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ORIGINAL PAPER

Epidemiology and antimicrobial resistance of uropathogens in a tertiary care setting in Yemen: A retrospective study

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Summary *Background: Urinary tract infections (UTIs) are a major global health concern, particularly in resource-limited regions where antimicrobial resistance (AMR) is increasingly prevalent. This study aimed to describe the demographic characteristics, pathogen distribution, and antimicrobial resistance patterns among UTI patients, and to identify clinical predictors of multidrug-resistant (MDR) and extensively drug-resistant (XDR) infections.*
Methods: A retrospective analysis was conducted on 216 clinically confirmed UTI cases processed at the Infectious Bacteriology and Biochemistry Laboratory affiliated with IBB University between January 2023 and September 2024. Data collected included patient demographics, clinical symptoms, comorbidities, bacterial isolates, and antimicrobial susceptibility profiles. MDR and XDR were classified according to internationally recognized definitions. Univariate and multivariate logistic regression analyses were performed to identify independent predictors of MDR/XDR infections.
Results: The majority of patients were adults aged 15-65 years (83.3%, n = 180), with a slight male predominance (53.2%, n = 115). Escherichia coli was the most frequently isolated pathogen (29.6%, n = 64), followed by Staphylococcus aureus (19.0%, n = 41) and Pseudomonas aeruginosa (6.0%, n = 13). A substantial proportion of isolates exhibited MDR or XDR phenotypes (80.1%, n = 173). Among E. coli isolates, resistance rates to ciprofloxacin and ceftriaxone exceeded 60%. Notably, all Klebsiella pneumoniae isolates were MDR (100%), and 92.3% of P. aeruginosa isolates were MDR. Nitrofurantoin and carbapenems demonstrated relatively higher susceptibility rates. Multivariate analysis identified prior hospitalization (adjusted odds ratio [aOR] = 3.15; 95% CI: 1.50-6.60; p = 0.002) and E. coli infection (aOR = 2.41; 95% CI: 1.02–5.70; p = 0.04) as significant predictors of MDR/XDR infections.
Conclusions: The high prevalence of MDR and XDR uropathogens, particularly E. coli, underscores the urgent need for sustained antimicrobial resistance surveillance and stewardship programs in resource-limited settings. Identifying key clinical predictors can inform empirical treatment strategies, improve patient outcomes, and help contain the spread of resistant organisms.

KEY WORDS: *Urinary tract infections; Uropathogenic Escherichia coli; Antimicrobial resistance; Multidrug resistance (MDR); extensively drug-resistant (XDR); Yemen; Resource-limited setting.*

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INTRODUCTION

Urinary tract infections (UTIs) are among the most common bacterial infections globally, with over 150 million cases reported annually (1, 2). They impose a significant clinical and economic burden on healthcare systems, ranging from uncomplicated cystitis to severe conditions such as pyelonephritis and urosepsis (1). The severity of clinical presentation often reflects the extent of disease progression (3). Gram-negative bacteria, particularly *Escherichia coli* (E. coli), remain the predominant uropathogens worldwide. However, recent epidemiological trends indicate a growing prevalence of non-E. coli organisms, including *Klebsiella pneumoniae* (K. pneumoniae), *Pseudomonas aeruginosa* (P. aeruginosa), and *Staphylococcus aureus* (S. aureus), which complicates empirical treatment decisions and highlights the need for continuous surveillance (4, 5).
The emergence of *antimicrobial resistance* (AMR), especially *multidrug-resistant* (MDR) and *extensively drug-resistant* (XDR) strains, has further complicated the management of UTIs (6). MDR is defined as resistance to at least three antimicrobial classes, while XDR refers to resistance to all but two or fewer antimicrobial classes (7). These resistance patterns are particularly concerning in resource-limited settings, where inadequate antimicrobial stewardship and limited diagnostic infrastructure contribute to the rapid dissemination of resistant organisms (7). Key molecular mechanisms underlying resistance include the production of *extended-spectrum β-lactamases* (ESBLs), carbapenemases (e.g., KPC and NDM), and the overexpression of efflux pumps. These mechanisms are associated with treatment failure, prolonged hospital stays, increased healthcare costs, and higher mortality rates (8).

