

Frequency of Different Bacteria Causing Urinary Tract Infection in Patients at University of Lahore Teaching Hospital, Lahore

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Author's Contribution

^{1,5}Conceptualized the study, curated the data, visualization, investigations, and methodology, ^{4,6}analysed the data and did the writing of the original draft, ²Supervised the project, ⁷Literature review

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ABSTRACT

Objective: To determine the frequency of different bacteria causing urinary tract infection in patients at University of Lahore Teaching Hospital, Lahore.

Methodology: This descriptive cross-sectional study was conducted in the Department of Medicine, University of Lahore Teaching Hospital, Lahore, from November 2025 to April 2026. A total of 168 patients with urinary tract infection were enrolled through non-probability consecutive sampling. Patients aged 20–80 years with pyuria (≥ 5 pus cells/high-power field) and positive urine culture were included. Patients with recent antibiotic use, fungal growth, pregnancy, menstruation, or refusal of consent were excluded. Urine samples were cultured on CLED medium, and bacterial isolates were identified using colony morphology and Gram staining, followed by antimicrobial susceptibility testing. Data was analyzed using SPSS version 26, and a p-value ≤ 0.05 was considered statistically significant.

Result: A total of 168 patients were included in the study, with a mean age of 55.78 ± 22.97 years, there were 84 (50%) male and 84 (50%) females enrolled. *Escherichia coli* was the most frequently isolated organism (28 n=47), followed by *Enterococcus* species and *Pseudomonas aeruginosa* (20.2%, n=34) respectively. The antimicrobial susceptibility pattern demonstrated high resistance to commonly used antibiotics, particularly ciprofloxacin (88.7%, n=149), norfloxacin (68.5%, n=115), fosfomycin (67.9%, n=114), gentamicin (64.3%, n=108), nitrofurantoin (53.6%, n=90), piperacillin–tazobactam (53.0%, n=89), cefuroxime (51.2%, n=86), ceftriaxone (47.6%, n=80), amikacin (47.0%, n=79), and trimethoprim–sulfamethoxazole (40.5%, n=68). Among the tested antibiotics, colistin demonstrated the highest susceptibility (73.2%, n=123), followed by meropenem (56.0%, n=94), whereas imipenem showed a comparatively lower susceptibility rate (20.2%, n=34).

Conclusion: The present study concluded that *Escherichia coli* remains the most common causative organism of urinary tract infections, followed by *Enterococcus* species and *Pseudomonas aeruginosa*, indicating a diverse spectrum of both Gram-negative and Gram-positive pathogens in the study population.

Keywords: E. Coli, Urinary Tract Infection, Gram-negative bacteria, Gram-positive bacteria

Introduction

Urinary tract infections (UTIs) are among the most common bacterial infections affecting people of all ages, especially women. They occur when harmful microorganisms enter and multiply within any part of the urinary system, including the bladder, urethra, ureters, or kidneys.¹ The condition can present in a variety of ways, ranging from mild symptoms such as burning urination, increased frequency, and urgency, to more severe complications like kidney infection (pyelonephritis) and, in extreme cases, bloodstream infections that can become life-threatening if not treated promptly.²

Across the world, UTIs place a considerable burden on healthcare systems due to their high frequency, tendency to recur, and the need for repeated medical visits and antibiotic use. In developing countries like Pakistan, this burden is even more significant.³ Factors such as limited access to clean water and sanitation, delayed healthcare seeking behavior, self-medication, and inappropriate antibiotic use contribute to both the

increased incidence of UTIs and the growing challenge of antibiotic resistance.⁴

Most UTIs are caused by bacteria, with *Escherichia coli* being the most common culprit. However, other organisms such as *Klebsiella pneumoniae*, *Proteus* species, *Pseudomonas aeruginosa*, *Enterococcus* species, and *Staphylococcus saprophyticus* are also frequently isolated.⁵ The distribution of these bacteria is not the same everywhere; it varies depending on geographic location, hospital environment, patient characteristics, and underlying health conditions.⁶ For example, hospital-acquired infections often show a higher proportion of resistant organisms compared to community-acquired cases.⁷

