

PATTERN OF ANTIBACTERIAL RESISTANCE IN URINARY TRACT INFECTIONS

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ABSTRACT

Background: Urinary Tract Infections (UTIs) represent one of the most prevalent bacterial infections encountered in clinical practice worldwide, affecting individuals of all ages and demographics. Despite advancements in science and healthcare, the management of UTIs continues to pose substantial challenges, primarily due to the emergence and proliferation of antibiotic-resistant strains of bacteria.

Objective: To determine the frequency of the most common gram-positive and gram-negative organisms causing urinary tract infections. To measure the frequency of their sensitivity/resistance to different antibiotics in patients.

Methods: It is cross-sectional study conducted at Department of Medicine, Railway Hospital, Rawalpindi. Its duration was six months. Non-probability, consecutive sampling technique was used. Patients with UTI proven by positive growth of microorganisms on urine culture and between 12-75 years of age were included in study. The WHO Sample Size Calculator was used to calculate the sample size. The sample size comes out to be 105 patients.

Results: This study demonstrates high rates of fluoroquinolone and third-generation cephalosporin resistance among uropathogens in our setting, with preserved susceptibility to aminoglycosides, carbapenems, fosfomycin, and nitrofurantoin.

Conclusions: These findings underscore the urgent need for antimicrobial stewardship, routine susceptibility surveillance, and adherence to evidence-based treatment guidelines. Future research should focus on molecular epidemiology of resistance, longitudinal resistance trends, and evaluation of stewardship interventions to preserve the efficacy of available antimicrobials.

Key words: Urinary Tract Infections, Uropathogens, multidrug-resistant, antimicrobial resistance

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INTRODUCTION

Urinary Tract Infections (UTIs) represent one of the most prevalent bacterial infections encountered in clinical practice worldwide, affecting individuals of all ages and demographics.¹ Despite advancements in science and healthcare, the management of UTIs continues to pose substantial challenges, primarily due to the emergence and proliferation of antibiotic-resistant strains of bacteria. The rise in antimicrobial resistance (AMR) not only compromises the efficacy of traditional treatment regimens but also underscores the urgent need for a deeper understanding of the evolving patterns of antibacterial resistance in UTIs.²

The misuse and overuse of antibiotics have facilitated the proliferation of resistant bacterial strains, rendering once-

effective treatment options ineffective.³ Understanding the specific patterns of antibacterial resistance in UTIs is paramount for guiding clinical decision-making and formulating effective therapeutic strategies. Analysis of surveillance data reveals varying resistance profiles across different geographical regions and patient populations^{4,5}, highlighting the dynamic nature of antimicrobial resistance and the importance of tailored treatment approaches. Moreover, the emergence of multidrug-resistant (MDR) and extensively drug-resistant (XDR) strains poses a grave threat to public health^{6,7}, limiting treatment options and increasing the risk of treatment failure and disease complications.^{8,9} A study done by Mortazavi et al¹ showed that the most common pathogens causing UTIs were *E. coli*, *Klebsiella*, *Staphylococcus*, and *Streptococcus* with a frequency of 62%, 13%, 12%, and 11%. Other bacteria such as *Citrobacter* and *Pseudomonas* had a marginal role in UTI with a combined frequency of 2%.

The rationale of this study is to determine bacterial etiologic agents responsible for urinary tract infection and to evaluate their in vitro susceptibility pattern to commonly used antimicrobial agents. This study is important for clinicians to initiate the effective empiric treatment and of patients with symptoms of urinary tract infection and to avoid unnecessary judicious use of these drugs to preserve their efficacies.

Development of unusual resistance among such strains could easily be detected, and thus, will help in better treatment and management of those infected by these pathogens.