In Yemen, the inappropriate use of antibiotics is a major driver of AMR. A prior study in Aden reported that antibiotics were prescribed in 84.2% of outpatient cases, a rate far exceeding *World Health Organization* (WHO) recommendations (9). This issue is compounded by the widespread availability of counterfeit and substandard medicines. It is estimated that up to 80% of pharmaceuticals entering Yemen are distributed through unregulated channels, with approximately 40% being of poor quality or counterfeit (10).

According to WHO analyses, 43% of counterfeit antibiotics contain no active ingredient, 24% fail to meet quality standards, 21% contain subtherapeutic concentrations, and 7% contain incorrect substances (11). The combination of irrational prescribing practices and the proliferation of ineffective antimicrobials creates a conducive environment for the emergence and spread of resistant uropathogens. Patients exposed to subtherapeutic or inactive treatments are at increased risk of treatment failure, facilitating the persistence and transmission of resistant strains in the community (12).

Despite national efforts to monitor AMR, there remains a significant gap in data regarding the distribution and resistance profiles of uropathogens in Yemen, particularly in tertiary care settings. This lack of local evidence limits the development of context-specific treatment guidelines and infection control strategies. Understanding the demographic and clinical factors associated with MDR and XDR UTIs – such as prior hospitalization, comorbidities, and healthcare exposure – is essential for improving patient outcomes and informing antimicrobial stewardship programs (12). This study aimed to describe the demographic characteristics, pathogen distribution, and antimicrobial resistance patterns among UTI cases at a tertiary referral laboratory in Ibb, Yemen. Additionally, it sought to identify clinical predictors of MDR and XDR infections to support evidence-based prescribing and enhance regional AMR surveillance.

Patients and methods

Study design and setting

This retrospective observational study was conducted at the *Infectious Bacteriology and Biochemistry* (IBB) Laboratory, affiliated with IBB University, located in Ibb City, Yemen. The IBB Laboratory functions as a tertiary referral center, receiving clinical specimens from diverse patient populations across multiple healthcare facilities. The study period spanned from January 1, 2023, to September 12, 2024.

Study population

The study included all patients with clinically confirmed UTIs whose urine samples were processed at the IBB Laboratory during the specified timeframe. A UTI was defined as the presence of typical clinical symptoms – such as dysuria, urinary frequency, and urgency – accompanied by a positive urine culture yielding ≥ 10^5 *colony-forming units per milliliter* (CFU/mL) of a single uropathogen. This definition aligns with internationally recognized diagnostic criteria for UTI (e.g., EMA and FDA guidelines) (13). Patients with contaminated samples (mixed flora), or duplicate isolates from the same infection episode were excluded. Consecutive sampling was employed to minimize selection bias, resulting in a final sample of 216 eligible cases.

Sample collection and microbiological analysis

Midstream urine specimens were collected using standardized aseptic techniques to reduce contamination risk. Initial screening was performed using urine dipstick tests to detect leukocyte esterase and nitrites, which are suggestive of infection. However, dipstick results were not used as diagnostic criteria. Samples were inoculated onto CLED agar, blood agar, and MacConkey agar and incubated aerobically at 35-37°C for 18-24 hours. Bacterial growth was quantified, and isolates with ≥ 10^5 CFU/mL were considered clinically significant.

Bacterial identification was performed using a combination of conventional biochemical tests and automated systems, including VITEK 2 (*bioMérieux, Durham, NC, USA*) (14). Where available, *matrix-assisted laser desorption/ionization time-of-flight* (MALDI-TOF) mass spectrometry was used for confirmatory identification.

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing (AST) was conducted in accordance with the *Clinical and Laboratory Standards Institute* (CLSI) guidelines (31st Edition) (15). The Kirby-Bauer disk diffusion method and/or broth microdilution techniques were used to determine susceptibility to a panel of antibiotics commonly used in UTI treatment, including fluoroquinolones, β-lactams, aminoglycosides, nitrofurantoin, and carbapenems.

Minimum inhibitory concentrations (MICs) were interpreted using CLSI clinical breakpoints. MDR was defined as resistance to at least one agent in three or more antimicrobial classes, while XDR was defined as resistance to all but two or fewer antimicrobial classes, based on international consensus definitions (7). Quality control was maintained by including reference strains such as E. coli ATCC 25922 in each testing batch to ensure the validity and reproducibility of results.