In recent years, the rising problem of antimicrobial resistance has made UTIs more difficult to treat effectively. Many of the commonly used antibiotics are becoming less effective due to misuse and overuse, making culture and sensitivity testing increasingly important before selecting treatment.⁸ Understanding which bacteria are most commonly responsible for

UTIs in a specific hospital setting is therefore essential for guiding appropriate antibiotic choices and improving patient outcomes.⁹

At the University of Lahore Teaching Hospital, Lahore, urinary tract infections are frequently seen among patients in both outpatient and inpatient departments. However, there is limited local data describing which bacterial organisms are most commonly responsible for these infections in this population. Without this information, it becomes challenging for clinicians to select the most effective empirical treatment and to develop updated antibiotic guidelines. For this reason, the present study aims to identify the frequency of different bacterial pathogens causing urinary tract infections among patients at the University of Lahore Teaching Hospital, Lahore. The findings will help build a clearer picture of local infection patterns and support better clinical decision-making, ultimately contributing to more effective treatment strategies and improved patient care.

Methodology

This descriptive cross-sectional study was conducted in the Department of Medicine at the University of Lahore Teaching Hospital, Lahore, over a period of six months (November 2025 to April 2026) after approval of the synopsis. A sample size of 168 patients was calculated using the prevalence of *Escherichia coli* (80%) as the most common causative organism in urinary tract infections, and a non-probability consecutive sampling technique was used for patient selection. Both male and female patients aged more than 20 years and less than 80 years who were admitted with urinary tract infection as per operational definition were included. Inclusion criteria required patients to have a urine complete examination showing pus cells ≥ 5 per high power field along with a positive urine culture and sensitivity report demonstrating bacterial growth and corresponding antimicrobial susceptibility patterns. Patients admitted in indoor wards and intensive care units were included in the study. Patients or attendants who refused consent, those who had used antibiotics within the previous two weeks, cases showing fungal growth on culture, and female patients who were pregnant or menstruating were excluded. After obtaining approval from the institutional ethical committee, informed consent was taken from each patient or attendant, and confidentiality as well as the non-invasive nature of the study was ensured. A structured proforma was used to collect detailed clinical history and relevant laboratory data, including complete blood count, urine analysis, and urine culture and sensitivity. Urine samples were inoculated on CLED medium, and after incubation, bacterial colonies were identified based on morphology and Gram staining, followed by antimicrobial susceptibility testing according to standard microbiological protocols under

the supervision of a qualified microbiologist. All collected data were entered and analyzed using SPSS version 27. Descriptive statistics such as mean and standard deviation were calculated for quantitative variables while frequencies and percentages were computed for categorical variables such as gender, isolated organisms, and antibiotic sensitivity patterns.

Results

In this study the mean age of the cases was 55.78 ± 22.97 years, there were 84 (50%) male and 84 (50%) females enrolled in this study. The mean of WBCs in this study was 9097.02 ± 2943.73 . In most of the cases 81 (48.2%) pus cells found were 11-15. In our data there were 71 (42.3%) smokers, 60 (35.7%) hypertensive, 74 (44%) diabetic, 67 (39.9%) patients with SGLT2 use and 54 (32.1%) patients with urinary catheter placed were found in this research. A total of 168 (100%) patients enrolled were having UTI. (Table I)

Table I: Descriptive statistics of demographic and risk factors.		
Age (Mean $\pm$ S.D)		55.78 $\pm$ 22.97
Min-Max		20-80
WBCs (Mean $\pm$ S.D)		9097.02 $\pm$ 2943.73
Pus Cells	5-10	43 (25.6%)
	11-15	81 (48.2%)
	16-20	44 (26.2%)
Gender	Male	84 (50%)
	Female	84 (50%)
Smoking	Yes	71 (42.3%)
	No	97 (57.7%)
Hypertension	Yes	60 (35.7%)
	No	108 (64.3%)
DM	Yes	74 (44%)
	No	94 (56%)
Urinary catheter placed	Yes	54 (32.1%)
	No	114 (67.9%)
SGLT2 Use	Yes	67 (39.9%)
	No	101 (60.1%)
UTI	Yes	168 (100%)
	No	0 (0%)

