

Bacteriological Profile and Antimicrobial Susceptibility Patterns of Urinary Tract Infections in a Tertiary Care Hospital of Multan, Southern Punjab, Pakistan

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ABSTRACT

Background: Urinary tract infections (UTIs) represent one of the most common bacterial infections encountered in both community and hospital settings. The increasing emergence of antimicrobial resistance among uropathogens has complicated empirical treatment strategies, particularly in developing regions where surveillance data remain limited. Local antimicrobial susceptibility patterns are essential for guiding rational antibiotic therapy and limiting resistance progression. **Objective:** To identify the prevalent bacterial pathogens and determine their antimicrobial susceptibility patterns among patients with urinary tract infections in a tertiary care hospital in Multan, southern Punjab, Pakistan. **Methods:** This cross-sectional study was conducted over four months and included 72 adult patients with culture-confirmed urinary tract infections. Midstream urine samples were processed using standard microbiological techniques. Bacterial identification was performed through Gram staining and biochemical profiling. Antimicrobial susceptibility testing was carried out using the Kirby–Bauer disk diffusion method in accordance with Clinical and Laboratory Standards Institute guidelines. Data were analyzed using SPSS version 26. Continuous variables were expressed as mean \pm standard deviation, and categorical variables as frequencies and percentages. Chi-square and independent t-tests were applied where appropriate, with $p < 0.05$ considered statistically significant. **Results:** The mean age of participants was 36.8 ± 14.2 years, with females comprising 65.3% of cases. Gram-negative organisms accounted for 86.1% of isolates, with *Escherichia coli* being the most common pathogen (54.2%), followed by *Klebsiella pneumoniae* (18.1%). High resistance rates were observed against ampicillin (76.4%) and ciprofloxacin (58.3%). Nitrofurantoin (81.9% sensitivity) and imipenem (94.4% sensitivity) demonstrated the highest effectiveness. Multidrug resistance was significantly more frequent among hospitalized patients ($p = 0.032$). **Conclusion:** Gram-negative bacteria, particularly *Escherichia coli*, predominated in urinary tract infections, with considerable resistance to commonly used oral antibiotics. Continuous surveillance and strengthened antimicrobial stewardship are essential to guide empirical therapy and curb antimicrobial resistance.

Keywords: Anti-Bacterial Agents; Anti-Infective Agents; Drug Resistance, Bacterial; *Escherichia coli*; Multidrug Resistance; Pakistan; Urinary Tract Infections

Received: 10 January 2026
Revised: 12 January 2026
Accepted: 17 February 2026
Published: 28 February 2026

Citation: [Click to Cite](#)

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INTRODUCTION

Urinary tract infections remain among the most frequently encountered bacterial infections worldwide and continue to impose a considerable burden on healthcare systems. They affect individuals across all age groups, with women disproportionately impacted due to anatomical and physiological factors.

Although many cases are uncomplicated and respond to short courses of antimicrobial therapy, the clinical and economic consequences of recurrent, complicated, and hospital-

acquired infections are substantial. In developing countries, where access to diagnostic facilities may be inconsistent and empirical therapy is often practiced without culture confirmation, the burden is amplified by delayed diagnosis and inappropriate antibiotic use. The microbial etiology of urinary tract infections has been extensively studied, and Gram-negative bacilli, particularly *Escherichia coli*, have consistently been identified as the predominant pathogens (1, 2).

Other organisms such as *Klebsiella* species, *Proteus* species, *Pseudomonas aeruginosa*, and certain Gram-positive cocci also contribute to disease burden, especially in hospitalized or catheterized patients. Despite the predictable dominance of certain pathogens, the antimicrobial susceptibility patterns of these organisms vary significantly across geographical regions and healthcare settings. These variations are influenced by prescribing practices, availability of antibiotics without prescription, infection control measures, and local antimicrobial stewardship policies (3, 4).

