IJMCM 15(1) (2025) 2214-2225 Doi: 10.22034/IJMCM.2025.710281

International Journal of
Molecular and Clinical Microbiology

Research Article

Frequency of Bacteria Causing Urinary Tract Infections in Patients Referring to Rasht Medical Centers and Analysis of Their Antibiotic Resistance Patterns

Alireza Massiha[1], Afsoon Shariat[1]*, Khosro Issazadeh[2]

1. Department of Microbiology, Kaz.C., Islamic Azad University, Kazerun, Iran
2. Department of Microbiology, La.C., Islamic Azad University, Lahijan, Iran

ARTICLE INFO

Article history:
Received 21 March 2025
Accepted 21 May 2025
Available online 1 June 2025

Keywords:
Urinary tract infection,
Antimicrobial resistance,
Multidrug resistance,
Escherichia coli, Iran

ABSTRACT

Urinary tract infections (UTIs) are among the most common bacterial diseases and present a significant public health challenge due to the increasing prevalence of multidrug-resistant (MDR) pathogens. Understanding local epidemiology and resistance profiles is essential for guiding empirical treatment and infection control strategies. This descriptive–analytical retrospective study analyzed 391 urine samples collected from patients with suspected UTIs at selected medical centers in Rasht, Iran, over a three-month period. Bacterial isolation and identification were performed using standard microbiological techniques, and antimicrobial susceptibility testing was conducted by the Kirby–Bauer disk diffusion method, with results interpreted according to CLSI 2023 guidelines. Statistical analyses were performed using the chi-square test and independent t-test. Of the 391 samples, 201 cases (52.4%) had positive urine cultures. Gram-negative bacilli accounted for 84.9% of isolates, while gram-positive cocci comprised 10.7%. *Escherichia coli* was the predominant pathogen and showed the highest resistance to tetracycline (58.5%), whereas tobramycin demonstrated the highest efficacy, with a sensitivity rate of 90.0%. The findings demonstrate a high burden of MDR uropathogens, particularly E. coli, in northern Iran. Continuous local surveillance of antimicrobial resistance patterns is essential to inform empirical therapy, and the implementation of targeted antibiotic stewardship policies is urgently recommended.

1. Introduction

Urinary tract infection (UTI) is among the most prevalent bacterial infections affecting humans, representing a major public health concern worldwide (Foxman, 2014; Stamm & Norrby, 2001). It is estimated that over 150 million people are diagnosed with a UTI each year, leading to significant healthcare costs and morbidity (Terlizzi et al., 2017). The urinary tract is normally sterile, owing to multiple host defense mechanisms that prevent microbial colonization. Nevertheless, UTIs can occur when these defenses are overcome by bacterial, viral, fungal, or, less commonly, parasitic pathogens (Puca, 2014; Medina & Castillo-Pino, 2019).UTIs may involve the lower urinary tract such as the bladder and urethra (cystitis and

*Corresponding author: Afsoon Shariat
E-mail address: afsoon571@iau.ac.ir

urethritis) or extend to the upper tract, including the ureters, renal pelvis, and kidney parenchyma (pyelonephritis) (Flores-Mireles et al., 2015). Although pyelonephritis is less frequent than cystitis, it typically presents with more severe clinical features such as fever and flank pain and poses a higher risk of permanent renal damage, especially in vulnerable populations like the elderly and young children (Hvidberg et al., 2000). The pathogenesis of ascending UTI is multifactorial, influenced by host anatomical and genetic factors and by bacterial virulence traits such as adhesion, motility, and biofilm formation (Paterson & Bonomo, 2005). Epidemiological studies consistently indicate that Gram-negative bacilli, particularly *Escherichia coli*, are the leading etiologic agents of both community-acquired and healthcare-associated UTIs, accounting for 70–90% of acute uncomplicated cases (Ranjan Dash et al., 2018; Iqbal et al., 2022). Other notable pathogens include *Klebsiella pneumoniae*, *Proteus mirabilis*, *Pseudomonas aeruginosa*, *Enterobacter spp.*, and Gram-positive species like *Staphylococcus aureus* and *Enterococcus faecalis*, which are more frequently associated with urinary tract abnormalities or catheterization (Flores-Mireles et al., 2015; Shrestha et al., 2022). In recent years, inappropriate and excessive use of antimicrobial agents has accelerated the emergence of multidrug-resistant (MDR) uropathogens, including extended-spectrum β-lactamase (ESBL)-producing *E. coli* and *K. pneumoniae* (Babakhani & Oloomi, 2018; Ventola, 2015; WHO, 2023). The prevalence and patterns of antibiotic resistance vary considerably between countries and even within regions of the same country, reflecting differences in prescribing practices, infection control measures, and accessibility of antibiotics (Farajnia et al., 2021; Shaikh et al., 2022). In Iran, several studies have reported alarmingly high rates of resistance among uropathogens, particularly in provinces with wider antibiotic availability and less stringent antimicrobial stewardship (Jalalvand et al., 2020; Pourakbari et al., 2021). This growing resistance complicates empirical therapy, prolongs treatment duration, and increases the risk of adverse outcomes. Consequently, continuous local surveillance of uropathogen distribution and drug susceptibility patterns is essential to guide empirical antibiotic choices, reduce treatment failures, and contain the spread of MDR strains (WHO, 2023).Given the dynamic nature of bacterial resistance and the regional variability in pathogen prevalence, the present study aims to identify the bacterial agents responsible for UTIs and determine their antibiotic resistance profiles in clinical urine specimens collected from patients referred to selected laboratories in Rasht, Iran.