In this research the most prevalent type of organism causing UTI was *Escherichia coli* found in 47 (28%) cases, *enterococcus* species and *pseudomonas aeruginosa* were found in 34 (20.2%) cases respectively. (Table II)

Table II: Descriptive statistics of different organisms causing UTI	
Organism	UTI
	Yes
Citrobacter species	27 (16.1%)
Enterococcus species	34 (20.2%)

Enterococcus species + Candida species	3 (1.8%)
Escherichia coli	47 (28%)
Klebsiella pneumonia	20 (11.9%)
Klebsiella species	3 (1.8%)
Pseudomonas aeruginosa	34 (20.2%)
Total	168 (100%)

Table II: Stratification of different types of organisms according to gender.

Organism	Gender		P-Value
	Female	No	
Citrobacter species	10 (11.9%)	17 (20.2%)	0.142
Enterococcus species	21 (25%)	13 (15.5%)	
Enterococcus species + Candida species	1 (1.2%)	2 (2.4%)	
Escherichia coli	29 (34.5%)	18 (21.4%)	
Klebsiella pneumonia	8 (9.5%)	12 (14.3%)	
Klebsiella species	2 (2.4%)	1 (1.2%)	
Pseudomonas aeruginosa	13 (15.5%)	21 (25%)	
Total	84 (100%)	84 (100%)	

The distribution of isolates also showed gender-related variation, with *Escherichia coli* and *Enterococcus* species being more common among female patients 29 (34.5%) versus 21 (25%) respectively, whereas *Pseudomonas aeruginosa* and *Escherichia coli* were more frequently isolated from male patients 21 (25%) versus 18 (21.4%). However, the p-value was insignificant 0.142. (Table III)

The antimicrobial susceptibility pattern revealed high resistance to commonly used antibiotics, particularly ciprofloxacin (88.7%, n=149), norfloxacin (68.5%, n=115), fosfomycin (67.9%, n=114), gentamicin (64.3%, n=108), nitrofurantoin (53.6%, n=90), piperacillin-tazobactam (53.0%, n=89), cefuroxime (51.2%, n=86), and ceftriaxone (47.6%, n=80). Among the tested antibiotics, colistin demonstrated the highest susceptibility (73.2%, n=123), followed by meropenem (56.0%, n=94), while aminoglycosides such as amikacin and gentamicin showed susceptibility rates of 30.4% (n=51) and 31.5% (n=53), respectively.

Table IV: Antibiotic resistance pattern

Antibiotic	Category	N	(%)
Ciprofloxacin	R	149	88.7%
	S	19	11.3%
Norfloxacin	I	6	3.6%
	R	115	68.5%
	S	47	28.0%
Ceftriaxone	I	38	22.6%
	R	80	47.6%

	S	50	29.8%
Cefuroxime	I	71	42.3%
	R	86	51.2%
	S	11	6.5%
Cefoperazone-Sulbactam	I	168	100.0%
	R	0	0.0%
	S	0	0.0%
Piperacillin-Tazobactam	I	38	22.6%
	R	89	53.0%
	S	41	24.4%
Imipenem	I	98	58.3%
	R	36	21.4%
	S	34	20.2%
Meropenem	I	38	22.6%
	R	36	21.4%
	S	94	56.0%
Gentamicin	I	7	4.2%
	R	108	64.3%
	S	53	31.5%
Amikacin	I	38	22.6%
	R	79	47.0%
	S	51	30.4%
Nitrofurantoin	I	3	1.8%
	R	90	53.6%
	S	75	44.6%
Fosfomycin	I	3	1.8%
	R	114	67.9%
	S	51	30.4%
Colistin	I	38	22.6%
	R	7	4.2%
	S	123	73.2%
SXT	I	71	42.3%
	R	68	40.5%
	S	29	17.3%