In recent years, antimicrobial resistance has emerged as a critical public health concern. The widespread and often irrational use of antibiotics has accelerated the development of resistant strains, rendering previously effective agents increasingly unreliable (5).

First-line oral antibiotics traditionally used for urinary tract infections, including ampicillin and fluoroquinolones, have shown diminishing efficacy in many regions. The rise of multidrug-resistant organisms, including extended-spectrum beta-lactamase-producing Enterobacteriaceae, has further complicated therapeutic decision-making. In resource-limited settings, where advanced diagnostic tools and second-line antibiotics may not be readily accessible, the implications are particularly concerning (6, 7).

In Pakistan, urinary tract infections constitute a common reason for outpatient visits and hospital admissions. However, antimicrobial resistance surveillance data remain fragmented and often limited to isolated institutional reports.

The southern region of Punjab, including the city of Multan, serves a large and diverse population, yet up-to-date local data on bacteriological profiles and susceptibility patterns are scarce (8, 9). In the absence of reliable local antibiograms, clinicians frequently rely on empirical treatment regimens that may not align with current resistance trends. This practice not only compromises patient outcomes but also contributes to further resistance development (10).

The importance of continuous local surveillance cannot be overstated. Microbiological monitoring enables the identification of prevalent pathogens and evolving resistance patterns, thereby informing evidence-based empirical therapy. Such data are essential for guiding hospital antibiotic policies and strengthening antimicrobial stewardship initiatives (11, 12).

Moreover, understanding differences between community-acquired and hospital-associated infections can help tailor targeted interventions to reduce the burden of multidrug-resistant organisms. Given the rising global concern regarding antimicrobial resistance and the limited region-specific data available from southern Punjab, there exists a clear need for systematic evaluation of urinary pathogens and their susceptibility patterns within this setting. Generating localized evidence is crucial to support rational antibiotic selection, optimize patient outcomes, and inform public health strategies aimed at combating resistance (13, 14).

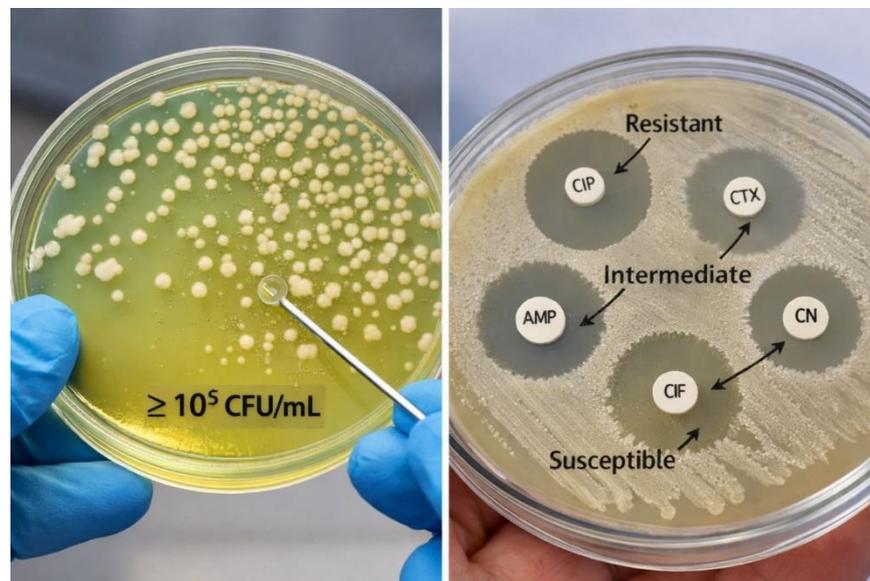
Therefore, the present study was conducted to identify the prevalent bacterial pathogens responsible for urinary tract infections in a tertiary care hospital in Multan and to determine

their antimicrobial susceptibility patterns. By providing current, institution-based data, this study sought to contribute to informed empirical treatment decisions and support the development of context-specific antimicrobial stewardship policies in the region.

