gram-negative bacilli (GNB) predominated (70%, n=341). Among the total 496 isolates, *Klebsiella* species was the most predominant organism, accounting for 109 isolates (22.0%), followed by *Escherichia* coli with 92 (18.5%) and Staphylococcus with 66 (13.3%). Other frequently encountered pathogens included *Acinetobacter* species (52, 10.5%), *Enterococcus* species (40, 8.1%), and *Pseudomonas aeruginosa* (23, 4.6%). Isolates such as *Pantoea spp*., *Ralstonia mannitolilytica*, *Stenotrophomonas maltophilia*, and *Haemophilus influenzae* were among the least represented, each contributing less than 1% of the total. Most of these pathogens were isolated from the general ICU, indicating a broader microbial spectrum in this unit compared to other ICU wards. The details are shown in Table 4.

Distribution of Bacterial Isolates from Clinical Samples

Out of a total of 496 clinical isolates, 143 were recovered from blood samples. Among these, 86 were identified as GPC and 57 as GNB. The most frequently isolated GPC from blood were *coagulase-negative staphylococci* (CoNS) (n = 61), followed by *Enterococcus spp*. (n = 9) and *Staphylococcus aureus* (n = 9). Among the GNB isolates, *Klebsiella spp*. (n = 14) and *Escherichia coli* (n = 13) were the predominant organisms. Out of 125 bacterial isolates obtained from urine samples, 19 were identified as GPC and 106 as GNB. Among the GPC, *Enterococcus spp*. was the predominant organism, accounting for 17 isolates. Among the GNB, *Escherichia coli* (n = 53) and *Klebsiella spp*. (n = 27) were the most commonly isolated organisms. Out of 105 bacterial isolates recovered from respiratory specimens, 12 were identified as GPC and 93 as GNB. Among the GPC, *Staphylococcus aureus* predominated (n = 9). Within the GNB, *Klebsiella spp*. were most frequently isolated (n = 42), followed by *Acinetobacter spp*. (n = 21) and *Escherichia coli* (n = 12). Out of 123 positive exudate samples, 34 isolates were GPC and 89 were GNB. Among the GPC, *Enterococcus spp*. was the most frequently isolated organism (n = 13), followed by *Staphylococcus aureus* (n = 8) and *Streptococcus spp*. (n = 6). Among the GNB, *Klebsiella spp*. accounted for the highest number of isolates (n = 27), followed by *Acinetobacter spp*. (n = 17) and *Escherichia coli* (n = 15). All the details are illustrated in Table 5.

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Table 1.Analysis of age and sex-wise distribution of organisms isolated from the patients admitted to the ICU

	Categories	GPC	GNB	Total
Age distribution	>1	1	8	9
	1-15	0	1	1
	16-30	10	35	45
	31-45	20	35	55
	46-60	37	101	138
	>61	83	165	248
Gender	Male	96	232	328
	Female	55	113	168

Table 2.Distribution across ICU wards

S.No	ICU Name	Total	Percentage
1	Cardio Thoracic ICU	38	8%
2	CATH ICU	34	7%
3	CT STEP DOWN ICU	4	1%
4	GENERAL ICU	410	83%
5	ICCU GENERAL	1	0%
6	NICU WARD	9	2%
	Grand total	496	100%

Table 3.Specimen distribution across different ICUs

Name of the ICU	BLOOD	BODY FLUID	BAL	CVC TIP	EAR SWAB	ET /S	Plural Fluid	PUS C/S	SPUTUM	SYNOVIAL FLUID	THROAT SWAB	TISSUE BIT	URINE	WOUND SWAB C/S	Grand Total
Cardio Thoracic ICU	6	0	1	0	0	3	0	0	4	0	0	1	11	12	38
CATH ICU	5	0	0	0	0	5	0	0	0	0	1	1	18	4	34
CT STEP DOWN ICU	2	0	0	0	0	2	0	0	0	0	0	0	0	0	4
GENERAL ICU	123	1	0	2	1	64	3	4	25	1	0	16	94	76	410
ICCU GENERAL	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1
NICU WARD	7	0	0	0	0	0	0	0	0	0	0	0	1	1	9
Grand Total	143	1	1	2	1	74	3	4	29	1	1	18	125	93	496