Data collection and management

Relevant demographic, clinical, and microbiological data were extracted from the laboratory information system and patient medical records using a standardized data collection form. Double data entry and cross-validation were performed to ensure accuracy and minimize transcription errors. All data were anonymized prior to analysis. Patient confidentiality was maintained throughout the study in accordance with institutional ethical standards and the principles of the Declaration of Helsinki.

Statistical analysis

Data were analyzed using IBM SPSS Statistics version 23 (*IBM Corp., Armonk, NY, USA*). Descriptive statistics were used to summarize demographic, clinical, and microbiological variables. Categorical variables were expressed as frequencies and percentages, while continuous variables were reported as means ± *standard deviations* (SD) or medians with *interquartile ranges* (IQR), depending on

data distribution. Group comparisons were performed using the chi-square (χ^2) test or Fisher's exact test for categorical variables, and the Student's t-test or Mann-Whitney U test for continuous variables, following normality assessment using the Shapiro-Wilk test. Variables with a p-value < 0.20 in univariate analysis were included in a multivariable logistic regression model to identify independent predictors of MDR/XDR UTIs. *Adjusted odds ratios* (aOR) with 95% *confidence intervals* (CI) were calculated. Multicollinearity was assessed using the *variance inflation factor* (VIF), with values > 5 indicating significant collinearity. Model calibration was evaluated using the Hosmer-Lemeshow goodness-of-fit test, with a p-value > 0.05 indicating adequate fit. Discriminatory ability was assessed using the area under the receiver operating characteristic curve (AUC), with values between 0.7 and 0.8 considered acceptable. A two-tailed p-value < 0.05 was considered statistically significant for all analyses.

Ethical considerations

The study protocol was reviewed and approved by the Institutional Ethics Committee of IBB University (Approval No. IBBUNI.AC.YEM.2024.79). Given the retrospective nature of the study and the use of anonymized data, the requirement for informed consent was waived. All procedures were conducted in accordance with the ethical standards of the institutional research committee and the Declaration of Helsinki.

Results

Demographic and clinical characteristics

A total of 216 patients with clinically confirmed UTIs were included in the study. The majority were adults aged 15-65 years, comprising 180 patients (83.3%). Pediatric patients aged 1-14 years accounted for 24 patients (11.1%), while geriatric patients over 65 years represented 12 patients (5.6%) (Table 1). Males slightly outnumbered females, with 115 (53.2%) and 101 (46.8%) patients, respectively.

Most patients presented with symptomatic UTIs (91.7%, n = 198), while 8.3% (n = 18) had asymptomatic bacteriuria. Comorbidities were present in 32.4% of patients. Diabetes mellitus was the most common (19.4%, n = 42), followed by other chronic conditions such as hypertension, chronic kidney disease, or immunosuppression (13.0%, n = 28). The remaining 67.6% (n = 146) had no documented comorbidities. A history of prior hospitalization within the last six months was reported in 26.9% (n = 58) of cases.

The prevalence of MDR or XDR infections was high across all age groups: 75.0% (18/24) in pediatric patients, 81.1% (146/180) in adults, and 83.3% (10/12) in geriatric patients. However, these differences were not statistically significant (p = 0.12). Similarly, no significant difference in MDR/XDR prevalence was observed between males (79.1%, 91/115) and females (82.2%, 83/101) (p = 0.45). Symptomatic patients had an MDR/XDR prevalence of 80.8% (160/198), compared to 77.8% (14/18) in those with asymptomatic bacteriuria (p = 0.62).

Patients with diabetes mellitus exhibited a higher MDR/XDR prevalence (88.1%, 37/42) compared to those without comorbidities (78.1%, 114/146), though this difference was not statistically significant (p = 0.08). In contrast, prior hospitalization was significantly associated with MDR/XDR UTIs (89.7% vs. 77.2%, p = 0.02), highlighting its importance as a risk factor (Table 1).

Pathogen distribution and resistance profiles

A total of 216 bacterial isolates were identified. E. coli was the most frequently isolated pathogen (29.6%, n = 64), followed by S. aureus (19.0%, n = 41), P. aeruginosa (6.0%, n = 13), and K. pneumoniae (5.6%, n = 12) (Table 2). Other Gram-negative organisms accounted for 24.1% (n = 52) of isolates, while other Gram-positive species represented 15.7% (n = 34).

