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ORIGINAL ARTICLE

Combating Antimicrobial Resistance in ICU-Related CAUTIs: Insights and Strategies" (A Cross Sectional Study)

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ABSTRACT

Keyword: Catheter-associated urinary tract infections, Antimicrobial resistance, Multidrug-resistant pathogens, ICU infections, Carbapenems, Amikacin, Therapeutic strategies

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Background and Objective: Catheter-associated urinary tract infections (CAUTIs) are a major source of morbidity in ICU patients, with antimicrobial resistance (AMR) complicating treatment. This study assesses resistance patterns and therapeutic options for CAUTIs in ICU patients at Aswan University Hospital. M**ethodology:** A total of 200 ICU patients with indwelling Foley catheters were included between June 2023 and June 2024. Urine samples were collected 48 hours post-catheterization under sterile conditions. Samples (10–20 cc) were processed for Gram staining and culture, with incubation at 37 °C for 18–24 hours. Antimicrobial susceptibility was tested using the Kirby-Bauer disc diffusion method per CLSI guidelines. **Results:** Gram-negative isolates showed high resistance to ampicillin, amoxicillin-clavulanic acid, and cephalosporins. Carbapenems and amikacin were the most effective antibiotics. Predominant pathogens included multidrug-resistant (MDR) Klebsiella spp. and E. coli. Most Gram-negative isolates were classified as MDR. Additionally, *E. coli* and *Klebsiella spp*. were more frequently isolated in patients with hypertension and diabetes, indicating a potential association with these comorbidities. **Conclusion:** The high prevalence of MDR organisms in CAUTIs highlights the urgent need for antimicrobial stewardship, routine resistance monitoring, and new therapeutic approaches to improve infection control in ICU settings.

INTRODUCTION

Catheter-associated urinary tract infections (CAUTIs) are a leading healthcare-associated infection globally, particularly in intensive care units (ICUs). These infections account for a significant proportion of hospital-acquired complications, often resulting in prolonged hospital stays and increased morbidity and mortality. The widespread emergence of antimicrobial resistance (AMR) among CAUTI pathogens exacerbates the challenge, limiting treatment options and increasing healthcare costs.(1)

In medical literature, the terms "multidrug-resistant" (MDR), "extensively drug-resistant" (XDR), and "pan drug-resistant" (PDR) are commonly used to describe the various resistance patterns seen in AMR bacteria. XDR was defined as non-susceptibility to at least one agent in all but two or fewer antimicrobial categories (i.e., bacterial isolates remain susceptible to only one or two categories), PDR as non-susceptibility to all agents in all antimicrobial categories, and MDR as acquired non-susceptibility to at least one agent in three or more antimicrobial categories.(2) The risk factors for UTIs caused by multidrug resistant organisms (MDROs) can be divided into two categories: individual variables, such as a history of UTIs, a diagnosis of dementia or malfunction, diabetes mellitus (DM), and prostate illness, and demographic factors, such as age and female sex. Urinary catheter use is one risk factor, as is previous hospitalization, residing in a nursing home, and prior antibiotic treatment.

Few research are available to assess the endemic antimicrobial resistance profile in low- and middle-income countries, despite the fact that numerous reports have shown the incidence and resistance patterns of numerous diseases(3).As a result, empirical antimicrobial therapy and the treatment of particular diseases are thought to require evidence-based understanding of the local pattern of antibiotic resistance.(4)

ICU patients are particularly vulnerable to CAUTIs due to factors such as extended catheterization periods, immunosuppression, and exposure to broad-spectrum antibiotics (5). Understanding pathogen resistance patterns and tailoring therapeutic approaches is critical to improving outcomes. This study aims to investigate the antimicrobial resistance profiles of CAUTI pathogens and update he antibiogram in Aswan University Hospital.

PATIENTS AND METHODS

Study Design

This prospective observational study was conducted at Aswan University Hospital between June 2023 and June 2024. Data collected from patients' records included: demographic data, diagnosis on admission, history of chronic diseases, duration of hospital stay, insertion of a urinary catheter and duration of the catheter in days.

Patients >18 years of age, having at least two calendar days of urinary catheterization after being admitted to the intensive care unit, and giving informed written consent was included in the study.