2. Materials and Methods

2.1. Study Design and Sample Collection

This descriptive analytical retrospective study was conducted on urine samples suspected of urinary tract infection (UTI) over a three-month period (July to September 2023) in Rasht, Iran. Patient demographic and clinical data including age, sex, and marital status, history of diabetes mellitus, previous UTIs, and prior antibiotic use were recorded anonymously using standardized data collection forms. Midstream, clean catch urine samples from all suspected UTI patients were collected in a sterile, dry, wide-neck, leak-proof, screw-capped container. The container was to be clearly labeled with a unique sample number, as well as the date and time of collection.. The samples were collected aseptically before the starting of antibiotic treatment. These sample were examined and processed within 24-28 hours. The urine was examined macroscopically for the color and turbidity and wet mount of urine samples were prepared. The wet mounts were observed microscopically to identify the presence of pus cells, red blood cells, epithelial cells, crystals, parasites and yeast. All the findings were recorded. All urine samples were inoculated aseptically on to Hi-Chrome UTI agar using a calibrated wire loop of 28G with an internal diameter of 3.26 mm holding 0.004 ml of urine. The plates were incubated at 37 0 C aerobically and after overnight incubation, they were checked for significant bacteriuria as under by enumeration of colonies [growth of 100 colonies equals to 105 colony forming units (CFU) of bacteria /ml of urine] (Patra. et al. 2020).

2.2. Culture and Bacterial Identification

Samples were inoculated directly onto Eosin Methylene Blue (EMB) agar and Blood Agar (Merck, Germany) using a calibrated 0.1 ml

loop, followed by incubation at 37 °C for 18–24 hours. Colony counts $\geq 10^5$ CFU/ml were considered indicative of significant bacteriuria. Bacterial identification was performed using standard microbiological and biochemical methods, including Gram staining, catalase, coagulase, triple sugar iron (TSI), oxidase, mannitol fermentation, and urease tests (Khoshbakht et al., 2012). Reference strains of *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* ATCC 25923 were used as quality controls throughout the study.

2.3. Antimicrobial Susceptibility Testing

Antibiotic susceptibility patterns were determined using the Kirby–Bauer disk diffusion method on Mueller–Hinton Agar (Merck, Germany), in accordance with the latest Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI, 2023). Antibiotic disks (MAST Group, UK) included: Ceftazidime (30 µg), Ceftriaxone (30 µg), Cephalothin (30 µg), Imipenem (10 µg), Amikacin (10 µg), Trimethoprim–Sulfamethoxazole (30 µg), Nalidixic acid (30 µg), Tetracycline (30 µg), Nitrofurantoin (300 µg), and Ciprofloxacin (30 µg). Plates were incubated at 35 ± 2 °C for 16–18 hours, and inhibition zone diameters were interpreted as Susceptible, Intermediate, or Resistant per CLSI breakpoints. (Humphries et al. 2021).

2.4. Definitions of Multidrug Resistance

Multidrug-resistant (MDR), extensively drug-resistant (XDR), and pandrug-resistant (PDR) phenotypes were defined according to the international consensus by Magiorakos et al. (2012), with updates based on recent literature (Momtaz et al., 2021; WHO, 2023).

2.5. Data Analysis

Descriptive statistics (frequency distributions, measures of central tendency and dispersion) were calculated. The chi-square test or Fisher's exact test, and where applicable, Student's t-test, were used to assess associations between categorical variables. All statistical analyses were performed using IBM SPSS Statistics version 26 (IBM Corp., Armonk, NY, USA) and a p-value <0.05 was considered statistically significant.