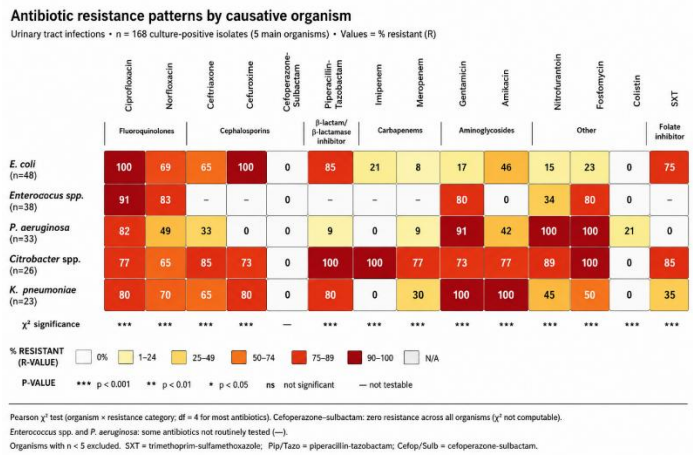
A marked level of resistance was observed against the fluoroquinolones. Ciprofloxacin demonstrated the highest resistance rate, with 149 isolates (88.7%) classified as resistant and only 19 isolates (11.3%) remaining susceptible. Norfloxacin also showed considerable resistance, with 115 isolates (68.5%) resistant, 47 (28.0%) susceptible, and 6 (3.6%) exhibiting an intermediate response. Resistance to cephalosporins was also evident in the study population. Ceftriaxone demonstrated resistance in 80 isolates (47.6%), susceptibility in 50 (29.8%), and intermediate sensitivity in 38 (22.6%). Likewise, cefuroxime showed resistance in 86 isolates (51.2%), while only 11 isolates (6.5%) were susceptible and 71 (42.3%) demonstrated intermediate sensitivity. All isolates were reported as intermediate to cefoperazone-sulbactam (100%, n=168).

The β -lactam/ β -lactamase inhibitor combination piperacillin-tazobactam demonstrated resistance in 89 isolates (53.0%), susceptibility in 41 (24.4%), and intermediate response in 38 (22.6%). Variations were also observed among the carbapenems. Imipenem demonstrated resistance in 36 isolates (21.4%),

susceptibility in 34 (20.2%), and intermediate sensitivity in 98 (58.3%). In comparison, meropenem showed greater activity, with 94 isolates (56.0%) classified as susceptible, 36 (21.4%) resistant, and 38 (22.6%) intermediate.

Aminoglycosides exhibited moderate to high resistance patterns. Gentamicin demonstrated resistance in 108 isolates (64.3%) and susceptibility in 53 (31.5%), whereas amikacin showed resistance in 79 isolates (47.0%) and susceptibility in 51 (30.4%). Evaluation of the urinary antimicrobial agents revealed resistance in 90 isolates (53.6%) to nitrofurantoin, while 75 isolates (44.6%) remained susceptible. Fosfomycin exhibited resistance in 114 isolates (67.9%) and susceptibility in 51 (30.4%).

The highest susceptibility among all tested antibiotics was observed with colistin, where 123 isolates (73.2%) were classified as susceptible and only 7 (4.2%) as resistant. Trimethoprim–sulfamethoxazole (SXT) demonstrated resistance in 68 isolates (40.5%), susceptibility in 29 (17.3%), and intermediate sensitivity in 71 (42.3%).



The chi-square analysis revealed statistically significant differences in antibiotic resistance patterns across the five bacterial organisms for 13 of the 14 antibiotics tested ($p < 0.05$). Ciprofloxacin resistance was high among all organisms, ranging from 77% in *Citrobacter* spp. to 100% in *Escherichia coli*. Norfloxacin resistance also remained high, with resistance rates of 69% in *Escherichia coli*, 83% in *Enterococcus* spp., 49% in *Pseudomonas aeruginosa*, 65% in *Citrobacter* spp., and 70% in *Klebsiella pneumoniae*. Marked variation was observed for cephalosporins. Ceftriaxone resistance was 65% in *Escherichia coli*, 33% in *Pseudomonas aeruginosa*, 85% in *Citrobacter* spp., and 65% in *Klebsiella pneumoniae*, while it was not routinely tested for *Enterococcus* spp. Cefuroxime resistance was highest in *Escherichia coli* at 100%, followed by *Klebsiella pneumoniae* at 80% and *Citrobacter* spp. at 73%, whereas no resistance was recorded for *Pseudomonas*

aeruginosa. Cefoperazone–sulbactam showed 0% resistance across all organisms.