The exclusion criteria for this study include patients who are not catheterized, those younger than 18 or older than 70, pregnant women, and patients undergoing chemotherapy. Additionally, patients with a history of sexually transmitted diseases or those who have been on antimicrobial therapy at least 48 hours prior to catheter insertion are excluded. If more than two types of organisms are grown from a clinical sample, the sample will be considered contaminated, and such cases will also be excluded from the study.

Methods:

Sample Collection

Samples were taken based on clinical suspicion in ICU patients who had been catheterized for more than 48 hours.

Following hospital guidelines and standard operating procedures, skilled medical professionals placed sterile indwelling urethral catheters in patients using aseptic techniques to minimize the risk of introducing bacteria into the bladder. To further reduce contamination during urine sample collection, strict aseptic protocols were adhered to, including performing hand hygiene, wearing gloves, and disinfecting the catheter sampling port with 70% isopropyl alcohol prior to aspiration. Urine was collected using a sterile syringe and transferred into a sterile container. If no urine was present in the catheter tubing, it was clamped to allow accumulation before collection.

After obtaining the sample, the tubing was unclamped, and all materials were properly disposed of. Samples were promptly transported to the laboratory or refrigerated if there was a delay. These procedures, in line with CDC and NICE guidelines[6], ensure sample sterility, reduce contamination risk, and enhance diagnostic accuracy.

In patients with short-term catheterization (<7 days), urine specimens were obtained via the catheter port using aseptic technique or, if no port was present, by puncturing the catheter tubing with a needle and syringe after clamping. For patients with long-term catheterization (>7 days), fresh catheter replacement was performed before urine collection.

Laboratory Analysis

• Gram Staining and Culture: Samples were subjected to Gram staining and inoculated onto culture media (Cysteine Lactose Electrolyte Deficient (CLED) agar, blood agar and MacConkey agar). Culture plates were incubated at 37 °C for 18–24 hours.

Routine methods for identifying pathogens in this study included Gram staining and biochemical reactions. In cases where biochemical results were inconclusive, the Vitek-2 compact system (Biomerieux) was utilized to ensure precise pathogen identification. However, the study primarily relied on the Kirby-Bauer disc diffusion method for antimicrobial susceptibility testing, adhering to CLSI guidelines.

The selective use of Vitek-2 in specific cases allowed the study to balance methodological rigor with practical constraints. Uniform application of automated systems could have further enhanced the reliability and accuracy of the resistance data.

• Antimicrobial Susceptibility Testing: The Kirby-Bauer disc diffusion method was used to evaluate susceptibility patterns, following Clinical Laboratory Standards Institute (CLSI) guidelines.

Each isolate's bacterial suspension was made in 0.5 milliliters of nutrient broth medium, and the turbidity was corrected to meet 0.5 McFarland standards. After dipping a sterile brush into the suspension, it was placed in the middle of the Muller Hinton agar plate and spread equally across the medium. After each isolate was seeded onto Muller Hinton agar, antibiotic discs were put on top and incubated for 24 hours at 35–37˚C. Inhibition zone (IZ) diameter was measured using a caliper and interpreted according to the Clinical and Laboratory Standards Institute (CLSI) guideline. as susceptible (S), intermediate (I), or resistant (R). *Staphylococcus aureus* (ATCC 25923), *Escherichia coli* (ATCC 25922), and *Pseudomonas aeruginosa* (ATCC 27853) were used as quality control strains (LSI2019).

Classes of antibiotics used. Antibiotic disc used in the present study were: Aminoglycosides (Gentamicin 10µg, Amikacin 10µg, Tobramycin 10µg), Cephalosporins (Cefotaxime 30µg, Ceftazidime 30µg Ceftriaxone 30µg) Nitrofurantoin (Nitrofurantoin 300µg),tetracyclines (tetracycline 30µg),Folate Pathway Inhibitors (trimethoprim- sulfamethoxazole 25µg), Penicillins (oxacillin 30µg, penicillin10µg, Ampicillin 10µg), Glycopeptides (vancomycin 30µg), Carbapenems (Imipenem 10µg, Meropenem 10µ), Fluoroquinolones(ciprofloxacin 5µg). All the antibiotics used in the study were the products of Oxoid, Basingstoke, and Hampshire, England

According to the recently updated CLSI standards[7], interpretative criteria for antibiotic susceptibility testing are revised annually to reflect current best practices.

Data management and Analysis:

Pathogen prevalence and antibiotic resistance patterns were analyzed, focusing on commonly used antibiotics and emerging multidrug-resistant organisms. Data was analyzed using SPSS statistical package (version 28).