METHODS

This cross-sectional descriptive study was conducted over a four-month period from May to August 2025 at a tertiary care hospital in Multan, located in the southern region of Punjab, Pakistan. The study aimed to determine the bacteriological profile and antimicrobial susceptibility patterns among patients presenting with clinical features suggestive of urinary tract infections (UTIs).

Based on previously published regional studies that reported sample sizes ranging from 50 to 100 participants for similar microbiological surveillance, a total sample size of 72 patients was determined to be adequate to provide reliable preliminary estimates within the available timeframe and laboratory capacity. Consecutive sampling was employed to recruit eligible participants.



Patients of either gender, aged 18 years and above, who presented to the outpatient department or were admitted to medical wards with symptoms suggestive of UTI (such as dysuria, urinary frequency, urgency, suprapubic pain, or fever) and had a positive urine culture were included. Patients who had received systemic antibiotics within the preceding 72 hours, those with polymicrobial growth suggestive of contamination, individuals with known structural urinary tract abnormalities, and patients unwilling to provide informed consent were excluded.

Midstream clean-catch urine samples were collected in sterile, wide-mouthed containers following standardized instructions. Samples were transported promptly to the hospital microbiology laboratory and processed within two hours of collection. Urine specimens were cultured on Cystine Lactose Electrolyte Deficient (CLED) agar and MacConkey agar using a calibrated 0.001 mL loop.

Plates were incubated aerobically at 37°C for 18–24 hours. Significant bacteriuria was defined as a colony count of $\geq 10^5$ colony-forming units (CFU)/mL. Bacterial identification was performed using standard microbiological techniques, including Gram staining, colony morphology assessment, catalase and coagulase tests for Gram-positive organisms, and biochemical profiling with Analytical Profile Index (API 20E) strips for Gram-negative

isolates. Antimicrobial susceptibility testing was carried out using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. Antibiotic discs included commonly prescribed agents such as ampicillin, amoxicillin-clavulanic acid, ciprofloxacin, ceftriaxone, nitrofurantoin, gentamicin, and imipenem. Zone diameters were measured in millimeters and interpreted as susceptible, intermediate, or resistant according to CLSI breakpoints.

Data were recorded on a structured proforma capturing demographic details, clinical features, isolated organisms, and susceptibility results. Data were entered and analyzed using SPSS version 26.0.

Continuous variables were expressed as mean \pm standard deviation after confirming normal distribution using the Shapiro–Wilk test. Categorical variables were summarized as frequencies and percentages. The independent t-test was applied to compare mean age between groups, while the chi-square test was used to assess associations between bacterial isolates and antimicrobial resistance patterns. A p-value of less than 0.05 was considered statistically significant.

RESULTS

A total of 79 patients were initially assessed for eligibility during the study period. Seven patients were excluded due to recent antibiotic use ($n=4$) or contaminated urine samples ($n=3$). Seventy-two patients fulfilled the inclusion criteria and were included in the final analysis, yielding a response rate of 91.1%. All collected samples demonstrated significant bacteriuria ($\geq 10^5$ CFU/mL) and were processed for identification and antimicrobial susceptibility testing.

The mean age of participants was 36.8 ± 14.2 years (range: 18–72 years), with the majority aged between 21–40 years (45.8%). Females constituted 47 (65.3%) of the cohort, resulting in a female-to-male ratio of approximately 1.9:1. Most patients were managed in the outpatient department (61.1%), while 38.9% were admitted to medical wards. Dysuria (81.9%) and urinary frequency (73.6%) were the most commonly reported symptoms. The demographic and baseline clinical characteristics are summarized in Table 1.

Gram-negative organisms predominated, accounting for 86.1% of isolates. *Escherichia coli* was the most frequently isolated pathogen (54.2%), followed by *Klebsiella pneumoniae* (18.1%), *Pseudomonas aeruginosa* (8.3%), and *Proteus mirabilis* (5.5%). Among Gram-positive isolates, *Staphylococcus saprophyticus* (6.9%) and *Enterococcus faecalis* (6.9%) were identified. The distribution of bacterial isolates is detailed in Table 2.