METHODS

This cross-sectional study was conducted in the Department of Medicine at Railway Hospital, Rawalpindi, over six months following ethical approval. The sample size of 105 patients was calculated using the WHO Sample Size Calculator based on a study by Mortazavi et al, with 6% absolute precision and 95% confidence level. Non-probability consecutive sampling was used to recruit participants. Patients aged 12-75 years with culture-proven UTI were included. Those with tubo-ovarian disorders, sexually transmitted diseases, appendicitis, prostatitis, epididymitis, pregnant patients, catheter associated urinary tract infections, and those already on antibiotics were excluded. Written informed consent was obtained from all participants. Data on age, gender, and antibiotic sensitivity patterns were collected.

Early morning mid-stream urine samples were collected in sterile bottles and labeled appropriately. For patients unable to provide clean-catch samples, catheterization was performed. Samples underwent microscopic examination after centrifugation to identify pus cells, epithelial cells, bacteria, and nitrites. Urine dipstick tests detected leukocyte esterase, nitrites, proteins, and blood. Urine cultures were performed by streaking samples onto agar plates and incubating at 37°C for 18-24 hours. Bacterial counts $>10^5$ CFU/mL indicated UTI. Bacterial identification was performed using Gram staining, culture characteristics, and biochemical tests. *E. coli* was identified as Gram-negative rods with pink colonies on MacConkey agar, indole-positive, and oxidase-negative. *Klebsiella pneumoniae* showed mucoid colonies and was urease-positive. *Staphylococcus aureus* appeared as Gram-positive cocci in clusters with golden colonies and was coagulase-positive. *Streptococcus* species were identified by hemolysis patterns and catalase negativity. *Citrobacter* was urease-positive and oxidase-negative. *Pseudomonas aeruginosa* produced greenish-blue colonies and was oxidase-positive. Antibiotic sensitivity testing was performed using the Kirby-Bauer disk diffusion method. Results were reported as sensitive or resistant based on inhibition zones. A consultant microbiologist prepared reports and uploaded them to the hospital's electronic medical record system.

Data were analyzed using SPSS version 22.0. Frequencies and percentages were calculated for qualitative variables including gender, organism type, and antibiotic sensitivity patterns. Mean and standard deviation were calculated for age and BMI. Data were stratified by age, BMI, and gender, and chi-square test was applied post-stratification. A p-value ≤ 0.05 was considered statistically significant.

RESULTS

The mean age of the study population was 54.1 ± 11.4 years, with a range of 20-74. Gender distribution showed 72.4% females and 27.6% males. The mean body mass index was 23.5 ± 4.1 kg/m². The most frequent comorbidities observed were Diabetes Mellitus, with 39 patients (37.14%) and Hypertension, affecting 26 patients (24.76%). Less common conditions included Ischemic Heart Disease (5 patients,

4.76%), Stroke (4 patients, 3.81%), and both Benign Prostatic Hyperplasia and End-Stage Renal Disease (3 patients each, 2.86%). COPD was present in 2 patients (1.90%), while other conditions including Parkinson's Disease, Rheumatoid Arthritis, Prostatic Carcinoma, Idiopathic Pulmonary Fibrosis, Urethral Stricture, Dementia, Paraplegia, Parkinsons Disease, Cerebral Palsy, Meningomyelocele and Obstructive Sleep Apnea each accounted for 1 patient (0.95%). A total of 12 patients (11.43%) were recorded as having no co-morbid condition. There were no difference of comorbidities between male and female patients ($p=0.286$).

Table 1: Antibiotic Sensitivity Patterns of Gram-Positive Organisms (n=21)