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Table 4.Distribution of bacterial species

Name of the Organism	CT ICU	CATH ICU	CT Step Down ICU	GICU	ICCU General	NICU Ward	Grand Total	Percentage
Acinetobacter species	4	2	-	46	-	-	52	10.48 %
Acinetobacter baumannii complex	-	-	-	1	-	1	2	0.40 %
Burkholderia pseudomallei	-	-	-	2	-	-	2	0.40 %
Citrobacter species	-	2	-	11	-	-	13	2.62 %
CoNS	4	4	-	57	-	1	66	13.31 %
Enterobacter species	-	1	-	8	-	-	9	1.81 %
Enterococcus species	5	4	-	31	-	-	40	8.06 %
Escherichia coli	6	7	-	78	1	-	92	18.55 %
Flavobacterium meningosepticum	-	-	1	1	-	-	2	0.40 %
Haemophilus influenza	-	-	-	1	-	-	1	0.20 %
Klebsiella species	7	6	1	92	-	3	109	21.98 %
Morganella morganii	-	-	-	2	-	-	2	0.40 %
Proteus species	1	1	-	8	-	-	10	2.02 %
Providencia species	-	-	-	1	-	-	1	0.20 %
Pantoea spp.	-	-	-	-	-	2	2	0.40 %
Pseudomonas aeruginosa	1	3	-	18	-	1	23	4.64 %
Pseudomonas species	4	-	-	16	-	-	20	4.03 %
Ralstonia mannitolilytica	-	-	-	1	-	-	1	0.20 %
Staphylococcus aureus	3	3	-	24	-	1	31	6.25 %
Stenotrophomonas maltophilia	1	-	-	-	-	-	1	0.20 %
Streptococcus pneumoniae	-	-	-	2	-	-	2	0.40 %
Streptococcus species	2	1	2	10	-	-	15	3.02 %
Total	38	34	4	410	1	9	496	100 %

Table 5.Distribution of Bacterial Isolates from different clinical Samples (n=496)

Sample Type	Total Isolates	GPC (n)	Common GPC (n)	GNB (n)	Common GNB (n)
Blood	143	86	*CoNS (61), Enterococcus spp. (9), S. aureus (9)*	57	*Klebsiella spp. (14), E. coli (13)*
Urine	125	19	*Enterococcus spp. (17)*	106	*E. coli (53), Klebsiella spp. (27)*
Respiratory	105	12	*S. aureus (9)*	93	*Klebsiella spp. (42), Acinetobacter spp. (21), E. coli (12)*
Exudate	123	34	*Enterococcus spp. (13), S. aureus (8), Streptococcus spp. (6)*	89	*Klebsiella spp. (27), Acinetobacter spp. (17), E. coli (15)*

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Antibiotics with significant sensitivity patterns

Among the *Escherichia coli* and *Klebsiella spp*. isolated from blood samples, the highest antibiotic efficacy was observed with tigecycline, which was estimated as 100% and 66.7%, followed by tobramycin, which showed good efficacy against *E. coli* (96.3%), and 82.6% against *Klebsiella spp*.; carbapenem classes of imipenem showed efficacy of 91.5% and 65.2% efficacy against *E.coli* and *Klebsiella spp*., and meropenem showed efficacy of 93.2% against E.coli and 66.0% against *Klebsiella spp*. Among the GPC isolated from blood samples, the highest antibiotic efficacy was observed with linezolid (100% sensitivity in *Staphylococcus aureus*, 100% in CoNS, and 95.5% in *Enterococcus spp*.), followed closely by vancomycin (100% for *S. aureus*, 99.4% for CoNS, and 83.3% for *Enterococcus spp*.) and teicoplanin (100% for *S. aureus*, 97.8% for CoNS, and 87.5% for *Enterococcus spp*.). Additionally, meropenem, imipenem, and piperacillin-tazobactam showed 100% sensitivity against *S. aureus*.