High resistance rates were observed against ampicillin (76.4%) and ciprofloxacin (58.3%), whereas nitrofurantoin (81.9% sensitivity) and imipenem (94.4% sensitivity) demonstrated the greatest efficacy. *Escherichia coli* showed significant resistance to ampicillin (82.1%) compared to non-*E. coli* isolates (65.2%), although this difference did not reach statistical significance ($p=0.091$). A statistically significant association was observed between Gram-negative isolates and resistance to ceftriaxone ($p=0.032$). Detailed antimicrobial susceptibility patterns are presented in Table 3.

Comparative analysis revealed that hospitalized patients exhibited a higher proportion of multidrug-resistant (MDR) isolates (57.1%) compared to outpatients (31.8%), and this difference was statistically significant ($\chi^2=4.62$, $p=0.032$). The comparative resistance patterns by patient setting are shown in Table 4. The findings collectively highlighted a predominance of Gram-negative uropathogens with considerable resistance to commonly prescribed oral antibiotics.

Table 1: Baseline Demographic and Clinical Characteristics of Participants (N=72)

Variable	Category	n (%) / Mean ± SD
Age (years)	Mean ± SD	36.8 ± 14.2
Age Group	18–20	6 (8.3%)
	21–40	33 (45.8%)
	41–60	21 (29.2%)
	>60	12 (16.7%)
Gender	Male	25 (34.7%)
	Female	47 (65.3%)
Patient Type	Outpatient	44 (61.1%)
	Inpatient	28 (38.9%)
Dysuria	Present	59 (81.9%)
Urinary Frequency	Present	53 (73.6%)
Fever	Present	29 (40.3%)

Table 2: Distribution of Bacterial Isolates (N=72)

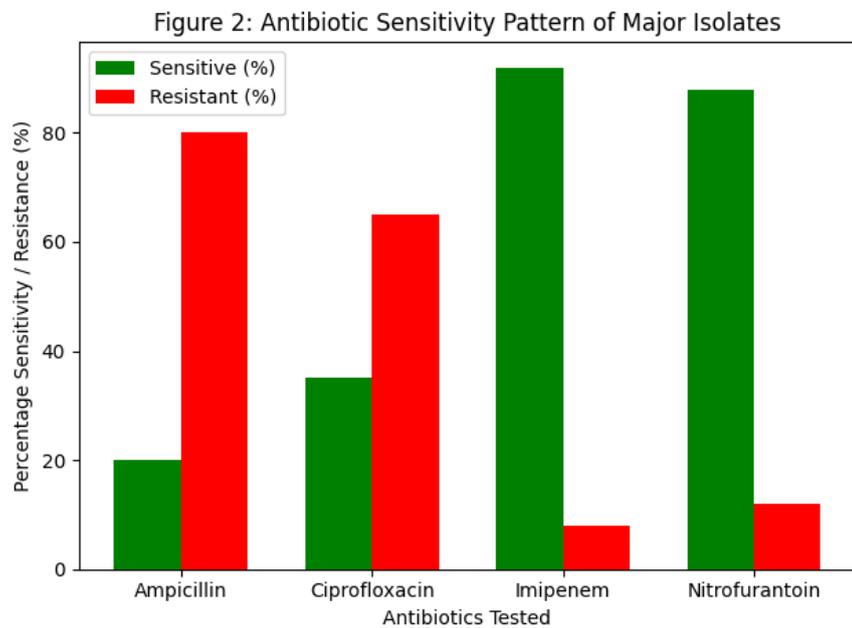
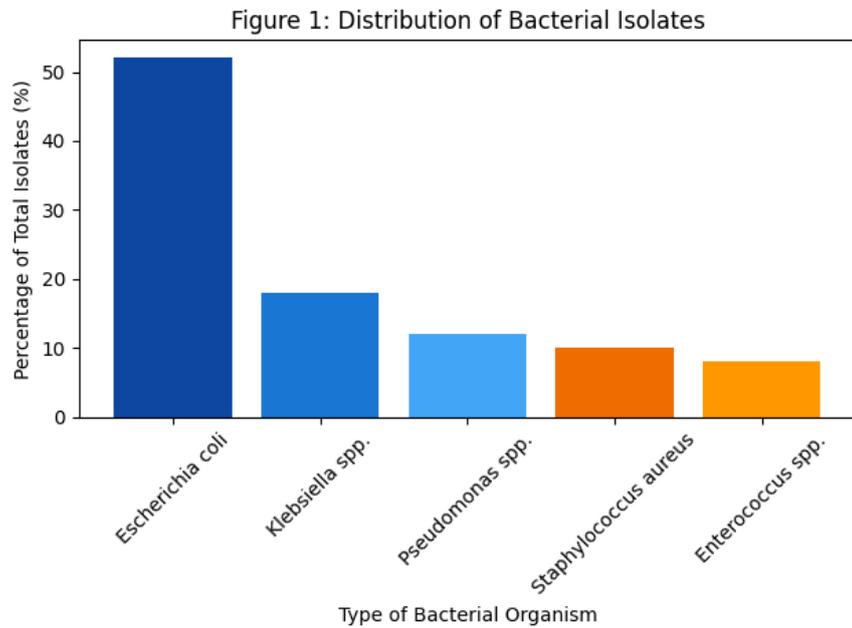
Organism	n (%)
Escherichia coli	39 (54.2%)
Klebsiella pneumoniae	13 (18.1%)
Pseudomonas aeruginosa	6 (8.3%)
Proteus mirabilis	4 (5.5%)
Staphylococcus saprophyticus	5 (6.9%)
Enterococcus faecalis	5 (6.9%)