RESULTS

Table 1: Distribution of Gram Negative and Gram Positive Organisms Isolated

Classification	Number	Percentage (%)
Gram-negative	194	96.98
Gram-positive	6	3.02

The table shows that Gram negative organisms were predominant, representing approximately 97% of the total isolates, while Gram positive organisms constituted only 3%.

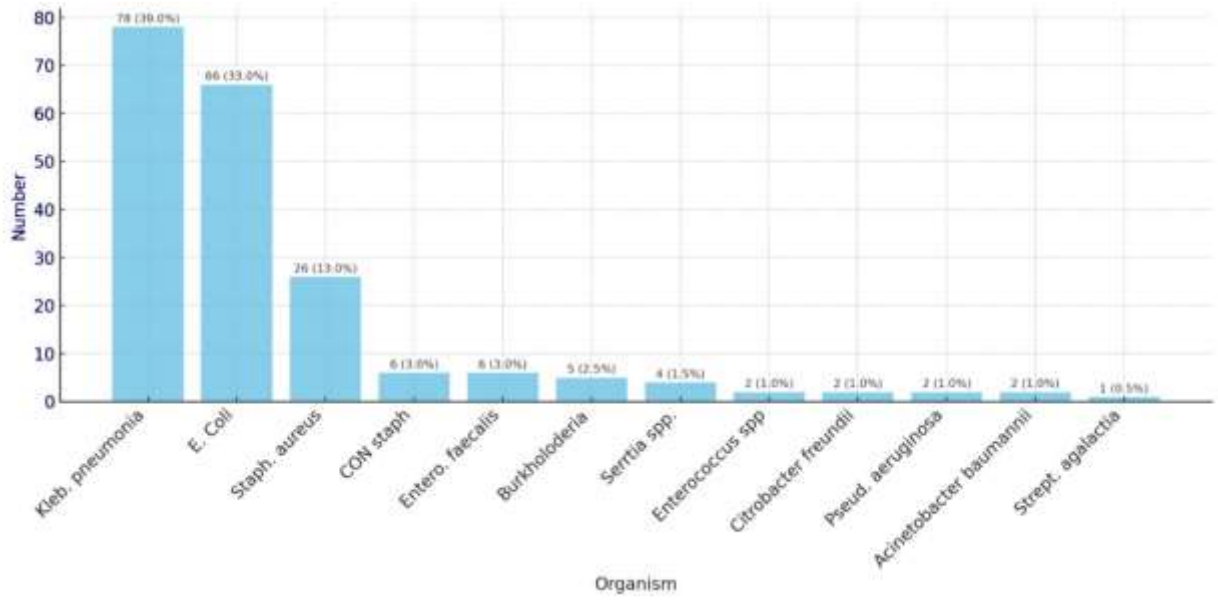

Figure 1: Bar chart showing Distribution of Clinical Bacterial Isolates

Note: *Klebsiella pneumoniae* was the most commonly isolated organism, representing 78 cases (39.0%) of the total isolates. In contrast, *Streptococcus agalactiae* was the least frequent, identified in only 1 case (0.5%).

Table 2: Antimicrobial Susceptibility and Resistance Distribution Across Major Bacterial Isolates and Antibiotics

All values reflect categorical interpretations (Sensitive (S)/Resistent (R)) based on standard clinical breakpoints (e.g., CLSI guidelines).

Antimicrobial Agents	**S/ R**	**Total No.(%)**	***E.coli No.(%)***	***Kleb.pneumoniae No.(%)***	***Staph.aureus No.(%)***	***Enterococcus spp. No.(%)***	***Serratia spp. No.(%)***	***Citrobacter freundii No.(%)***	***Pseud. aeruginosa No.(%)***
Amikacin	S	110 (69%)	50 (90%)	35 (60%)	7 (58%)	5 (63%)	4 (67%)	3 (75%)	2 (22%)
	R	50 (31%)	6 (10%)	23 (40%)	5 (42%)	3 (37%)	2 (33%)	1 (25%)	7 (78%)
Gentamicin	S	125 (72%)	55 (93%)	40 (65%)	8 (62%)	6 (66%)	5 (71%)	4 (80%)	2 (20%)
	R	48	4	22	5	3	2	1	8