	Antibiotic Sensitivity	Frequency	%age
Enterococcus (n=11)	Vancomycin	11	100%
	Linezolid	10	90.91%
	Doxycycline	7	63.64%
	Ampicillin	3	27.27%
	Piperacillin-Tazobactam	2	18.18%
	Ciprofloxacin	2	18.18%
	Chloramphenicol	2	18.18%
	Fosfomycin	2	18.18%
	Meropenem	1	9.09%
	Clindamycin	1	9.09%
	Amikacin	1	9.09%
Methicillin-Resistant Staphylococcus Aureus (MRSA) (n=7)	Cefaparazone-Sulbactam	1	9.09%
	Nitrofurantoin	1	9.09%
	Cotrimoxazole	1	9.09%
	Linezolid	7	100%
	Vancomycin	5	71.43%
	Clindamycin	3	42.86%
	Meropenem	3	42.86%
	Cotrimoxazole	1	14.29%
	Ampicillin	1	14.29%
	Cloxacillin	1	14.29%
	Doxycycline	2	28.57%
Staphylococcus aureus (n=2)	Piperacillin-Tazobactam	1	14.29%
	Clindamycin	1	50%
	Cloxacillin	1	50%
	Vancomycin	1	50%
	Gentamicin	1	50%
Streptococcus pyogenes (n=1)	Cefaparazone-Sulbactam	1	50%
	Levofloxacin	1	50%
	Clindamycin	1	100%
	Doxycycline	1	100%
	Chlormaphenicol	1	100%

The microbiological profile was dominated by gram-negative organisms, which comprised 84 isolates, while gram-positive organisms accounted for 21 isolates. Among gram-negatives, *Escherichia coli* was the leading pathogen, followed by *Klebsiella pneumoniae* and smaller proportions of *Pseudomonas aeruginosa*, *Proteus mirabilis*, and *Acinetobacter baumannii*. Rare isolates included *Klebsiella oxytoca* and *Providencia stuartii*. Within gram-positives, *Enterococcus* species were most frequent, followed by

methicillin-resistant *Staphylococcus aureus* (MRSA), with few isolates of *Staphylococcus aureus* and *Streptococcus pyogenes*.

Table 2: Antibiotic Resistance Patterns of Gram-Positive Organisms

	Antibiotic Resistance	Frequency	%age
Enterococcus (n=11)	Azithromycin	5	45.45%
	Cloxacillin	2	18.18%
	Ampicillin	2	18.18%
	Erythromycin	2	18.18%
	Ceftriaxone	2	18.18%
	Ciprofloxacin	2	18.18%
	Levofloxacin	2	18.18%
	Cefapazone-Sulbactam	2	18.18%
	Nitrofurantoin	2	18.18%
	Fosfomycin	2	18.18%
	Doxycycline	2	18.18%
	Colistin	1	9.09%
	Piperacillin-Tazobactam	1	9.09%
	Clindamycin	1	9.09%
	Cotrimoxazole	1	9.09%
	Flucloxacillin	1	9.09%
	Norfloxacin	1	9.09%
	Ofloxacin	1	9.09%
	Cefotaxime	1	9.09%
	Tetracycline	1	9.09%
Methicillin-Resistant <i>Staphylococcus aureus</i> (MRSA) (n=7)	Azithromycin	5	71.43%
	Clindamycin	4	57.14%
	Levofloxacin	3	42.86%
	Doxycycline	2	28.57%
	Cotrimoxazole	2	28.57%
	Cloxacillin	2	28.57%
	Erythromycin	1	14.29%
	Ampicillin	1	14.29%
	Amoxicillin	1	14.29%
	Clindamycin	1	50%
Staphylococcus aureus (n=2)	Ciprofloxacin	1	50%
	Fosfomycin	1	50%
	Erythromycin	1	50%
	Ampicillin	1	50%
	Azithromycin	1	50%
Streptococcus pyogenes (n=1)	Clindamycin	1	100%
	Ciprofloxacin	1	100%
	Fosfomycin	1	100%
	Erythromycin	1	100%
	Ampicillin	1	100%

Gram-positive organisms demonstrated preserved susceptibility to vancomycin and linezolid, particularly among *Enterococcus* and MRSA isolates, although resistance to macrolides and selected beta-lactams was notable. *Enterococcus* showed limited sensitivity to ampicillin and fluoroquinolones, while MRSA exhibited substantial resistance to azithromycin and clindamycin. Sensitivity and resistance patterns of gram-positive organisms are demonstrated in table 1 and 2.