Piperacillin–tazobactam showed wide variation, with resistance of 85% in *Escherichia coli*, 9% in *Pseudomonas aeruginosa*, 100% in *Citrobacter* spp., and 80% in *Klebsiella pneumoniae*. Carbapenem resistance also varied across organisms. Imipenem resistance was 21% in *Escherichia coli*, 0% in *Pseudomonas aeruginosa*, 100% in *Citrobacter* spp., and 0% in *Klebsiella pneumoniae*. Meropenem resistance was lower in *Escherichia coli* and *Pseudomonas aeruginosa* at 8% and 9%, respectively, but higher in *Citrobacter* spp. at 77% and *Klebsiella pneumoniae* at 30%. Aminoglycoside resistance showed mixed patterns. Gentamicin resistance was 17% in *Escherichia coli*, 80% in *Enterococcus* spp., 91% in *Pseudomonas aeruginosa*, 73% in *Citrobacter* spp., and 100% in *Klebsiella pneumoniae*. Amikacin resistance was highest in *Klebsiella pneumoniae* at 100%, followed by *Citrobacter* spp. at 77%, *Escherichia coli* at 46%, and *Pseudomonas aeruginosa* at 42%, while *Enterococcus* spp. showed 0% resistance.

For urinary agents, nitrofurantoin resistance was highest in *Pseudomonas aeruginosa* at 100%, followed by *Citrobacter* spp. at 89%, *Klebsiella pneumoniae* at 45%, *Enterococcus* spp. at 34%, and *Escherichia coli* at 15%. Fosfomycin resistance was 100% in *Pseudomonas aeruginosa* and *Citrobacter* spp., 80% in *Enterococcus* spp., 50% in *Klebsiella pneumoniae*, and 23% in *Escherichia coli*. Colistin resistance remained low, with 0% resistance in *Escherichia coli*, *Enterococcus* spp., *Citrobacter* spp., and *Klebsiella pneumoniae*, while *Pseudomonas aeruginosa* showed 21% resistance. Trimethoprim–sulfamethoxazole resistance was highest in *Citrobacter* spp. at 85%, followed by *Escherichia coli* at 75% and *Klebsiella pneumoniae* at 35%, while *Pseudomonas aeruginosa* showed 0% resistance.

Discussion

Urinary tract infections (UTIs) remain among the most common bacterial infections encountered in clinical practice, and their causative organisms and antimicrobial resistance patterns vary across geographical regions and healthcare settings. The present study assessed the frequency of bacterial pathogens causing UTIs and their antimicrobial susceptibility profile among patients at the University of Lahore Teaching Hospital, Lahore.

In this study, *Escherichia coli* was identified as the predominant uropathogen, accounting for 28% of isolates, followed by *Enterococcus* species (20.2%) and *Pseudomonas aeruginosa* (20.2%). These findings

are consistent with previous studies reporting *Escherichia coli* as the leading cause of UTIs because of its ability to adhere to and colonize the urinary tract. Similar findings have been reported in Pakistani studies where *Escherichia coli* remained the most prevalent isolate, followed by *Klebsiella* and *Enterococcus* species. However, the relatively lower proportion of *Escherichia coli* compared with community-based studies may reflect the inclusion of hospitalized patients, where a broader range of organisms such as *Pseudomonas aeruginosa* and *Enterococcus* species are frequently encountered.¹¹

The antimicrobial susceptibility profile revealed substantial resistance to commonly prescribed antibiotics. Ciprofloxacin demonstrated the highest resistance rate (88.7%), followed by fosfomycin (67.9%), norfloxacin (68.5%), gentamicin (64.3%), nitrofurantoin (53.6%), piperacillin-tazobactam (53.0%), cefuroxime (51.2%), and ceftriaxone (47.6%). These findings are comparable to regional reports documenting increasing resistance to fluoroquinolones and cephalosporins among urinary pathogens.¹³ These findings collectively highlight a growing public health concern regarding the declining effectiveness of first-line antibiotics in urinary infections.¹⁴