2.6. Ethical Considerations

The study protocol was approved by the Ethics Committee of Kazerun Branch, Islamic Azad University, (Approval Code: [Approval Code: IR.IAU.REC.2021.064]). Patient confidentiality was maintained in accordance with the Declaration of Helsinki.

3. Results

During the three-month study period, 391 urine samples from patients suspected of urinary tract infection (UTI) were analyzed. Significant bacteriuria (≥ 10^5 CFU/mL) was detected in 205 samples (52.4%).

3.1. Demographic characteristics

The patients' ages ranged from 1 to 83 years (mean ± SD: 37.5 ± 21.8 years). Of the culture-positive cases, 171 (83.4%) were female (mean ± SD: 36.1 ± 22.3 years) and 34 (16.6%) were male (mean ± SD: 46.7 ± 20.3 years). Table 1 presents the demographic comparison between sexes. Women had a significantly higher history of previous UTI, diabetes mellitus, and prior antibiotic use compared with men ($p = 0.001$). No significant difference was observed in the prevalence of prostatitis between sexes.

3.2. Clinical manifestations

Table 2 summarize the frequency of clinical symptoms. Dysuria, urinary frequency, and flank pain were significantly associated with positive culture results ($p < 0.001$).

3.4. Urinalysis findings

Urinalysis parameters, including leukocytes, red blood cells (RBCs), glucose, nitrite, casts, protein, stones, and crystals, are shown in Table 3. Leukocyturia and hematuria were significantly more common in culture-positive samples (61.9% and 37.1%, respectively) compared with culture-negative samples. Nitrite was detected in 29.7% of positive samples versus 2.1% of negative samples ($p = 0.001$), while differences for glucose, protein, and casts were not statistically significant.

3.5. Age and sex distribution

The highest prevalence of infection was recorded among men aged 26–35 years and women aged 56–65 years. Across all age groups, women exhibited a significantly higher prevalence of UTI than men ($p < 0.001$).

3.6. Bacterial isolates

Gram-negative bacilli accounted for 84.9% of culture-positive UTIs, with *Escherichia coli* being the most frequent isolate (60.9% of Gram-negatives). Gram-positive cocci comprised 10.7% of isolates, with coagulase-negative *Staphylococcus* species being the most common among them (17.5% of Gram-positives). Gender distribution analysis showed similar pathogen spectra in men and women, with no statistically significant differences (Table 4).

3.7. Antibiotic resistance patterns

The antibiotic susceptibility profile revealed high resistance rates among Gram-negative isolates to tetracycline (74.3%), cephalothin (48.7%), nalidixic acid (43.4%), ceftriaxone (37.1%), and ceftazidime (32.4%). *E. coli* isolates exhibited the highest resistance to tetracycline (73.7%) and the lowest to Tobramycin, Ciprofloxacin, Amikacin, and Nitrofurantoin. Among Klebsiella spp., resistance to β-lactams and trimethoprim-sulfamethoxazole was reported at 66.7% and 77.8%, respectively, while partial susceptibility to amikacin (33.3%) and imipenem (44.4%). Enterobacter spp. showed the highest resistance to cefixime (66.7%), cephalothin (88.9%), and ampicillin; resistance to cefotaxime and ceftazidime was also about 55%. Pseudomonas spp. showed high resistance to most β-lactams and quinolones, but were completely sensitive to amikacin and tobramycin in women. Other gram-positives such as Streptococcus and Enterococcus, although isolated in small numbers, showed a high resistance pattern to penicillins and ampicillin. (Table 5).

3.8. Multidrug resistance (MDR/XDR) profiles

Among 201 bacterial isolates, 63 (31.3%) were single-drug resistant (SDR), 115 (57.2%) were MDR, and 14 (7.0%) were XDR. No pandrug-resistant (PDR) strains were detected (Table 7).

- *E. coli* accounted for the majority of MDR (47.7%) and XDR (5.9%) strains.
- Other MDR/XDR isolates included *Enterococcus faecalis*, *Klebsiella spp*., *Pseudomonas spp*., and *coagulase-negative Staphylococcus spp.*
- Fisher's exact tests indicated that the distribution of drug resistance patterns in *E. coli* was significantly different from other pathogens ($p = 0.0001$). The overall comparison across all species also showed a significant difference ($p = 0.0004$).

3.9. Resistance patterns by genus

- *Klebsiella spp*. High resistance to β-lactams (including penicillins and cephalosporins), aminoglycosides, fluoroquinolones, tetracyclines, and nitrofurans; some isolates exhibited carbapenem resistance.