Among the urine isolates, *Escherichia coli* and *Klebsiella* species were the most highly isolated GNB, which exhibited the highest sensitivity to tetracycline and tobramycin, with both species showing 100% sensitivity. The most commonly isolated GPC from urine samples, *Enterococcus species* and *Staphylococcus aureus*, showed the highest efficacy to linezolid, which was estimated as 99.4% and 100%, followed by teicoplanin, which showed 99.1% efficacy against *Enterococcus spp*. and 100% efficacy against vancomycin, indicating that these antibiotics remain highly effective treatment options for GPC-related urinary tract infections.

Among the respiratory isolates, *Acinetobacter* species showed the highest sensitivity to minocycline (100%), followed by piperacillin-tazobactam (90%) and meropenem and tobramycin (88%). *Escherichia coli* exhibited maximum efficacy against imipenem and meropenem (99%) and tobramycin (98%). *Klebsiella species* were most effective to tigecycline (100%), imipenem/meropenem (93%), and gentamicin/tobramycin (90%). Among the *Staphylococcus aureus* isolates from respiratory samples, the highest antibiotic sensitivity was observed with multiple agents, including cefepime, cefotaxime, imipenem, linezolid, meropenem, piperacillin-tazobactam, teicoplanin, tobramycin, and vancomycin, all showing 100% efficacy.

Among the tested antibiotics against exudate isolates, *Klebsiella species* showed the highest sensitivity to tigecycline (100%), followed by meropenem (66%), and *Acinetobacter species* demonstrated the greatest susceptibility to tobramycin (48%) and meropenem (46%), though overall sensitivity was relatively low, suggesting limited treatment choices. *E. coli* exhibited the highest sensitivity to meropenem (83%) and imipenem (79%), highlighting carbapenems as the most potent antibiotics against this pathogen. Among GPC samples, *Enterococcus spp*. showed the highest efficacy to azithromycin and gentamicin (100%), followed by teicoplanin and vancomycin (98%). *S. aureus* was 100% sensitive to cefotaxime, chloramphenicol, oxacillin, teicoplanin, and vancomycin. *Streptococcus spp*. showed 100% efficacy to azithromycin and gentamicin (HL), with high response to cefazolin (99%) and penicillin, vancomycin (98%).

Discussion

This study was carried out to assess the common etiological agents and their antibiotic sensitivity patterns isolated from ICU samples. In this study, 496 clinical isolates from different ICU settings were analyzed.

Our study revealed a significant age-related variation in the distribution of bacterial isolates among ICU patients. The highest number of isolates was observed in patients aged above 61 years (n=248), followed by those in the 46-60-year age group (n=138). Furthermore, a study conducted by da Silva et al., in Brazil, reported that GNB accounted for 64.9% of the total isolates, with *Klebsiella pneumoniae* being the most common pathogen. The study also noted that older patients had a higher incidence of bloodstream infections caused by GNB, which is in line with our finding of a higher number of isolates in patients aged above 61 years.[8]

In our study, male patients showed a higher number of isolates (328) compared to female patients (168), with 96 Gram-positive cocci (GPC) and 232 Gram-negative bacilli (GNB) from males, and 55 GPC and 113 GNB from females. Overall, GNB were the predominant organisms isolated in both age and gender categories. These findings are consistent with a study by Ibrahim ME, who observed that GNB were the most commonly isolated pathogens in ICU patients, with a male predominance. (9)In our study, the general ICU accounted for the highest proportion of positive culture samples (83%), followed by the cardiothoracic ICU (8%), CATH ICU (7%), NICU (2%), and CT Step-down ICU (1%). This high prevalence in the general ICU may be attributed to the greater patient load, higher frequency of invasive procedures, prolonged hospital stays, and the presence of critically ill individuals requiring mechanical ventilation and indwelling devices, all of which are known risk factors for hospital-acquired infections. Our findings are in agreement with those of Vincent et al., who reported a significantly higher rate of nosocomial infections in general and medical ICUs compared to specialized units due to similar risk factors and patient demographics.[8] A similar pattern was observed in a study by Rosenthal et al., where device-associated infection rates were highest in general ICUs across multiple countries in the INICC surveillance data.[9] In our study, the distribution of clinical specimens across ICU wards showed a predominance in the General ICU, which accounted for 410 (82.6%) of the total 496 specimens. Within this ICU,