Among gram-negative organisms, *E. coli* retained high sensitivity to amikacin and carbapenems, with reasonable activity of fosfomycin and nitrofurantoin. However,

resistance to fluoroquinolones and third-generation cephalosporins was high, limiting empirical options. *Klebsiella pneumoniae* displayed reduced carbapenem sensitivity and significant fluoroquinolone resistance, suggesting emerging multidrug resistance. Non-fermenters, particularly *Pseudomonas aeruginosa* and *Acinetobacter baumannii*, showed variable but clinically relevant resistance to carbapenems, aminoglycosides, and beta-lactams, consistent with a multidrug-resistant trend.

Among the three isolates of *Acinetobacter baumannii*, all three isolates (100%) were sensitive to vancomycin. Two isolates (66.67%) showed sensitivity to doxycycline, linezolid and cloxacillin. One isolate (33.33%) was sensitive to clindamycin, gentamicin, meropenem and chloramphenicol.

Among the 56 isolates of *Escherichia coli*, the highest sensitivity was with amikacin, 52 isolates (91.23%) showing sensitivity, followed by meropenem, to which 51 isolates (89.47%) were sensitive. Fosfomycin showed sensitivity in 44 isolates (77.19%), while 42 isolates (73.68%) were sensitive to imipenem. Nitrofurantoin demonstrated sensitivity in 40 isolates (70.18%), followed by piperacillin-tazobactam in 35 isolates (61.40%). Gentamicin showed sensitivity in 24 isolates (42.11%), while 23 isolates (40.35%) were sensitive to cefoperazone-sulbactam. Ciprofloxacin showed sensitivity in 18 isolates (31.58%). Lower sensitivity was observed with ceftriaxone, with 7 isolates (12.28%) showing sensitivity. Colistin, cefotaxime and amoxicillin each demonstrated sensitivity in 2 isolates (3.51%), while cefixime showed sensitivity in only 1 isolate (1.75%).

Among the 12 isolates of *Klebsiella pneumoniae*, gentamicin demonstrated the highest sensitivity, with 9 isolates (75.00%) showing sensitivity. Meropenem and nitrofurantoin were each sensitive in 7 isolates (58.33%), while piperacillin-tazobactam and amikacin were each sensitive in 6 isolates (50.00%). Fosfomycin showed sensitivity in 4 isolates (33.33%), followed by imipenem in 4 isolates (33.33%). Tigecycline, ceftriaxone, cefoperazone-sulbactam and colistin-polymyxin B each showed sensitivity in 3 isolates (25.00%). Ciprofloxacin and cefotaxime were each sensitive in 2 isolates (16.67%), while ofloxacin showed sensitivity in 1 isolate (8.33%). The only isolate of *Klebsiella oxytoca* showed 100% sensitivity to all tested antibiotics, including amikacin, ciprofloxacin, gentamicin, imipenem, meropenem, nitrofurantoin, and piperacillin-tazobactam.

Four isolates of *Proteus mirabilis*, three isolates (75%) were sensitive to vancomycin. Doxycycline, linezolid, and cloxacillin each showed sensitivity in 2 isolates (50%), while clindamycin, gentamicin, meropenem, and chloramphenicol each demonstrated sensitivity in 1 isolate (25%).

The single isolate of *Providencia stuartii* showed 100% sensitivity to ciprofloxacin, meropenem, imipenem, amikacin, piperacillin-tazobactam, and ampicillin.

Out of seven isolates of *Pseudomonas aeruginosa*, amikacin and imipenem demonstrated the highest sensitivity, with 5 isolates (71.43%) sensitive to each antibiotic. Gentamicin, meropenem, and piperacillin-tazobactam each showed sensitivity in 4 isolates (57.14%). Cefoperazone-sulbactam, ceftriaxone, and colistin were each sensitive in 3 isolates (42.86%). Ciprofloxacin showed sensitivity in 2 isolates (28.57%). Cefoperazone, ofloxacin, ceftazidime,

fosfomycin, tigecycline, polymyxin B, and levofloxacin each demonstrated sensitivity in 1 isolate (14.29%).