- *Enterobacter spp.* Resistance to multiple classes including β-lactams, penicillins, fluoroquinolones, aminoglycosides, tetracyclines, and carbapenems.
- *Pseudomonas spp.* Notable resistance to carbapenems, β-lactams (especially extended-spectrum cephalosporins), fluoroquinolones, aminoglycosides, and partial resistance to nitrofurans and tetracyclines.
- *Staphylococcus spp.* Resistance to β-lactams (particularly in MRSA strains), fluoroquinolones, folate pathway inhibitors, and tetracyclines in some cases.
- *Enterococcus spp*. MDR to tetracyclines, β-lactams, penicillins, and nitrofurans; vancomycin resistance not documented in this cohort.
- *Streptococcus spp.* MDR mainly to tetracyclines, β-lactams, penicillins, and folate pathway inhibitors.

Table 1: Frequency Distribution of Demographic Factors Among Patients Referred to Selected Laboratories

Specification	Woman		Man		P-value
	Quantity	Percentage	Quantity	Percentage	
History of Urinary Tract Infection	84	49	11	32	0.001
History of Diabetes	15	8.8	1	2.9	0.001
Prostatism	–	–	3	–	0
History of Antibiotic Use	69	40	7	21	0.001
Employment Status	53	31	26	76	0.001
Marital Status	155	91	19	56	0.002

Table 2: Frequency Distribution of Clinical Symptom Comparisons Among the Studied Clients

Symptoms	**Woman**		**Man**		P-value
	Quantity	**Percentage**	**Quantity**	**Percentage**	
Burning	87	50.8	9	26.4	0.0
Urination Frequency	63	36.8	3	8.8	0.0
Flank Pain	49	28.6	8	23.5	0.0
Fever	28	16.3	15	44.1	0.1
Reproductive System Disorders	19	11.1	4	11.7	0.3
Dark Urine	23	13.4	5	14.7	0.1
Foul odor of urine	24	14.0	6	17.6	0.1

Table 3: Frequency Distribution of Urine Analysis and Culture Findings in the Studied Clients

Parameters	**Negative Culture**		**Positive Culture**		P-value
	Negative	Positive	Negative	Positive	
WBC	168 (90.3)	18 (9.7)	78 (38.1)	127 (61.9)	0.0
RBC	161 (86.6)	25 (13.4)	129 (62.9)	76 (37.1)	0.0
Sugar	176 (94.6)	10 (5.4)	189 (92.2)	16 (7.8)	0.3
Nitrite	182 (97.1)	4 (2.1)	144 (70.3)	61 (29.7)	0.0
Acetone	181 (97.3)	5 (2.7)	202 (98.6)	3 (1.4)	0.2
Protein	183 (98.4)	3 (1.6)	197 (96.1)	8 (3.9)	0.5
Cylinder	185 (99.5)	1 (0.5)	199 (97.1)	6 (2.9)	0.7
Crystal	139 (84.7)	47 (25.3)	168 (82.5)	63 (17.5)	0.0

Table 4: Comparison of the Frequency of Bacteria Isolated from Urine Culture Samples

Microorganism	**Frequency**	**Frequency percentage**
Escherichia coli	163	81.1%
Klebsiella	9	4.48%
Enterobacter	12	5.97%
Pseudomonas	7	3.48%
Staphylococcus coagulase-negative	5	2.49%
Streptococcus	1	0.50%
Enterococcus faecalis	3	1.49%
Staphylococcus aureus	1	0.50%
Total	201	100

Table 5: Frequency of Isolated Bacterial Agents from Patients by Age Group and Gender