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the most frequently collected samples were blood 123 (24.8%), ET aspirates 64 (12.9%), urine 94 (18.9%), and wound swabs 76 (15.3%), suggesting a high incidence of bloodstream, respiratory, urinary, and wound-related infections in critically ill patients. These findings are in line with the report by Alp et al. (2011), who observed that respiratory tract infections, catheter-associated urinary tract infections, and bloodstream infections were the most common ICU-acquired infections, often associated with mechanical ventilation and invasive procedures.[10] Contrary to our findings, Sohn et al. (2001) reported that NICUs often experience high rates of bloodstream infections, primarily due to the vulnerability of neonates and frequent use of central lines.[11] This discrepancy might reflect differences in sample collection practices, patient volume, or infection control protocols between institutions.

Our study revealed that *Klebsiella species* (21.98%), *Escherichia coli* (18.5%), and *CoNS* (13.31%) were the most common pathogens isolated from ICU patients, with the highest number of isolates obtained from the General ICU. These findings are similar to earlier reports by Moolchandani et al.[12,] who observed that *E. coli* and *Klebsiella spp*. were the most frequently isolated gram-negative organisms in ICU settings in India, often linked with ventilator-associated pneumonia and urinary tract infections. In our study, blood isolates from ICU patients demonstrated that *Escherichia coli* and *Klebsiella spp*. exhibited notable susceptibility to several antibiotics. A study conducted by Manoharan et al. on evaluating tigecycline activity in clinical isolates among Indian patients found that tigecycline had good activity against tested *E. coli* and *Klebsiella spp*.[14]

In the present study, linezolid demonstrated the highest efficacy against GPC isolated from blood cultures, showing 100% sensitivity in *Staphylococcus aureus*. This was closely followed by vancomycin, which also showed 100% efficacy against *S. aureus*, 99.4%. Teicoplanin exhibited similarly high sensitivity, 100% in *S. aureus*. Similar to our findings, Shas et al. stated that *S. aureus* showed 100% efficacy against tigecycline, teicoplanin, linezolid, and vancomycin.[15] Among the GPC isolated from blood samples, the highest antibiotic efficacy was observed with Linezolid (100% in CoNS and 95.5% in *Enterococcus spp*.), followed closely by vancomycin (99.4% for CoNS and 83.3% for *Enterococcus spp*.), and teicoplanin 97.8% for CoNS and 87.5% for *Enterococcus spp*. Similar to our findings, Nikita Vasudeva et al. reported 100% sensitivity of linezolid, vancomycin, and teicoplanin against *CoNS* and *Enterococcus spp*. from bloodstream infections.[16]

In urine isolates, out of 125, the highest number of isolates were identified as GNB, which is 106, and the common strains are *E. coli*, followed by *Klebsiella spp*., which are estimated as 53 and 27. And 17 out of 19 GPC in urine samples were identified as *Enterococcus spp*. Tobramycin demonstrated 100% efficacy against both *Escherichia coli* and *Klebsiella spp*. in our urine isolates, followed by meropenem, which showed high efficacy with sensitivity rates of 82.2% for *E. coli* and 92.8% for *Klebsiella spp*. These findings are consistent with those reported by Shas et al., who observed 100% susceptibility of urinary *E. coli* isolates to both tobramycin and meropenem.[15] Similarly, a recent study by Worku et al. (2024) reported that *Klebsiella spp*. demonstrated notable sensitivity to tobramycin (67.9%) and meropenem (79%) in urinary isolates.[17] *Enterococcus spp*. showed significant efficacy against linezolid (99.4% sensitive), followed by teicoplanin, which showed an efficacy of 99.1. This study was supported by a recent study conducted by Ferede et al. (2024), reported that linezolid and teicoplanin showed maximum efficacy against *Enterococcus spp*. isolated from clinical samples.[18]