		(28%)	(7%)	(35%)	(38%)	(34%)	(29%)	(20%)	(80%)
Meropenem	S	100 (64%)	45 (85%)	30 (55%)	0 (0%)	4 (50%)	3 (75%)	3 (60%)	4 (44%)
	R	56 (36%)	8 (15%)	25 (45%)	0 (0%)	4 (50%)	1 (25%)	2 (40%)	5 (56%)
Nitrofuranto-in	S	90 (60%)	38 (79%)	30 (55%)	8 (50%)	6 (70%)	4 (57%)	2 (50%)	0 (0%)
	R	60 (40%)	10 (21%)	25 (45%)	8 (50%)	3 (30%)	3 (43%)	2 (50%)	3 (100%)
Ciprofloxacin	S	80 (50%)	30 (55%)	25 (45%)	6 (40%)	4 (44%)	3 (43%)	2 (40%)	2 (22%)
	R	80 (50%)	25 (45%)	30 (55%)	9 (60%)	5 (56%)	4 (57%)	3 (60%)	7 (78%)
TMP-SMX	S	70 (56%)	28 (60%)	22 (50%)	6 (46%)	5 (58%)	3 (60%)	3 (67%)	1 (25%)
	R	55 (44%)	19 (40%)	22 (50%)	7 (54%)	4 (42%)	2 (40%)	1 (33%)	3 (75%)
Piperacillin-Tazobactam	S	60 (53%)	25 (62%)	20 (50%)	5 (42%)	3 (50%)	2 (67%)	2 (50%)	1 (17%)
	R	53 (47%)	15 (38%)	20 (50%)	7 (58%)	3 (50%)	1 (33%)	2 (50%)	5 (83%)
Vancomycin	S	65 (67%)	-	-	35 (78%)	20 (63%)	-	-	-
	R	32 (33%)	-	-	10 (22%)	12 (37%)	-	-	-
Ceftriaxone	S	50 (41%)	20 (48%)	15 (40%)	4 (44%)	3 (50%)	2 (50%)	2 (50%)	1 (17%)
	R	72 (59%)	22 (52%)	23 (60%)	5 (56%)	3 (50%)	2 (50%)	2 (50%)	5 (83%)

The table shows high resistance rates among Gram-negative bacteria, particularly *Klebsiella pneumoniae, Citrobacter freundii, and Pseudomonas aeruginosa*, to commonly used antibiotics such as ciprofloxacin, TMP-SMX, and ceftriaxone. P. aeruginosa exhibited the highest resistance, reaching 100% for ciprofloxacin and 83% for ceftriaxone. In contrast, amikacin and meropenem showed better efficacy across most isolates, especially *E. coli and Enterococcus spp.*.

Table 3: Association of Top Comorbidities with Pathogen Distribution and Statistical Significance calculated using the Chi-square test (Fischer's exact test was applied when counts where below 5).

Note: * refer to p value with significant importance (p value < 0.05).

Organism	HTN(n/%) P-value	DM(n/%) P-value	CKD P-value
Kleb.pneumonia	30(38%) 0.03*	28(36%) 0.04*	10(13%) 0.08
E. coli	35(53%) 0.02*	20(30%) 0.05*	11(17%) 0.06
Staph.aureus	12(46%) 0.07	6(23%) 0.09	3(12%) 0.12
Enterococcus spp.	1(50%) 0.15	1(50%) 0.18	0(0%) 0.20
Pseud.aeruginosa	1(50%) 0.22	-	-

This table reveals that hypertension and diabetes are significantly associated with **Klebsiella pneumoniae** and **Escherichia coli* infections, suggesting these comorbidities may influence pathogen susceptibility patterns. Chronic kidney disease did not show significant organism-specific associations.

DISCUSSION

When it comes to health sector governance, antimicrobial stewardship is more stringent in underdeveloped nations. Antimicrobial resistance levels differ among hospital settings and geographical regions, making it difficult to assess the severity of the issue. MDR pathogen infections cause therapy to be delayed, which has a detrimental effect on the patient's health, particularly in immunocompromised patients. [8] Furthermore, one of the main causes of the development of resistance is the lack of awareness on the appropriate use of antibiotics in each community. The goal of the current study was to identify the most common diseases in our community and the patterns of antibiotic resistance they exhibit.

The data presented in Table 1 highlights a statistically significant disparity in the distribution of Gram-negative versus Gram-positive organisms isolated in the clinical setting. Gram-negative bacteria accounted for 96.98% of isolates. Compared to Gram-positive organisms, which consti-

tuted only 3.02%. This finding is similar to **Poddar et al.'s** study, reported a clear predominance of Gram-negative isolates.