Bacteria Type	Age Categories									
	gender	5> quantity	6-15 quantity	16-25 quantity	26-35 quantity	36-45 quantity	46-55 quantity	56-65 quantity	>66 quantity	Total
Escherichia coli	Male	0	1 (9.1)	2 (18.2)	2 (18.2)	1 (9.1)	1 (9.1)	1 (9.1)	3 (27.3)	11 (50.0)
	Female	0	3 (2.0)	17 (11.2)	4 (2.6)	9 (5.9)	39 (25.7)	57 (37.5)	23 (15.1)	152 (84.9)
Staphylococcus coagulase-negative	Male	0	0	0	1 (100)	0	0	0	0	1 (4.5)
	Female	0	0	0	0	2 (50)	1 (25)	1 (25)	0	4 (2.2)
Klebsiella	Male	0	0	0	1 (50)	1 (50)	0	0	0	2 (9.1)
	Female	0	0	3 (42.9)	1 (14.3)	1 (14.3)	2 (28.6)	0	0	7 (3.9)
Enterobacter	Male	0	0	0	0	1 (50)	1 (50)	0	0	2 (9.1)
	Female	0	0	0	2 (20)	4 (40)	2 (20)	1 (10)	1 (10)	10(5.6)
Pseudomonas	Male	0	0	1 (20)	1 (20)	1 (20)	2 (40)	0	0	5 (22.7)
	Female	0	0	0	0	2 (100)	0	0	0	2 (1.1)
Staphylococcus aureus	Male	0	0	0	0	0	0	0	0	0 (0)
	Female	0	0	1 (100)	0	0	0	0	0	1 (0.6)
Streptococcus	Male	0	0	0	0	0	0	0	0	0 (0)
	Female	0	0	0	1 (100)	0	0	0	0	1 (0.6)
Enterococcus	Male	0	0	0	1 (100)	0	0	0	0	1 (4.5)
	Female	0	0	0	1 (50)	1 (50)	0	0	0	2 (1.1)
Total	Male	0	1 (4.5)	3 (13.6)	6 (27.3)	4 (18.2)	4 (18.2)	1 (4.5)	3 (13.6)	22 (10.9)
	Female	0	3 (1.68)	21 (11.7)	9 (5.0)	11 (6.1)	44 (24.6)	59 (33.0)	24 (13.4)	179 (89.1)

Table 6: Frequency of Antibiotic Resistance Patterns in Isolated Cases from Urinary Tract Patients by Gender

Antibiotic	Class	Isolated bacteria from culture							
		gender	***Escherichia coli* N=163**	***Staphylococcus* N=6**	***Klebsiella* N=9**	***Enterobacter* N=12**	***Pseudomonas* N=7**	***Streptococcus* N=1**	***Enterococcus* N=3**
Imipenem (IMI)	Carbapenems	Male	4 (2.5)	0	1 (11.1)	1 (16.7)	3 (43.0)	0	0
		Female	32 (19.6)	0	3 (33.3)	2 (10.5)	1 (14.3)	0	0
Cefotaxime (CTX)	Beta-lactams	Male	3 (1.8)	1 (16.7)	1 (11.1)	1 (16.7)	5 (71.4)	0	1 (33.3)
		Female	29 (17.8)	4 (30.7)	1 (11.1)	3 (15.8)	0	0	1 (33.3)
Tobramycin (TOB)	Aminoglycosides	Male	1 (0.6)	0	0	0	2 (28.5)	0	0
		Female	8 (4.9)	0	1 (11.1)	0	0	1 (100)	0
Trimethoprime (TS)	Folate pathway inhibitors	Male	5 (3.1)	2 (40)	1 (11.1)	2 (33.3)	4 (57.1)	0	0
		Female	45 (27.6)	6 (46.1)	6 (66.7)	5 (31.6)	0	1 (100)	0
Nitrofurantoin (NI)	Nitrofuran	Male	3 (1.8)	0	1 (11.1)	0 (33.3)	3 (43.0)	0	0
		Female	24 (14.7)	1 (16.7)	3 (33.3)	1 (36.8)	1 (14.3)	0	1 (33.3)
Tetracycline (T)	Tetracyclines	Male	11 (6.8)	0	1 (11.1)	1 (50)	4 (57.1)	0	0
		Female	109 (66.9)	1 (16.7)	4 (44.4)	11 (47.4)	1 (14.3)	1 (100)	2 (67.0)
Ciprofloxacin (CIP)	Fluoroquinolones	Male	2 (1.2)	1 (16.7)	1 (11.1)	1 (16.7)	5 (71.4)	0	0
		Female	19 (11.7)	3 (50)	5 (55.6)	1 (10.5)	0	1 (100)	0
Nalidixic acid (NA)	Quinolones	Male	7 (4.3)	2 (40)	2 (22.2)	2 (33.3)	3 (43)	0	0
		Female	59 (36.2)	6 (100)	1 (11.1)	7 (42.1)	0	0	0
Amikacin AK)	Aminoglycosides	Male	2 (1.2)	1 (16.7)	1 (11.1)	0 (16.7)	0	0	0
		Female	22 (13.5)	2 (15.4)	3 (33.3)	1 (26.3)	0	0	0
Ampicillin (AMP)	Penicillins	Male	6 (3.7)	1 (16.7)	1 (11.1)	3 (50)	2 (28.5)	0	0
		Female	48 (29.4)	4 (66.7)	7 (77.8)	9 (57.9)	0	1 (100)	1
Ceftazidime (CAZ)	Beta-lactams	Male	6 (3.7)	4 (66.7)	1 (11.1)	-	0	0	0
		Female	50 (30.7)	3 (50)	5 (55.6)	-	0	0	1 (33.3)
Ceftriaxon (CTR)	Beta-lactams	Male	6 (3.7)	2 (40)	1 (11.1)	0 (0)	5 (71.4)	0	0
		Female	49 (30.1)	4 (30.7)	6 (66.7)	3 (73.7)	1 (14.3)	0	0
Cefalotin (CEP)	First generation cephalosporins	Male	8 (4.9)	4 (66.7)	2 (66.7)	3 (50)	0	0	0
		Female	71 (43.6)	4 (30.7)	8 (88.9)	1 (63.1)	0	0	0
Cefixime (CT)	Beta-lactams	Male	7 (20.6)	1 (16.7)	1 (33.3)	0 (0)	0	0	0
		Female	64 (57.1)	3 (50)	6 (66.7)	0	0	1 (100)	0

