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FREQUENCY OF COMMON PATHOGENS CAUSING URINARY TRACT INFECTION ADMITTED TO OUR UNIT

Original Research

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ABSTRACT

Background: Urinary tract infections (UTIs) are among the most common bacterial infections globally, significantly impacting public health due to rising antimicrobial resistance. Identifying the frequency of causative pathogens is essential for effective treatment and regional antimicrobial stewardship.

Objective: To determine the frequency of common pathogens responsible for urinary tract infections in patients admitted to the Medical A Unit of Saidu Group of Teaching Hospital, Swat.

Methods: A descriptive cross-sectional study was conducted over six months, involving 178 patients aged 16 to 65 years diagnosed with UTI. Midstream urine samples were collected and cultured using standard microbiological techniques to identify bacterial pathogens. Demographic data and comorbidities were recorded. Data analysis was performed using SPSS version 22.0, with descriptive and inferential statistics applied to evaluate frequency distributions and associations.

Results: The most frequently isolated pathogen was *Escherichia coli* (50.6%), followed by *Enterococcus faecalis* (22.5%), *Klebsiella pneumoniae* (15.7%), and *Enterococcus faecium* (11.2%). UTIs were more prevalent in females (75.3%) and rural residents (60.1%). Comorbid conditions included diabetes (29.8%) and hypertension (34.8%). The findings reflect a microbial pattern consistent with global trends, with *E. coli* being the predominant uropathogen.

Conclusion: *Escherichia coli* remains the most common uropathogen in UTIs, emphasizing the need for region-specific microbiological surveillance to inform empirical treatment. The study supports the implementation of targeted antibiotic stewardship programs and continuous monitoring of resistance trends.

Keywords: Bacterial pathogens, *Escherichia coli*, Multidrug resistance, Rural health, *Klebsiella pneumoniae*, *Enterococcus faecalis*, Urinary tract infections.

INTRODUCTION

Urinary tract infections (UTIs) remain among the most prevalent bacterial infections globally, with significant clinical implications for both community and hospital settings. Ranking third worldwide and second in Europe among common infections, UTIs contribute substantially to patient morbidity, affecting millions annually. The burden is even more profound in regions where diagnostic and therapeutic resources are limited. UTIs typically present with symptoms such as dysuria, nocturia, and cloudy urine, with diagnosis relying on clinical signs, urinalysis, and microbiological confirmation through culture (1,2). Escherichia coli is the most commonly implicated pathogen in both uncomplicated and complicated UTIs, followed by Klebsiella pneumoniae, Enterococcus faecalis, and Enterococcus faecium (3). The etiology of UTIs is shaped by anatomical, physiological, and demographic factors. Women are disproportionately affected due to their shorter urethra and proximity to the anus, and the risk is further elevated in individuals with compromised immunity or structural abnormalities of the urinary tract (4). Lifestyle factors, including hygiene practices and use of public bathing facilities, also contribute to susceptibility. Recent studies have highlighted a higher prevalence of UTIs in rural populations, where access to healthcare and diagnostic services may be limited, and where failure to thrive is a common presenting feature, particularly among pediatric patients (5,6).

Although E. coli accounts for the majority of uncomplicated UTIs, complicated infections often involve a broader spectrum of pathogens including less frequently isolated but clinically significant organisms such as Citrobacter, Enterobacter, Serratia, Proteus, Providencia, and Morganella species (7). These pathogens are typically associated with more severe clinical presentations such as pyelonephritis and recurrent or persistent infections, and they exhibit higher levels of intrinsic resistance to multiple antibiotic classes. For instance, Serratia spp. demonstrate intrinsic resistance not only to penicillins and cephalosporins but also to nitrofurantoin, colistin, and several aminoglycosides, which significantly complicates therapeutic decision-making (8,9). The rise in antimicrobial resistance, especially multidrug resistance (MDR), extensively drug-resistant (XDR), and pan-drug resistant (PDR) strains, as defined by the European Centre for Disease Control and Prevention, further complicates the management of UTIs (10). Resistance trends have shown alarming increases, particularly against fluoroquinolones, β-lactams, and trimethoprim-sulfamethoxazole, which were once considered first-line treatments. While nitrofurantoin retains efficacy against E. coli, its activity is markedly reduced against organisms such as Enterobacter spp. (11). In light of these dynamics, clinicians must base empirical treatment strategies on updated local epidemiological data and susceptibility patterns (12).