Table 3: Antimicrobial Susceptibility Patterns of Isolates

Antibiotic	Sensitive n (%)	Resistant n (%)
Ampicillin	17 (23.6%)	55 (76.4%)
Amoxicillin-Clavulanate	36 (50.0%)	36 (50.0%)
Ciprofloxacin	30 (41.7%)	42 (58.3%)
Ceftriaxone	34 (47.2%)	38 (52.8%)
Gentamicin	46 (63.9%)	26 (36.1%)
Nitrofurantoin	59 (81.9%)	13 (18.1%)
Imipenem	68 (94.4%)	4 (5.6%)

Table 4: Comparison of Multidrug Resistance by Patient Setting

Variable	Outpatients (n=44)	Inpatients (n=28)	p-value
MDR Isolates n (%)	14 (31.8%)	16 (57.1%)	0.032
Non-MDR Isolates n (%)	30 (68.2%)	12 (42.9%)	



DISCUSSION

The present study delineated the bacteriological spectrum and antimicrobial susceptibility patterns among patients with urinary tract infections in a tertiary care hospital in Multan, southern Punjab. The findings demonstrated a clear predominance of Gram-negative organisms, with *Escherichia coli* emerging as the principal uropathogen, followed by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. This distribution aligned with

established global and regional trends, where *E. coli* consistently accounts for the majority of community- and hospital-acquired urinary tract infections. The higher proportion of female patients and the concentration of cases in the younger adult age group further reflected known epidemiological patterns attributable to anatomical and behavioral factors that predispose women to urinary tract infections. The antimicrobial susceptibility profile revealed a concerning degree of resistance to commonly prescribed oral antibiotics, particularly ampicillin, ciprofloxacin, and ceftriaxone. These findings were consistent with increasing antimicrobial resistance trends reported in South Asia, where widespread empirical use and over-the-counter availability of antibiotics have contributed to selective pressure (9, 15). The relatively preserved sensitivity to nitrofurantoin and imipenem suggested that these agents remain effective therapeutic options in this setting. Nitrofurantoin, in particular, demonstrated high sensitivity against most isolates, reinforcing its role as a first-line agent for uncomplicated lower urinary tract infections (16). The high efficacy of imipenem reflected limited resistance to carbapenems, although its parenteral administration and cost restrict its routine empirical use and necessitate stewardship-driven prescription (17, 18).