Table 7: Distribution of Drug-Resistance Pattern among the Isolated Pathogens

Isolated Uropathogens	Non Drug Resistance (NDR)	Single Drug Resistance (SDR)	Multi Drug Resistance (MDR)	Extensively Drug Resistance (XDR)	Total	p-value (Fisher's exact)
	No. (%)	No. (%)	No. (%)	No. (%)	No. (%)	
Escherichia coli	7 (3.5)	48 (23.9)	96 (47.7)	12 (5.9)	163 (81.1)	0.0
Enterobacter	0 (0)	2 (0.9)	6 (3)	1 (0.5)	9 (4.4)	0.2
Klebsiella	2 (1)	6 (3)	4 (2)	0 (0)	12 (6)	0.2
Pseudomonas	0 (0)	4 (2)	2 (1)	1 (0.5)	7 (3.5)	0.4
Staphylococcus aureus	0 (0)	0 (0)	1 (0.5)	0 (0)	1 (0.5)	0.3
Streptococcus	0 (0)	1 (0.5)	0 (0)	0 (0)	1 (0.5)	0.5
Enterococcus faecalis	0 (0)	1 (0.5)	2 (1)	0 (0)	3 (1.5)	0.7
Staphylococcus coagulase-negative	0 (0)	1 (0.5)	4 (2)	0 (0)	5 (2.5)	0.6
Total	9 (4.5)	63 (31.3)	115 (57.2)	14 (7)	201 (100)	* p < 0.001

*Overall p-value for all drug resistance patterns and pathogens (Fisher's Exact Test)

As shown in the table above, the p-value for each pathogen, calculated via Fisher's exact test compared to all other pathogens, is presented in the final column. The results indicate a statistically significant difference in the drug resistance pattern of *E. coli* compared to other organisms ($p<0.001$). The overall p-value for the entire table was 0.0004, confirming a significant difference in resistance distribution among all isolated pathogens.