Among the tested agents, colistin demonstrated the highest susceptibility (73.2%), followed by meropenem (56.0%). Although meropenem retained comparatively better activity than many other antibiotics, resistance and intermediate responses were still observed. Imipenem showed susceptibility in only 20.2% of isolates, while 58.3% demonstrated intermediate sensitivity and 21.4% were resistant. These findings suggest reduced effectiveness of several broad-spectrum agents and may indicate increasing antimicrobial pressure within the hospital environment.¹⁵

Aminoglycosides demonstrated limited effectiveness, with gentamicin and amikacin showing susceptibility rates of 31.5% and 30.4%, respectively. Similarly, nitrofurantoin demonstrated susceptibility in 44.6% of isolates, whereas fosfomycin showed susceptibility in 30.4%. These findings suggest variable activity of urinary antimicrobial agents and highlight the importance of culture-directed therapy before antibiotic selection.¹⁶

The relatively high isolation frequency of *Enterococcus* species (20.2%) and *Pseudomonas aeruginosa* (20.2%) further reflects the changing microbiological profile of UTIs in hospitalized patients. Previous studies have reported an increasing prevalence of non-*Escherichia coli* pathogens, particularly among catheterized, elderly, and immunocompromised individuals, where *Enterococcus* species and *Pseudomonas aeruginosa* are frequently encountered.¹⁷

Overall, the findings demonstrate a substantial burden of antimicrobial resistance among uropathogens. The high resistance rates observed for fluoroquinolones and cephalosporins emphasize the importance of antimicrobial stewardship, rational antibiotic prescribing, and continuous local surveillance to support evidence-based empirical therapy and reduce the progression of antimicrobial resistance.

Conclusion

Escherichia coli was the most frequently isolated uropathogen, followed by *Enterococcus* species and *Pseudomonas aeruginosa*, demonstrating the presence of both Gram-negative and Gram-positive organisms among patients with urinary tract infections. The antimicrobial susceptibility profile revealed substantial resistance to commonly prescribed antibiotics, particularly fluoroquinolones and cephalosporins, indicating reduced effectiveness of several first-line treatment options. In contrast, colistin and meropenem demonstrated comparatively higher susceptibility rates against the isolated pathogens. These findings highlight the importance of continuous antimicrobial surveillance, culture-guided therapy, and antimicrobial stewardship strategies to optimize treatment outcomes and limit the further spread of antimicrobial resistance.

LIMITATIONS

- The study included 168 culture-positive isolates, which may limit the generalizability of the findings to larger populations.
- The study was conducted at a single tertiary care hospital; therefore, the observed bacterial distribution and antimicrobial resistance patterns may primarily reflect the local epidemiological profile.
- The cross-sectional design provided information at a single point in time and did not allow assessment of temporal trends in antimicrobial resistance.
- Molecular characterization of bacterial isolates and resistance mechanisms was not performed, limiting the identification of specific genetic determinants associated with antimicrobial resistance.
- Important patient-related factors, including previous antibiotic exposure, duration of hospitalization, catheterization status, recurrent urinary tract infections, and underlying comorbidities, were not evaluated in detail and may have influenced the observed resistance patterns.

RECOMMENDATIONS

- Routine urine culture and antimicrobial susceptibility testing should be performed whenever possible before initiating antibiotic therapy to facilitate evidence-based treatment decisions.
- Antimicrobial stewardship programs should be strengthened to promote the rational use of antibiotics and reduce the development of antimicrobial resistance.

- Regular surveillance of uropathogens and their antimicrobial susceptibility patterns should be conducted to support the development of updated local treatment guidelines.
- Healthcare professionals should receive continuous education and training regarding emerging antimicrobial resistance trends and appropriate antibiotic prescribing practices.
- Strict adherence to infection prevention and control measures should be maintained to reduce the transmission of multidrug-resistant organisms within healthcare facilities.
- Future studies should include larger multicenter populations and incorporate molecular techniques to investigate the genetic mechanisms underlying antimicrobial resistance.

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