The distribution pattern seen in the bar chart further emphasizes the clinical dominance of Gram-negative pathogens, particularly *Klebsiella pneumoniae* and *Escherichia coli*, which together represent over 60% of all bacterial isolates. *Klebsiella pneumoniae*, being the most prevalent organism (n = 78, 39.0%), is known for its capacity to acquire multidrug resistance and cause a broad range of infections. *E. coli* follows closely with 66 cases (33.0%), a finding consistent with its role as a common etiological agent in both community- and hospital-acquired infections. The presence of other Gram-negative organisms such as *Pseudomonas aeruginosa, Citrobacter freundii, and Acinetobacter baumannii*, although in smaller numbers, is clinically significant due to their intrinsic resistance mechanisms and association with high morbidity in hospitalized patients.

In contrast, Gram-positive organisms such as *Staphylococcus aureus* (13.0%), *coagulase-negative staphylococci* (3.0%), and *Enterococcus spp*. (3.0%) were considerably less frequent. Of note, *Streptococcus agalactiae* was detected in only one instance (0.5%), reinforcing its relatively minor role in the infection. This disparity in prevalence could be influenced by several factors, including differences in host susceptibility, hospital infection control practices, and local antibiotic prescribing patterns. The higher standard deviation observed among Gram-positive isolates also suggests greater variability and less predictability in their distribution. These findings underline the urgent need for Gram-negative-targeted infection control measures and guide empirical therapy toward coverage of the most prevalent and resistant organisms.

Additionally, **The Bereanu et al.'s** study [10] published in Antibiotics in 2024 reported that *Klebsiella pneumoniae* was the most commonly isolated microorganism in ICU patients, accounting for 38.7% of infections, followed by *Acinetobacter baumannii* (20.6%) and *Pseudomonas aeruginosa* (8.7%). Similarly, research in the Journal of Infection and Public Health identified *Acinetobacter baumannii* (30.6%), *Klebsiella pneumoniae* (27%), and *Pseudomonas aeruginosa* as the most prevalent Gram-negative bacterial species in healthcare-related infections.

According to **Ma et al.** [11] the prominence of these pathogens is particularly concerning due to their association with multidrug resistance (MDR). The ESKAPE group of pathogens—*Enterococcus faecium, Staphylococcus aureus, Klebsiella pneumoniae, Acinetobacter baumannii, Pseudomonas aeruginosa*, and *Enterobacter species*—are known for their ability to "escape" the effects of antibacterial drugs, leading to challenging treatment scenarios.

The comprehensive antimicrobial susceptibility profile table 2 demonstrated notable variability in resistance patterns among common clinical bacterial isolates. *Escherichia coli* exhibited high susceptibility to aminoglycosides such as amikacin (90%) and gentamicin (93%), as well as to carbapenems like meropenem (85%). However, resistance was more pronounced against commonly used oral agents, with ciprofloxacin and TMP-SMX showing lower susceptibility rates of 55% and 60%, respectively. *Klebsiella pneumoniae* displayed a more resistant phenotype overall, with moderate susceptibility to amikacin (60%) and meropenem (55%), but considerably lower sensitivity to fluoroquinolones and β-lactam/β-lactamase inhibitor combinations. *Staphylococcus*

aureus isolates showed expected high susceptibility to vancomycin (78%) and moderate resistance to other tested agents including gentamicin (62%) and ceftriaxone (44%). These findings emphasize the continued efficacy of certain broad-spectrum agents, especially aminoglycosides and carbapenems, against Gram-negative pathogens.

Among other organisms, *Enterococcus spp*. showed moderate susceptibility to vancomycin (63%) and gentamicin (66%), underscoring the need for vigilant monitoring of resistance among Gram-positive cocci. Non-fermenting Gram-negative bacilli such as *Pseudomonas aeruginosa* and *Acinetobacter baumannii* demonstrated high resistance levels across most tested agents, particularly piperacillin-tazobactam and ciprofloxacin, with susceptibility rates as low as 17–22%. Rare isolates like *Serratia spp*. and *Citrobacter freundii* displayed relatively preserved sensitivity to gentamicin, amikacin, and TMP-SMX, albeit from limited sample sizes.