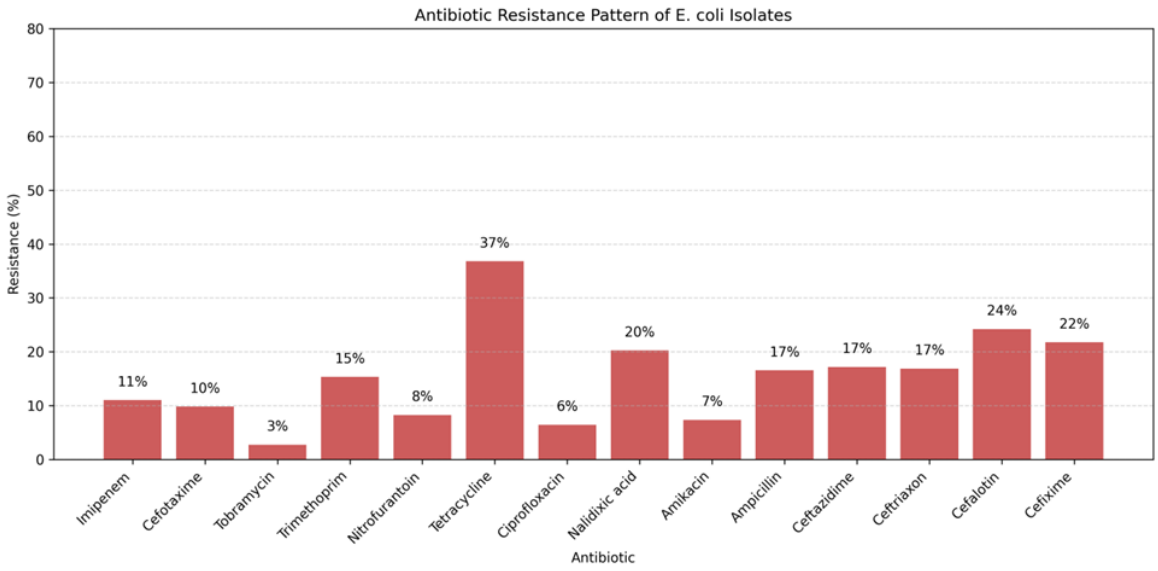

Figure 1. Bar chart showing the frequency (%) of antibiotic resistance among *Escherichia coli* isolates from community-acquired urinary tract infections in Rasht, Iran.

4. Discussion

This study evaluated the distribution of uropathogenic microorganisms isolated from patients with urinary tract infections (UTIs) referred to medical centers in Rasht, Iran, and analyzed their antimicrobial susceptibility patterns. It also examined associations between gender, clinical manifestations, laboratory findings, and the isolated bacterial species.UTI remains one of the most common bacterial infections worldwide, affecting an estimated 150 million people annually (Einabadi et al., 2018). Epidemiological data indicate that approximately one in three women will require antimicrobial therapy for UTI before the age of

24, and 40–50% will experience at least one episode during their lifetime (Moniri et al., 2003). Consistent with previous studies (Flores‐Mireles et al., 2015), our results show a clear female predominance, with women constituting 89.1% of positive cultures. This is largely attributed to female anatomical factors a shorter urethra and proximity to the anal region which facilitate ascending infection, as well as behavioral and hygienic practices (Ghaffar et al., 2019; AHB, 2006). Sexual activity has also been linked to increased UTI risk in women. In men, the lower incidence of UTI is attributed to the longer urethra and the protective antimicrobial properties of prostatic secretions containing zinc and cationic proteins (Flores‐Mireles et al., 2015).In line with national and global reports, *Escherichia coli* was the predominant pathogen (81.1%), followed by *Enterobacter spp.* (5.97%) and *Klebsiella spp.* (4.48%) (Saleh et al., 2018; Jabrodini et al., 2018; Rossignol et al., 2017). The pathogenic success of *E.* coli is linked to its intestinal abundance, adhesive fimbriae facilitating attachment to the uroepithelium, motility via flagella, and evasion of local immune defenses such as IgA (Oluremi et al., 2011). Among Gram-positive organisms, *coagulase-negative Staphylococcus* was the most frequently isolated agent, supporting recent evidence of its clinical relevance in UTIs (Farajnia et al., 2009).Urinalysis findings demonstrated significantly higher leukocyturia, hematuria, nitrite, crystals, and proteinuria in culture-positive specimens compared to negative ones. However, as in other studies, a notable proportion of infected patients lacked these diagnostic urinalysis markers (Gerber et al., 2002; Huppert et al., 2003), underscoring the importance of culture confirmation. Antimicrobial susceptibility testing revealed alarmingly high resistance rates in *E. coli*, particularly to tetracycline (73.7%), Cephalothin (48.5%), and Nalidixic acid (40.5%). Lower resistance was observed for tobramycin (5.5%), ciprofloxacin (12.9%), and Amikacin (14.7%). These results align with prior data from both Iran and other countries (Moniri et al., 2003; Einabadi et al., 2018; Rossignol et al., 2017). *Coagulase-negative Staphylococcus* isolates exhibited high resistance to Nalidixic acid, trimethoprim, ceftriaxone, and cefotaxime, with comparatively better activity for nitrofurantoin, ciprofloxacin, and ampicillin, showing partial divergence from other Iranian and international studies (Murray et al., 2005).Consistent with global patterns, increasing resistance was found for commonly used agents such as ceftriaxone, Cefixime, and ciprofloxacin a likely outcome of widespread and often empirical prescription practices (Amin et al., 2011). Conversely, drugs less frequently used in routine treatment, such as Ceftazidime and Imipenem, maintained better activity profiles. Alarmingly, a high prevalence of multidrug resistance (MDR) was documented in *E. coli isolates:* 76.8% were resistant to at least three antibiotic classes, with resistance patterns extending up to eight concurrent agents. Only 18% of isolates were fully susceptible. Comparable MDR prevalence rates have been reported in Pakistan (77.5%; Sheikholeslami & Hassanshahi, 2010) and Iran (77%; Mohammadi et al., 2016). These findings reinforce the urgent need for antibiotic stewardship programs, region-specific prescribing guidelines, and regular surveillance to monitor trends in uropathogen resistance (Jalilian et al., 2014; Habibi-Asl et al., 2018).Given the regional variability in uropathogen prevalence and resistance profiles, annual antimicrobial susceptibility mapping is warranted to support evidence-based empirical therapy and reduce inappropriate antibiotic use.