Overall, 56.0% (n = 121) of isolates were classified as MDR, and 25.9% (n = 56) as XDR. The highest MDR rates were observed in K. pneumoniae (100.0%, 12/12), followed by P. aeruginosa (92.3%, 12/13), E. coli (81.3%, 52/64), and S. aureus (73.2%, 30/41). XDR rates were also notable in K. pneumoniae (50.0%, 6/12), P. aerugi-

Characteristic	Category	N (%)	MDR/XDR cases n (%)	P-value
Age group	Pediatric (1-14 years)	24 (11.1)	18 (75.0)	0.12 *
	Adult (15-65 years)	180 (83.3)	146 (81.1)	
	Geriatric (> 65 years)	12 (5.6)	10 (83.3)	
Sex	Male	115 (53.2)	91 (79.1)	0.45 *
	Female	101 (46.8)	83 (82.2)	
Clinical presentation	Symptomatic UTI	198 (91.7)	160 (80.8)	0.62 *
	Asymptomatic Bacteriuria	18 (8.3)	14 (77.8)	
Comorbidities	Diabetes Mellitus	42 (19.4)	37 (88.1)	0.08 *
	Hypertension	15 (6.9)	12 (80.0)	0.83 *
	Chronic Kidney Disease	8 (3.7)	7 (87.5)	0.50 **
	Immunocompromised	5 (2.3)	4 (80.0)	1.00 **
	None (Reference)	146 (67.6)	114 (78.1)	–
Prior Hospitalization	Yes	58 (26.9)	52 (89.7)	0.02 *
	No	158 (73.1)	122 (77.2)	

** Chi-square test; ** Fisher's exact test (used for small cell counts).*
MDR/XDR percentages represent the proportion of resistant cases within each subgroup.

Table 1.
Demographic and clinical characteristics of patients with urinary tract infections and their association with multidrug-resistant/extensively drug-resistant status (n = 216).

Pathogen	Frequency n (%)	MDR Cases n (%)	XDR Cases n (%)
Escherichia coli	64 (29.6)	52 (81.3)	12 (18.8)
Staphylococcus aureus	41 (19.0)	30 (73.2)	10 (24.4)
Pseudomonas aeruginosa	13 (6.0)	12 (92.3)	5 (38.5)
Klebsiella pneumoniae	12 (5.6)	12 (100.0)	6 (50.0)
Other Gram-negative spp. *	52 (24.1)	38 (73.1)	14 (26.9)
Other Gram-positive spp. **	34 (15.7)	22 (64.7)	9 (26.5)

MDR = resistance to ≥ 3 antimicrobial classes; XDR = resistance to all but ≤ 2 classes.
** Includes Proteus spp. (n = 9), Enterobacter spp. (n = 8), Citrobacter spp. (n = 6), and others (n = 29).*
*** Includes Enterococcus spp. (n = 17), Streptococcus spp. (n = 5), and other species (n = 12).*
Overall MDR rate = 56.0% (121/216); XDR rate = 25.9% (56/216).

Table 2.
Frequency and resistance patterns of uropathogens isolated from patients with urinary tract infections (n = 216 Isolates).

Antibiotic (Class)	Resistant Isolates n (%)	Overall Resistance Rate	Pathogens with High Resistance (>75%)
Ciprofloxacin (Fluoroquinolone)	140 (64.8)	64.8%	Escherichia coli
Ceftriaxone (3rd-gen Cephalosporin)	164 (75.9)	75.9%	Klebsiella pneumoniae
Gentamicin (Aminoglycoside)	114 (52.8)	52.8%	Pseudomonas aeruginosa
Nitrofurantoin (Nitrofuran)	57/198 (28.8)	28.8%	Enterococcus faecalis (low resistance)
Meropenem (Carbapenem)	29 (13.4)	13.4%	Klebsiella pneumoniae

3rd-gen = Third-generation cephalosporin.
High resistance defined as > 75% resistance rate among isolates tested.
Nitrofurantoin was not tested against Pseudomonas spp. (n = 13) and non-UTI pathogens (n = 5).