Among the three isolates of *Acinetobacter baumannii*, resistance was most frequently observed against vancomycin, with 3 isolates (23.08%) showing resistance. Two isolates (15.38%) were resistant to doxycycline and linezolid. Resistance to clindamycin, gentamicin, chloramphenicol, cloxacillin, cefotaxime, and meropenem was observed in 1 isolate each (7.69%).

Among the 57 isolates of *Escherichia coli*, ciprofloxacin demonstrated the highest resistance, with 31 isolates (54.39%) showing resistance, followed by ceftriaxone, with 30 isolates (52.63%). Resistance to cefotaxime was observed in 25 isolates (43.86%). Fosfomycin showed resistance in 12 isolates (21.05%), while nitrofurantoin, gentamicin, and cefoperazone-sulbactam each demonstrated resistance in 11 isolates (19.30%). Eight isolates (14.04%) were resistant to amikacin and amoxicillin-clavulanate. Resistance to ofloxacin was observed in 7 isolates (12.28%), while 6 isolates (10.53%) were resistant to meropenem. Cefixime showed resistance in 3 isolates (5.26%). Amoxicillin, ampicillin, levofloxacin, and ceftazidime each demonstrated resistance in 2 isolates (3.51%). Resistance to piperacillin-tazobactam, ceftazidime, imipenem, colistin, minocycline, and azithromycin was observed in 1 isolate each (1.75%).

Among the 12 isolates of *Klebsiella pneumoniae*, ciprofloxacin showed the highest resistance, with 7 isolates (58.33%) demonstrating resistance. Amikacin showed resistance in 4 isolates (33.33%), while meropenem, cefoperazone-sulbactam, piperacillin-tazobactam, and fosfomycin each showed resistance in 3 isolates (25.00%). Nitrofurantoin and the category recorded as "Nil" each accounted for 2 isolates (16.67%). Gentamicin, ofloxacin, amoxicillin, ceftriaxone, cefotaxime, and imipenem each demonstrated resistance in 1 isolate (8.33%).

The single isolate of *Klebsiella oxytoca* demonstrated resistance to ceftriaxone, cefotaxime, and cefixime, with each antibiotic showing resistance in 1 isolate (100%).

Among the four isolates of *Proteus mirabilis*, resistance was highest for fosfomycin, with 3 isolates (75%) showing resistance. Ciprofloxacin, ceftriaxone, and nitrofurantoin each demonstrated resistance in 2 isolates (50%). Ofloxacin and amoxicillin-clavulanic acid each showed resistance in 1 isolate (25%). The single isolate of *Providencia stuartii* demonstrated resistance to gentamicin, nitrofurantoin, and fosfomycin, with each antibiotic showing resistance in 1 isolate (100%). Among the seven isolates of *Pseudomonas aeruginosa*, ciprofloxacin showed the highest resistance, with 5 isolates (71.43%) demonstrating resistance. Piperacillin-tazobactam and ceftazidime each showed resistance in 3 isolates (42.86%). Cefoperazone-sulbactam, ceftriaxone, imipenem, and nitrofurantoin each demonstrated resistance in 2 isolates (28.57%). Amikacin, gentamicin, meropenem, fosfomycin, and cefotaxime each showed resistance in 1 isolate (14.29%). Among the seven isolates of *Pseudomonas aeruginosa*, ciprofloxacin showed the highest resistance, with 5 isolates (71.43%) demonstrating resistance. Piperacillin-tazobactam and ceftazidime each showed resistance in 3 isolates (42.86%). Cefoperazone-sulbactam, ceftriaxone, imipenem, and nitrofurantoin each demonstrated resistance in 2 isolates (28.57%). Amikacin, gentamicin, meropenem, fosfomycin, and cefotaxime each showed resistance in 1

isolate (14.29%). Overall, the data indicate a predominance of gram-negative pathogens with substantial resistance to commonly prescribed empirical agents, while last-line drugs such as carbapenems, vancomycin, and linezolid largely retained activity in this cohort. The resistance pattern signals a narrowing therapeutic window and underscores the need for targeted antimicrobial stewardship strategies.