These results align with **Saleem et al.'s** [(12)] findings, which noted *Klebsiella pneumoniae* isolates exhibited high resistance rates to ceftriaxone, tigecycline, and nitrofurantoin, with 80% resistance to the former two antibiotics. Similarly, *Escherichia coli* isolates demonstrated some sensitivity to nitrofurantoin and amikacin (both 19.2%), followed by gentamicin (18.8%) and meropenem (13.9%).

For *Staphylococcus aureus*, susceptibility was highest for nitrofurantoin (13.2%) and gentamicin (10.5%), with lower responses to rifampin, levofloxacin, and vancomycin. *CoNS* exhibited modest sensitivity to vancomycin, gentamicin, and nitrofurantoin (20% each), which remains consistent with current treatment recommendations, although resistance is emerging as in **Kawasuji et al.'s** study. [(13)]

Additionally, the study by **Sader et al.** [(14)] reported that *Klebsiella spp*. exhibited high resistance rates to multiple antibiotics, including ampicillin and cephalosporins, while *E. coli* strains showed significant resistance to cephalosporins but retained susceptibility to carbapenems.

The table 3 illustrates the statistical association between major bacterial pathogens and common comorbidities—Hypertension (HTN), Diabetes Mellitus (DM), and Chronic Kidney Disease (CKD)—. The analysis employed the Chi-square test, with Fisher's exact test applied for low-frequency values (counts < 5). Among the pathogens analyzed, *Klebsiella pneumoniae* and *E. coli* demonstrated statistically significant associations with both HTN and DM, with p-values of 0.03 and 0.04 for *Klebsiella* and 0.02 and 0.05 for *E. coli*, respectively. These findings suggest that patients harboring these organisms were more likely to have these metabolic comorbidities, supporting the hypothesis that such conditions may influence microbial colonization or infection susceptibility.

In contrast, *Staphylococcus aureus, Enterococcus spp.*, and *Pseudomonas aeruginosa* did not show statistically significant associations with any of the studied comorbidities, as indicated by p-values above the 0.05 threshold. For CKD, none of the organisms reached statistical significance, although *E. coli* and *Klebsiella* displayed higher frequencies among CKD patients (17% and 13%, respectively), suggesting a possible trend that may warrant further investigation with a larger sample size. Overall, the data highlight a noteworthy association between gram-

negative pathogens and metabolic diseases such as HTN and DM, potentially guiding targeted prevention and therapeutic strategies in susceptible patient populations.

Preventive antibiotic treatment may theoretically reduce the risk of CAUTIs. However, such prophylaxis is generally not recommended due to concerns about cost, potential adverse effects, and the promotion of antibiotic resistance. The Health Service Executive (HSE) advises against long-term antibiotic prophylaxis in catheterized patients, citing risks such as adverse events and the development of antimicrobial resistance.

Effective CAUTI prevention strategies include appropriate use of urinary catheterization and prompt catheter removal. The National Institute for Health and Care Excellence (NICE) emphasizes the importance of removing or changing catheters as soon as possible when no longer needed to reduce infection risk. Additional preventive measures involve maintaining unobstructed urine flow, using a sterile closed drainage system, and ensuring that trained personnel insert and maintain catheters aseptically. Also, non-antibiotic strategies, such as catheter coatings, probiotics, and bacteriophage therapy, represent promising avenues for future research. CDC recommend these practices as part of a comprehensive approach to prevent CAUTIs.[15]

CONCLUSION

This study confirms the high prevalence of multidrug-resistant pathogens in ICU-related CAUTIs, particularly among *Klebsiella spp.* and *E. coli*. While carbapenems and amikacin remain effective therapeutic options, the reliance on these drugs must be balanced with antimicrobial stewardship initiatives. Hypertention and diabetes are significantly associated with *Klebsiella spp* and *E. coli*. Ongoing surveillance, innovative therapies, and infection prevention measures are critical to mitigating the impact of AMR in ICU settings.

ETHICS AND LIMITATIONS

The study was conducted in accordance with ethical guidelines and approved by the institutional ethics committee at Aswan University Hospital. Informed written consent was obtained from all participants.
Despite its strengths, the study has limitations. The single-center design restricts the generalizability of findings. The exclusion of patients with prior antibiotic use or advanced age (>70 years) may have led to an underestimation of resistance prevalence. Future multicenter studies incorporating broader patient demographics are needed to validate and extend these results.

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