Table 3.
Antimicrobial resistance profiles of uropathogens (n = 216 isolates).

nosa (38.5%, 5/13), S. aureus (24.4%, 10/41), and E. coli (18.8%, 12/64) (Table 2).

Antimicrobial resistance patterns

Antibiotic susceptibility testing revealed high resistance rates to several commonly used agents (Table 3). Ciprofloxacin resistance was observed in 64.8% (140/216) of isolates, with particularly high rates among E. coli (78.1%, 50/64) and P. aeruginosa (84.6%, 11/13). Ceftriaxone resistance was detected in 75.9% (164/216) of isolates, especially among K. pneumoniae (91.7%, 11/12). Gentamicin resistance was present in 52.8% (114/216) of isolates, with the highest rate observed in P. aeruginosa (76.9%, 10/13).

Nitrofurantoin resistance was relatively low, affecting 28.8% (57/198) of tested isolates. Enterococcus faecalis demonstrated the lowest nitrofurantoin resistance (12.0%, 3/25). Meropenem resistance was observed in 13.4% (29/216) of isolates, with a notably higher rate among K. pneumoniae (33.3%, 4/12) (Table 3).

Resistance phenotype classification

Based on resistance phenotypes, 17.6% (n = 38) of isolates were non-MDR, 56.0% (n = 121) were MDR, 25.9% (n = 56) were XDR, and 0.5% (n = 1) were pandrug-resistant (PDR) (Table 4). Among E. coli isolates, 18.8% (12/64) were non-MDR, 62.5% (40/64) were MDR, and 18.8% (12/64) were XDR. For S. aureus, 26.8% (11/41) were non-MDR, 48.8% (20/41) were MDR, and 24.4% (10/41) were XDR. P. aeruginosa isolates were predominantly MDR (53.8%, 7/13) or XDR (38.5%, 5/13). No PDR isolates were identified among these species, with the exception of one Acinetobacter baumannii isolate (Table 4).

Predictors of MDR/XDR urinary tract infections

Multivariable logistic regression analysis identified two independent predictors of MDR/XDR UTIs (Table 5). Infection with E. coli was significantly associated with an increased risk of MDR/XDR status aOR = 2.41; 95% CI, 1.02-5.70; p = 0.04). Prior hospitalization within the last six months was also a strong predictor (aOR = 3.15; 95% CI, 1.50-6.60; p = 0.002).

In contrast, age over 65 years (aOR = 1.82; 95% CI, 0.38-8.72; p = 0.45) and female sex (aOR = 0.91; 95% CI, 0.44-1.89; p = 0.80) were not significantly associated

Pathogen	Non-MDR n (%)	MDR n (%)	XDR n (%)	PDR n (%)
Escherichia coli	12 (18.8)	40 (62.5)	12 (18.8)	0 (0.0)
Staphylococcus aureus	11 (26.8)	20 (48.8)	10 (24.4)	0 (0.0)
Pseudomonas aeruginosa	1 (7.7)	7 (53.8)	5 (38.5)	0 (0.0)
Klebsiella pneumoniae	0 (0.0)	6 (50.0)	6 (50.0)	0 (0.0)
Total	38 (17.6)	121 (56.0)	56 (25.9)	1 (0.5)

MDR = resistance to ≥3 antimicrobial classes; XDR = resistance to all but ≤ 2 classes; PDR = resistance to all tested agents.
One Acinetobacter baumannii isolate was classified as pandrug-resistant (PDR).

Table 4.
Resistance phenotypes of major uropathogens isolated from patients with UTIs (n = 216 Isolates).

Predictor	Reference category	Unadjusted OR (95% CI)	p-value	Adjusted OR (95% CI)	p-value	VIF
Age > 65 years	≤ 65 years	1.42 (0.51-3.95)	0.50	1.82 (0.38-8.72)	0.45	1.12
Female sex	Male	0.84 (0.45-1.56)	0.58	0.91 (0.44-1.89)	0.80	1.04
Escherichia coli	Other pathogens	2.15 (1.12-4.13)	0.02	2.41 (1.02-5.70)	0.04	1.32
Prior hospitalization	No hospitalization	3.40 (1.78-6.50)	< 0.001	3.15 (1.50-6.60)	0.002	1.18
Diabetes mellitus	No diabetes	2.01 (0.93-4.35)	0.08	1.95 (0.82-4.65)	0.13	1.21