In respiratory isolates, out of 105 bacteria, the highest number of them were found to be GNB.[93] followed by GPC.[12] In GNB isolates, *Klebsiella spp*. was the most predominant one.[42] followed by *Acinetobacter spp*. and *E. coli*, which were estimated as 21 and 12. And in GPC, 9 out of 12 were identified as *S. aureus*. Tobramycin showed 75% efficacy against *Klebsiella spp*. In contrast to our findings, More et al. (in 2020) showed that a high resistance percentage was observed from *Klebsiella spp*., which was isolated from respiratory samples, indicating significant changes in antibiotic profiles across different regions and geographical locations.[19] Imipenem and tobramycin showed 100% efficacy against all isolated *E. coli*. This is supported by findings from a study conducted by Mai et al., which reported that imipenem showed the highest sensitivity against *E. coli* isolates (0% resistance), followed by tobramycin, which exhibited a resistance rate of 21.4%, thereby confirming the effectiveness of these antibiotics in managing such infections.[20] Notably, *Acinetobacter spp*. showed 100% resistance against all the antibiotics. Similar to our findings, Kaur et al. reported that Acinetobacter showed high resistance against different classes of antibiotics, including cephalosporins, fluoroquinolones, and aminoglycosides.[21] In GPC, linezolid, Teicoplanin, and vancomycin showed 100% efficacy against *S. aureus*. These findings are similar to a recent study conducted by Gaire et al. (2024), who also reported 100% sensitivity to linezolid, teicoplanin, and vancomycin against *S. aureus* infections from respiratory sources.[22]

In the overall exudate culture-positive samples (123), the highest number of them were identified as GNB, which was estimated as 89. Out of the 89 highest isolates *Klebsiella spp*. was followed by *Acinetobacter spp*. and *E. coli*, which were further estimated as 21, 17, and 15. In GPC, out of 34, the most common of them was *Enterococcus spp*. (13), followed by *S. aureus*.[8] and *Streptococcus spp*.*6* Overall, isolates of

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E. coli showed good sensitivity against meropenem (87%), followed by tobramycin (81%). Similar to our findings, Naqid stated that the highest sensitivity was observed to imipenem (96.1% sensitive), followed by tobramycin (61.1% sensitive) in various clinical isolates.[23] In this present study, *Klebsiella spp*. isolated from exudate samples showed high efficacy against ceftriaxone 100%. However, Bushra et al., in 2016, reported a significantly lower sensitivity rate of 65% against clinically isolated *Klebsiella*, which indicates variability in different antibiotic susceptibility patterns across different settings and indicates the need for continuous antimicrobial monitoring surveillance.[24] In GPC, inezolid showed 100% efficacy against *Enterococcus spp., S. aureus*, and *Streptococcus spp*. Similar to our findings, Jones (2001) reported 100% efficacy of *S. aureus, Streptococcus spp*., and *Enterococcus spp*., which were reported as 100%, 99.4%, and 96% respectively.[25]

Conclusion:

This one-year retrospective analysis highlights the significant burden of ICU-acquired infections, with the General ICU demonstrating the highest incidence of multidrug-resistant organisms. The predominance of *Klebsiella spp., Escherichia coli* and *CoNS* reflects the evolving microbial landscape in critically ill patients. Although carbapenem and glycopeptide remain effective against several major pathogens, the emergence of resistance to first-line antibiotics and the observation of polymyxin resistance and pan-drug resistance in *Acinetobacter spp*. raise serious public health concerns. These findings underscore the urgent need for strengthened antibiotic stewardship programs, rational empirical therapy based on local antibiograms, and strict infection prevention and control practices within ICU settings. Furthermore, continuous regional AMR surveillance is essential to monitor evolving resistance trends and to guide evidence-based policy decisions aimed at mitigating the growing threat of multidrug-resistant infections.

Conflict of Interest: None

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