An important observation was the significantly higher proportion of multidrug-resistant isolates among hospitalized patients compared to outpatients. This finding highlighted the impact of healthcare exposure and potential prior antibiotic use on resistance patterns. It underscored the importance of tailored antimicrobial policies within inpatient settings and strengthened the argument for regular local antibiogram surveillance to guide empirical therapy (19, 20). The statistically significant association between Gram-negative isolates and ceftriaxone resistance further emphasized the evolving resistance mechanisms among Enterobacteriaceae, including the possible presence of extended-spectrum beta-lactamase-producing strains. The study possessed several strengths. It relied on standardized microbiological techniques and adherence to CLSI guidelines for susceptibility testing, thereby ensuring methodological rigor and reproducibility. The use of consecutive sampling minimized selection bias, and the inclusion of both outpatient and inpatient populations allowed comparison across different clinical settings (21). Additionally, laboratory processing within a defined timeframe preserved specimen integrity and enhanced reliability of culture results (22).

However, certain limitations warranted acknowledgment. The relatively small sample size and short study duration restricted the generalizability of the findings beyond the study setting. Seasonal variations in infection patterns could not be assessed due to the limited timeframe (23). Molecular characterization of resistant isolates was not performed, which precluded confirmation of specific resistance mechanisms such as extended-spectrum beta-lactamase or carbapenemase production. Furthermore, prior antibiotic exposure beyond 72 hours and comorbid conditions were not extensively evaluated, limiting insight into risk factors associated with resistance. The cross-sectional design also constrained the ability to establish temporal trends in antimicrobial resistance. The findings carried important clinical and public health implications. The high resistance rates to first-line oral agents highlighted the urgent need for antibiotic stewardship programs, rational prescribing practices, and continuous monitoring of local resistance patterns. Empirical therapy for urinary tract infections in this region should be reconsidered in light of the documented resistance, particularly against ampicillin and fluoroquinolones. Strengthening laboratory capacity for routine culture and sensitivity testing could reduce inappropriate empirical treatment and mitigate the progression of resistance (24, 25).

Future research should focus on multicenter studies with larger sample sizes to enhance representativeness across southern Punjab. Longitudinal surveillance would provide

valuable insight into evolving resistance trends over time. Incorporating molecular diagnostics could elucidate specific resistance genes and transmission dynamics within hospital settings. Investigating patient-related risk factors and treatment outcomes would further inform targeted interventions. Through sustained surveillance and integrated antimicrobial stewardship strategies, improved management of urinary tract infections in the region could be achieved while limiting the escalation of antimicrobial resistance.

CONCLUSION

This study demonstrated that Gram-negative organisms, particularly *Escherichia coli*, were the predominant causative agents of urinary tract infections in the studied tertiary care hospital in Multan. High resistance rates to commonly prescribed oral antibiotics, including ampicillin and ciprofloxacin, were observed, whereas nitrofurantoin and imipenem retained substantial efficacy. These findings underscore the necessity for routine culture-based diagnosis, continuous local antibiogram surveillance, and strengthened antimicrobial stewardship to guide empirical therapy and curb the growing threat of antimicrobial resistance.

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DECLARATIONS

Ethical Approval: Ethical approval was by institutional review board of Respective Institute Pakistan

Informed Consent: Informed Consent was taken from participants.

Authors' Contributions:

Concept: MAW; Design: AN, MTA; Data Collection: AS, WS; Analysis: MZ, UAS; Drafting: MAW, AN

Conflict of Interest: The authors declare no conflict of interest.

Funding: This research received no external funding.

Data Availability: The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request.

Acknowledgments: NA

Study Registration: Not applicable.