Model Diagnostics:

· *Hosmer-Lemeshow test: p = 0.62 (indicating good model fit).*

· *Area under the curve (AUC): 0.72 (95% CI: 0.65-0.79), indicating moderate discriminatory ability..*

· *Variance Inflation Factor (VIF): All values < 5, suggesting no significant multicollinearity.*

Table 5.
Multivariable logistic regression analysis of predictors for multidrug-resistant and extensively drug-resistant urinary tract infections.

with MDR/XDR status. Diabetes mellitus showed a non-significant elevation in odds (aOR = 1.95; 95% CI, 0.82-4.65; p = 0.13), which should be interpreted cautiously. Model diagnostics indicated adequate fit (Hosmer-Lemeshow test, p = 0.62) and moderate discriminative ability (area under the curve = 0.72; 95% CI, 0.65-0.79) (Table 5).

Discussion

Pathogen distribution and resistance trends

This study reveals a high prevalence of MDR and XDR uropathogens among patients with UTIs, consistent with emerging trends in both regional and global contexts (2, 16). E. coli was the most frequently isolated pathogen, accounting for 29.6% of cases, which aligns with data from across Africa and other *low- and middle-income countries* (LMICs) (17-19). The predominance of E. coli as a uropathogen is well-documented, and its high rates of MDR (81.3%) and XDR (18.8%) phenotypes in this study mirror findings from sub-Saharan Africa and other resource-constrained settings (10, 18-20). This trend is largely driven by the global spread of *extended-spectrum beta-lactamase* (ESBL)-producing strains, which significantly limit therapeutic options and complicate clinical management (21, 22).

Similarly, the elevated resistance observed in K. pneumoniae (100% MDR, 50% XDR) and P. aeruginosa (92.3% MDR, 38.5% XDR) reflects a broader pattern of increasing antimicrobial resistance among Gram-negative pathogens in UTIs (10, 23-25). The universal resistance of K. pneumoniae to ampicillin is consistent with its intrinsic resistance mechanisms, including chromosomal beta-lactamase production and the acquisition of plasmid-mediated ESBLs and carbapenemases (23). These enzymatic defenses severely restrict antibiotic choices and underscore the need for enhanced surveillance and stewardship.

Resistance to commonly prescribed antibiotics such as ciprofloxacin (64.8%) and ceftriaxone (75.9%) was notably high, consistent with reports from Saudi Arabia, Iran, and other parts of Africa, where fluoroquinolone and third-generation cephalosporin resistance often exceed 60% (2, 3, 17, 26, 27). In contrast, nitrofurantoin and carbapenems retained relatively higher susceptibility rates (71.2% and 86.6%, respectively), supporting their continued use as empirical treatment options in selected cases (28, 29). However, the emergence of carbapenem resistance – particularly among K. pneumoniae isolates (33%) – is concerning and highlights the urgent need for judicious use of last-resort antibiotics.

Risk factors for MDR/XDR infections

Multivariate analysis identified prior hospitalization (aOR = 3.15; 95% CI: 1.50-6.60; p = 0.002) and E. coli infection (aOR = 2.41; 95% CI: 1.02-5.70; p = 0.04) as independent predictors of MDR/XDR UTIs. These findings are consistent with existing literature that links healthcare exposure to increased risk of resistant infections due to selective antibiotic pressure and nosocomial transmission (30, 31). The association between E. coli and MDR/XDR status may reflect the widespread dissemination of ESBL-producing strains in both community and hospital settings. This pathogen's genetic adaptability and frequent exposure to antibiotics make it a key driver of resistance in UTIs (25). These findings emphasize the importance of targeted diagnostic approaches and tailored empirical therapy, particularly in high-risk populations.