Data Stratification: Although the proportions of organism types differed across the demographic variables, the differences were not statistically significant in this sample for age, gender, or BMI. Specifically, the older age group showed a higher proportion of Gram-positives, but this was not statistically significant ($p=0.292$). Similarly, males had a higher proportion of Gram-positives than females, but this difference also lacked statistical significance ($p=0.103$) and might be confounded by differences in BMI distribution. Finally, there was no statistically significant association found between BMI group and organism type.

DISCUSSION

This study examined the distribution of uropathogens and their antibiotic resistance patterns in a cohort of 105 patients with culture-proven urinary tract infections at Railway Hospital, Rawalpindi. The predominance of gram-negative organisms (80.0%) in our study aligns with established global patterns, where gram-negative bacteria account for approximately 80-90% of UTI cases.¹⁰ *Escherichia coli* emerged as the most prevalent pathogen, representing 66.67% of gram-negative isolates, consistent with recent international studies reporting *E. coli* prevalence ranging from 55-80% in UTI cases.^{11,12} A recent multi-center study across Europe and the United States documented *E. coli* as the causative agent in 79% of initial UTI episodes, declining to 73% in recurrent cases.¹³ Similarly, research from Gabon demonstrated *E. coli* prevalence of 31.4% in UTI patients¹⁴, while studies from Romania and Bangladesh reported rates of 55.34% and 65.84%, respectively.^{15,16} *Klebsiella pneumoniae* constituted 14.29% of gram-negative isolates in our study, which corresponds well with recent literature. Ku et al. reported *K. pneumoniae* in 7% of index UTIs, increasing to 11% in subsequent infections¹³, while a Turkish emergency department study found *K. pneumoniae* in 19% of positive urine cultures.¹⁷ The high prevalence of comorbidities, particularly diabetes mellitus (37.14%) and hypertension (24.76%), reflects the well-documented association between chronic diseases and UTI susceptibility. Diabetes mellitus is recognized as a significant risk factor for UTI development, with diabetic patients showing distinct uropathogen profiles and increased antimicrobial resistance.¹⁸

Our study revealed alarming resistance rates among *E. coli* isolates, with ciprofloxacin resistance at 54.39% and ceftriaxone resistance at 52.63%. These findings are comparable to recent studies from India where fluoroquinolone resistance in *E. coli* ranged from 74.5-82.9% and cephalosporin resistance approached 89%.¹⁹ A comprehensive analysis from a Californian healthcare system demonstrated that 57% of index UTIs exhibited resistance to at least one antibiotic class, increasing to 65% with subsequent infections¹³, underscoring the progressive nature of antimicrobial resistance.

The high sensitivity of *E. coli* to amikacin (91.23%) and carbapenems (meropenem 89.47%, imipenem 73.68%) in

our study is encouraging and consistent with global trends. Recent literature confirms aminoglycosides retain activity against 60-70% of multidrug-resistant *E. coli*, while carbapenem resistance in *E. coli* remains relatively uncommon at 1.75-5.26%.²⁰ However, emerging data from genomic surveillance indicates the rise of carbapenem-resistant *E. coli* clones, particularly ST167, which showed 89% carriage of carbapenem and cephalosporin resistance genes in recent sequencing studies.²¹

Notably, our findings of preserved sensitivity to fosfomycin (77.19%) and nitrofurantoin (70.18%) align with recommendations from the Infectious Diseases Society of America (IDSA), which advocates these agents as preferred first-line options for uncomplicated cystitis due to maintained susceptibility in ESBL-producing strains.²² *Klebsiella pneumoniae* in our study demonstrated concerning resistance patterns, with ciprofloxacin resistance at 58.33% and reduced carbapenem sensitivity (meropenem 58.33%, imipenem 33.33%). These findings are consistent with the global emergence of carbapenem-resistant Enterobacterales (CRE), which represent an urgent public health threat.²³ Recent guidelines emphasize that *K. pneumoniae* frequently harbors *fosA* hydrolase genes, limiting fosfomycin efficacy and necessitating alternative therapeutic approaches.²²