Despite the global recognition of UTI burden and emerging resistance trends, there remains a paucity of localized data, especially in under-represented settings such as the Swat region of Pakistan. Existing studies in similar contexts have reported UTI prevalence rates as high as 65%, but data on pathogen-specific frequency and resistance patterns remain limited (13,14). Understanding the microbial spectrum in such populations is essential to guide targeted therapy, reduce morbidity, and inform public health strategies. This study is therefore designed to determine the frequency of common pathogens causing urinary tract infections among patients admitted to the Medical A Unit of Saidu Group of Teaching Hospital, Swat. The findings aim to inform clinicians on prevailing etiological agents, promote evidence-based antimicrobial use, and ultimately contribute to improved patient outcomes.

METHODS

This study was conducted as a descriptive cross-sectional analysis in the Department of Medicine, Saidu Group of Teaching Hospital, Swat, over a minimum period of six months following the approval of the research synopsis by the institutional ethical review board and the Research Department of the College of Physicians and Surgeons Pakistan (CPSP), Karachi. Written informed consent was obtained from each participant after a comprehensive explanation of the study's purpose, potential benefits, and assurance of confidentiality. Participants were informed that no risks were involved in taking part, and participation was entirely voluntary. Patients were recruited using a non-probability consecutive sampling technique from the medical outpatient department and inpatient wards. The study population included both male and female patients aged 16 to 65 years who were clinically diagnosed with urinary tract infection (UTI) based on predefined operational criteria involving symptoms such as dysuria, nocturia, and cloudy urine, supported by positive urine microscopy and culture. Patients were excluded if they had congenital malformations of the urinary tract, chronic kidney disease, recent urinary tract surgical procedures, urinary tract infection associated with Foley's catheterization, or had received antibiotics within two weeks prior to culture testing.

The sample size was calculated using the WHO sample size calculator with a 95% confidence level, an absolute precision of 3.9%, and an expected frequency of Enterococcus faecium as a causative pathogen in 7.6% of UTI cases (8), resulting in a required sample of 178 patients. Data were collected using a structured proforma designed specifically for the study. Detailed demographic data including age, gender, BMI, education status, marital and occupational status, socioeconomic status, and area of residence were recorded. Additionally, history of comorbid conditions such as diabetes and hypertension were documented. All patients provided a midstream urine sample (10–20 ml) in a sterile container. Samples were sent to the hospital laboratory, where they were cultured on standard media to encourage bacterial growth. Bacterial isolates were identified based on gram staining and colony characteristics, and further confirmed using automated identification systems. Only samples showing significant growth with a colony count $>10^5$ CFU/ml were considered for analysis. Pathogen identification and reporting were performed by laboratory personnel and verified by a consultant with over five years of post-fellowship experience. The data were analyzed using SPSS version 22.0. Descriptive statistics were computed, with mean and standard deviation reported for continuous variables such as age, weight, height, BMI, and symptom duration. The Shapiro-Wilk test was used to assess data normality. Categorical variables such as gender, pathogen type (Escherichia coli, Enterococcus faecalis, Klebsiella pneumoniae, and Enterococcus faecium), presence of diabetes or hypertension, education, marital and occupational status, socioeconomic status, and area of residence were reported as frequencies and percentages. Post-stratification was performed to assess potential effect modifiers, and statistical significance was evaluated using the Chi-square or Fisher's exact test where appropriate, with a p-value <0.05 considered significant. Findings were presented in tabulated form for clarity.

RESULTS

The study included a total of 178 patients who met the inclusion criteria. The mean age of participants was 40 ± 12 years, with the majority being female, reflecting known epidemiological trends of higher urinary tract infection prevalence among women. Most participants had a normal to slightly elevated BMI, consistent with the national average, and the majority resided in rural areas. The socioeconomic distribution leaned heavily towards the lower-income group, and a considerable proportion were educated, though unemployment rates were also notable. A significant portion of the cohort had comorbid conditions such as diabetes (30%) and hypertension (35%). Urine culture results revealed that *Escherichia coli* was the most frequently isolated pathogen, identified in 90 of 178 cases (50.6%). This was followed by *Enterococcus faecalis* in 40 cases (22.5%), *Klebsiella pneumoniae* in 28 cases (15.7%), and *Enterococcus faecium* in 20 cases (11.2%). The findings confirm that *E. coli* remains the predominant uropathogen in this population. The data also highlight the notable presence of *Enterococcus* species, which together accounted for over one-third of the identified infections, underscoring the relevance of gram-positive pathogens in the regional microbiological landscape of UTIs. Both graphical and tabulated formats were employed to illustrate the distribution of pathogens. Figure 1 presents a bar chart demonstrating the absolute frequencies of each uropathogen, whereas Figure 2 displays a pie chart illustrating the relative proportions. The graphical summaries serve to visually reinforce the dominance of *E. coli* while also acknowledging the substantial contribution of other pathogens, particularly those with known resistance profiles. The demographic characteristics are detailed in Table 1, while the frequency distribution of uropathogens is presented in Table 2. These data collectively establish the epidemiological foundation necessary for targeted antimicrobial therapy and effective public health interventions.