Demographic and clinical characteristics

Although age and gender were not identified as a statistically significant predictor of MDR/XDR urinary tract infections in this study, the majority of patients were adults aged 15-65 years (83.3%), with a slight male predominance (53.2%). This contrasts with many regional studies that report a higher UTI prevalence among females (26, 27, 32). The observed male predominance may be attributable to differences in healthcare-seeking behavior, referral patterns, or underlying comorbidities in this setting. Notably, *Khanal et al.* reported higher MDR rates among males, possibly due to increased antibiotic exposure in this group (33). These sex-specific trends warrant further investigation and should inform future risk stratification strategies. Moreover, our findings align with regional epidemiological data from the Middle East and North Africa. *Amiri et al.* reported that UTI incidence peaked in younger adults, particularly females aged 20-24 and males aged 35-39, followed by a gradual decline with age (2). While our study did not observe a significant difference in MDR/XDR prevalence across age groups, the concentration of cases in the 15-65 age range is consistent with these regional patterns (2). This suggests that while age remains a key factor in UTI epidemiology, the emergence of resistance may be influenced more by healthcare exposure and antibiotic use than by age alone.

Although several factors previously reported to be associated with MDR urinary tract infections – such as prior antibiotic use, duration of catheterization, urological procedures and the presence of comorbidities – were not fully captured in our analysis due to the retrospective nature of the study, their role in the development of resistance remains well established (34-38). These patient-specific factors, along with broader determinants such as healthcare exposure and environmental influences, significantly contribute to the emergence and persistence of MDR and XDR uropathogens. In our study, a notably high proportion of patients with diabetes mellitus (88.1%) were affected by resistant infections, a finding that aligns with existing literature linking diabetes to increased susceptibility to complicated and antimicrobial-resistant UTIs (39). The underlying pathophysiology includes immune dysfunction due to chronic hyperglycemia, urinary stasis, and frequent healthcare contact, all of which facilitate bacterial colonization and the selection of resistant strains (40). These findings underscore the importance of targeted infection control measures and individualized antimicrobial strategies in high-risk populations, particularly those with chronic comorbidities such as diabetes mellitus.

Clinical and public health implications

The findings of this study have important implications for clinical practice and public health policy. The high prevalence of MDR and XDR uropathogens – particularly E. coli – highlights the urgent need for continuous antimicrobial resistance surveillance and the implementation of stewardship programs in resource-limited settings. Empirical treatment guidelines should be updated regularly to reflect local resistance patterns and minimize the risk of treatment failure.

Moreover, the emergence of carbapenem resistance in Klebsiella spp. and other Gram-negative pathogens signals a critical threat to available treatment options. This trend necessitates the development of novel therapeutic strategies and the reinforcement of infection prevention and control measures in both hospital and community settings.

Study limitations

Several limitations should be considered when interpreting the results of this study. First, its retrospective design limits the ability to control for confounding variables, and some clinical data may be incomplete or inconsistently documented. Second, variations in UTI definitions across studies may affect comparability. Although our use of clinical symptoms combined with culture results aligns with current guidelines, misclassification – particularly in cases of asymptomatic bacteriuria – cannot be ruled out (41, 42). Third, while antimicrobial susceptibility testing followed CLSI guidelines, we did not systematically investigate specific resistance mechanisms such as ESBL or carbapenemase production. This limits the depth of our resistance analysis and may obscure important epidemiological trends. Fourth, the study was conducted at a single tertiary care center, which may limit the generalizability of the findings to primary care or community settings. Finally, the study did not assess patient outcomes or treatment efficacy, which are essential for linking resistance patterns to clinical impact and guiding therapeutic decisions.

Conclusions

In summary, this study highlights a high burden of MDR and XDR uropathogens in a resource-limited setting, with E. coli playing a central role in resistance dissemination. Prior hospitalization and E. coli infection were identified as key predictors of resistant infections. These findings underscore the need for ongoing resistance monitoring, antimicrobial stewardship, and context-specific treatment guidelines to improve patient outcomes and curb the spread of antimicrobial resistance.

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Declarations

Ethical approval and consent for participate: *The study protocol was reviewed and approved by the Institutional Review Board (IRB) of Ibb University (Approval Code: IBBUNI.AC.YEM.2024.79, dated February 3, 2024). Due to the retrospective nature of the study and the use of anonymized data, the requirement for informed consent was waived. The study was conducted in accordance with the principles of the Declaration of Helsinki.*

Availability of data and material: *The datasets analyzed during the current study are available in the Mendeley Data repository and can be accessed via the following DOI: 10.17632/26hn6wmb8x.1.*

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