The relatively high sensitivity to gentamicin (75%) and nitrofurantoin (58.33%) in *K. pneumoniae* isolates provides valuable treatment options. However, the emergence of extended-spectrum β -lactamase (ESBL) production in *Klebsiella* species, as evidenced by our *Klebsiella oxytoca* isolate showing complete resistance to third-generation cephalosporins, reflects a worrying trend documented extensively in recent literature.¹

Pseudomonas aeruginosa isolates exhibited the highest sensitivity to amikacin and imipenem (71.43% each), with substantial resistance to ciprofloxacin (71.43%). This pattern aligns with the IDSA guidance on difficult-to-treat resistance (DTR) *P. aeruginosa*, which defines DTR as resistance to carbapenems, fluoroquinolones, and piperacillin-tazobactam.²² Recent studies confirm that multidrug-resistant *P. aeruginosa* in UTI settings shows variable but clinically significant resistance to multiple antibiotic classes.²⁴

Enterococcus species, representing 10.48% of total isolates, demonstrated 100% sensitivity to vancomycin and 90.91% sensitivity to linezolid, consistent with international guidelines recommending these agents for enterococcal UTI.²⁵ Recent studies from Bangladesh reported similar patterns, with *Enterococcus* showing 100% sensitivity to vancomycin, linezolid, and piperacillin-tazobactam, but extensive resistance to cephalosporins and carbapenems.²⁶

MRSA isolates (6.67% of total sample) exhibited 100% sensitivity to linezolid and 71.43% sensitivity to vancomycin, consistent with current treatment guidelines recommending glycopeptides and linezolid as first-line therapy for MRSA infections.²⁷ The high resistance to azithromycin (71.43%) and clindamycin (57.14%) reflects widespread macrolide and lincosamide resistance among MRSA strains globally.

A recent Ethiopian study reported MRSA prevalence of 42.59% among *S. aureus* isolates from UTI patients, with 53.7% resistance to nitrofurantoin²⁸, higher than our findings. UK guidelines caution against linezolid use for MRSA UTI

due to poor renal excretion, recommending investigation of the underlying cause of MRSA bacteriuria and consideration of glycopeptides for complicated cases.²⁹

Several limitations merit consideration. The single-center design may limit generalizability to other healthcare settings in Pakistan. The sample size of 105 patients, while statistically powered, provides limited data for less common organisms such as *Providencia stuartii* and *Klebsiella oxytoca*. The cross-sectional design precludes assessment of resistance trends over time. Additionally, molecular characterization of resistance mechanisms (ESBL types, carbapenemase genes) was not performed, limiting our understanding of the genetic basis of resistance patterns observed.

CONCLUSION

This study demonstrates high rates of fluoroquinolone and third-generation cephalosporin resistance among uropathogens in our setting, with preserved susceptibility to aminoglycosides, carbapenems, fosfomycin, and nitrofurantoin. These findings underscore the urgent need for antimicrobial stewardship, routine susceptibility surveillance, and adherence to evidence-based treatment guidelines. Future research should focus on molecular epidemiology of resistance, longitudinal resistance trends, and evaluation of stewardship interventions to preserve the efficacy of available antimicrobials.

ETHICAL APPROVAL

Ethical approval of article was granted by the Institutional Review Committee of Islamic International Medical College vide Appl. # Riphah /IRC/ 24/1012 on dated: December, 23rd 2025.

AUTHOR'S CONTRIBUTIONS

NM: Concept, design, manuscript writing, data collection

AZ: Supervision, data analysis, critical revision

IR: Data collection, data analysis & interpretation

MA: Manuscript writing, Critical analysis,

All Authors: Approval of the final version of the manuscript to be published

CONFLICT OF INTEREST

Authors declare no conflict of interest.

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