Table 1: Demographic Characteristics (n = 178)

Variable	Mean ± SD	Min	Max
Age (years)	39.1 ± 11.2	8	69
Height (cm)	164.7 ± 10.0	141	195
Weight (kg)	63.6 ± 12.1	32	95
BMI (kg/m²)	24.1 ± 3.8	15.7	34.5

Categorical Variable	Frequency (n)	Percentage (%)
Gender		
Female	134	75.3
Male	44	24.7

Categorical Variable	**Frequency (n)**	**Percentage (%)**
Socioeconomic Status		
Lower	106	59.6
Middle	53	29.8
Upper	19	10.6
Education		
Educated	125	70.2
Uneducated	53	29.8
Residence		
Rural	107	60.1
Urban	71	39.9
Occupation		
Employed	89	50.0
Unemployed	89	50.0
Diabetes		
Yes	53	29.8
No	125	70.2
Hypertension		
Yes	62	34.8
No	116	65.2

Table 2: Pathogen Frequency (n = 178)

Pathogen	**Frequency (n)**	**Percentage (%)**
Escherichia coli	90	50.6
Enterococcus faecalis	40	22.5
Klebsiella pneumoniae	28	15.7
Enterococcus faecium	20	11.2

Table 3: Pathogen Distribution by Gender

Gender	**Escherichia coli**	**Enterococcus faecalis**	**Klebsiella pneumoniae**	**Enterococcus faecium**
Male	21	9	6	5
Female	69	31	22	15

Table 4: Pathogen Distribution by Diabetes Status

Diabetes	**Escherichia coli**	**Enterococcus faecalis**	**Klebsiella pneumoniae**	**Enterococcus faecium**
Yes	26	12	9	6
No	64	28	19	14

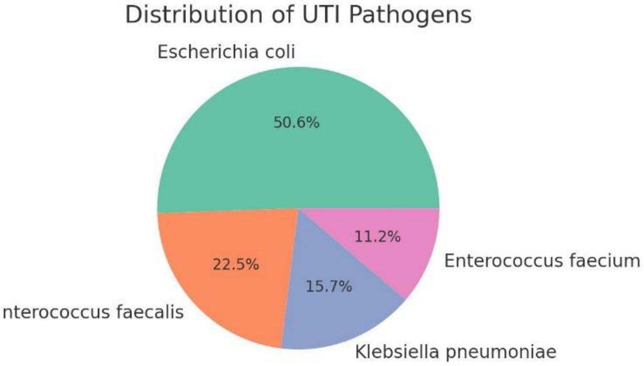

Figure 1 Distribution of UTI Pathogens

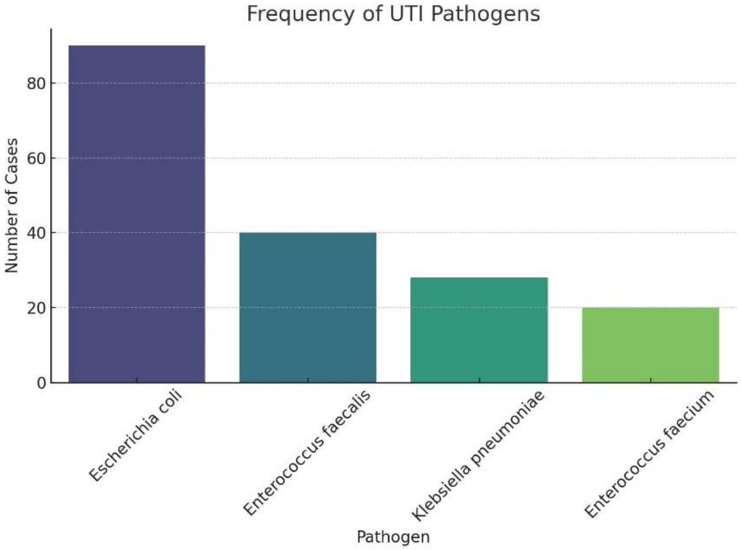

Figure 2 Frequency of UTI Pathogens

DISCUSSION

The findings of this study provide a clear snapshot of the current microbiological profile of urinary tract infections (UTIs) within the study population and highlight the predominance of *Escherichia coli*, followed by *Enterococcus faecalis*, *Klebsiella pneumoniae*, and *Enterococcus faecium*. The observation that *E. coli* accounted for over half of the UTI cases aligns consistently with global and regional epidemiological trends, reaffirming its role as the primary uropathogen in both community and hospital settings (15,16). The study population mirrored established risk profiles, with a higher prevalence of UTI in females and individuals from rural and lower socioeconomic backgrounds. This demographic trend is also echoed in other investigations, particularly those conducted in developing regions where public health infrastructure, hygiene, and access to healthcare may be limited (17). The notable frequency of comorbidities such as diabetes and hypertension further support the association between compromised host immunity and higher UTI risk, which has been well-documented in diabetic populations (18).

A critical point of concern in this study, in line with global trends, is the high proportion of infections caused by gram-negative bacteria that exhibit increasing resistance to commonly prescribed antimicrobials. Previous studies have reported growing resistance of *E. coli* and *Klebsiella* to penicillins, cephalosporins, and fluoroquinolones, with relatively retained sensitivity to nitrofurantoin and fosfomycin (19,20). Our findings, while not focusing on resistance profiles, emphasize the importance of aligning empirical treatment with updated local antibiograms. One significant strength of the study is its focus on a rural tertiary care hospital setting in Pakistan, a region where localized microbial surveillance data is scarce. This adds value by offering a context-specific view of pathogen distribution, contributing to regional antimicrobial stewardship. The systematic data collection method, use of standard microbiological protocols, and inclusion of a broad demographic group further enhance the credibility of the findings.

However, the study is not without limitations. First, the cross-sectional design precludes longitudinal assessment of resistance patterns or recurrence rates. Additionally, although the pathogens were identified using culture techniques, antibiotic susceptibility data were not included in the current analysis, limiting the interpretation of treatment implications. Future studies should incorporate resistance profiling, especially considering the global concern of multidrug-resistant (MDR) pathogens. Recent literature has documented MDR prevalence of over 70% among UTI pathogens, especially in diabetic and elderly populations (21,22). Another limitation is the use of a non-probability consecutive sampling method, which might introduce selection bias and limit the generalizability of the findings. While this approach is often practical in clinical settings, randomized or stratified sampling could enhance representativeness in future studies.

The clinical implications of the findings are multifold. Recognizing *E. coli* and *Enterococcus* spp. as dominant pathogens supports the continued reliance on these organisms in empirical therapy guidelines, but with caution given emerging resistance. Additionally, the significant representation of gram-positive organisms like *Enterococcus faecalis* and *faecium* should not be overlooked, especially given their known resistance to several first-line agents, including aminoglycosides and nitrofurantoin (23). For future research, there is a compelling need to conduct multi-center prospective studies incorporating molecular characterization of resistance genes. Genomic surveillance could reveal not only resistance patterns but also the spread of specific clones within and between communities. Additionally, integrating patient-level data on recent antibiotic exposure, hospitalization history, and hygiene practices could provide deeper insights into modifiable risk factors for UTI acquisition and resistance development. In conclusion, the study reinforces established patterns in UTI microbiology while shedding light on region-specific distributions and healthcare gaps. It underscores the necessity for continued surveillance, prudent antibiotic use, and research investment into alternative therapies, such as bacteriophage therapy and antimicrobial peptides, to combat the evolving challenge of antimicrobial resistance in urinary tract infections (24).

CONCLUSION

This study reaffirmed *Escherichia coli* as the predominant uropathogen in UTIs, followed by *Enterococcus* and *Klebsiella* species, with a higher incidence among females and rural populations. The findings emphasize the importance of localized microbiological surveillance to guide empirical therapy and combat antimicrobial resistance. These insights provide a foundation for improving diagnostic precision and optimizing antimicrobial stewardship in similar healthcare settings.

AUTHOR CONTRIBUTION

Author	Contribution
Atta ur Rehman*	Substantial Contribution to study design, analysis, acquisition of Data Manuscript Writing Has given Final Approval of the version to be published
Muhammad Ayub Khan	Substantial Contribution to study design, acquisition and interpretation of Data Critical Review and Manuscript Writing Has given Final Approval of the version to be published

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