Conclusion

UTIs in this study were predominantly caused by Gram-negative bacteria, particularly *E. coli*, with alarmingly high resistance rates to several commonly prescribed antibiotics. MDR and XDR strains are emerging as major clinical threats. Routine culture and susceptibility testing, early detection of resistant strains, and judicious antibiotic prescription are essential to control the spread of resistance. Antibiotic policies tailored to local resistance patterns should be developed and strictly implemented to safeguard the efficacy of available treatments.

Acknowledgement

This study was derived from the Ph.D. thesis at Islamic Azad University, Kazerun Branch. The authors gratefully acknowledge the support of the university's Research Unit.

Conflict of interest

None

Refereces

Adedeji B, Abdulkadir O. Etiology and antimicrobial resistance pattern of bacterial agents of urinary tract infections in students of tertiary institutions in Yola Metropolis. Biol Res. 2009; 3(3-4):67-70.

Afsharpaiman S, Bairaghdar F, Torkaman M, Kavehmanesh Z, Amirsalari S, Moradi M, et al. Bacterial Pathogens and Resistance Patterns in Children With Community-Acquired Urinary Tract Infection: A Cross Sectional Study. J Compr Pediatr. 2012; 3(1):16–2

Afsharpaiman S, Bairaghdar F, Torkaman M, Kavehmanesh Z, Amirsalari S, Moradi M, et al. Bacterial pathogens and resistance patterns in children with community-acquired urinary tract infection: a cross-sectional study. J Compr Pediatr. 2012; 3(1):16-2.

Ahmadzadeh Barzegar R, Nejad Soleimani S, Bahrami F, Jafari S, Javanmard A, Rouhi S. Determination of bacterial factors causing urinary infections and its antibiotic resistance patterns in patients referred to Khorramabad Hospital, Iran. Pajouhan Sci J. 2018; 16(4):1-5.

Al-Naqshbandi AA, Chawsheen MA, Abdulqader HH. Prevalence and antimicrobial susceptibility of bacterial pathogens isolated from urine specimens received in Rizgary hospital - Erbil. J Infect Public Health. 2019; 12:330–336.

Amin M, Mehdinejad M, Pourdangchi Z. Study of bacteria isolated from urinary tract infections and determination of their susceptibility to antibiotics. Jundishapur J Microbiol. 2011; 2(3):118-23. https://sites.kowsarpub.com/jjm/articles/86746.html

Ayoyi AO, Kikuvi G, Bii C, Kariuki S. Prevalence, etiology and antibiotic sensitivity profile of asymptomatic bacteriuria isolates from pregnant women in selected antenatal clinic from Nairobi, Kenya. Pan Afr Med J. 2017; 26(1):41.https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5614176/

Babakhani S, Oloomi M. Transposons: The agents of antibiotic resistance in bacteria. J Basic Microbiol. 2018; 58:905–917. https://doi.org/10.1002/jobm.201800181

Babakhani, S., & Oloomi, M. (2018). Antibiotic resistance patterns in uropathogenic bacteria. Journal of Infection and Public Health, 11(6), 784–792. https://doi.org/10.1016/j.jiph.2018.05.007

Beyene G, Tsegaye W. Bacterial uropathogens in urinary tract infection and antibiotic susceptibility pattern in Jimma university specialized hospital, southwest Ethiopia. Ethiop J Health Sci. 2011; 21(2):141-6. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3596303/

Clinical and Laboratory Standards Institute (CLSI). Performance Standards for Antimicrobial SusceptibilityTesting, 27th ed., 2017. https://clsi.org/standards/products/microbiology/documents/m100/

Einabadi M, Abdolerahmani F, Yousefi Mashoof R, Vazini H, Khaledi A, Piroozmand A, et al. Study of drug resistance of Staphylococcus aurous and Pseudomonas aeruginosa strains isolated from environmental samples of Hamadan educational hospitals in 2017 using disk diffusion and minimum inhibitory concentration. Feyz 2018; 22(2): 206-13.

Farajnia S, Alikhani MY, Ghotaslou R, Naghili B, Nakhlband A. Causative agents and antimicrobial susceptibilities of urinary tract infections in the northwest of Iran. Int J Infect Dis. 2009; 13(2):140-4. https://doi.org/10.1016/j.ijid.2008.04.018

Farajnia, S., et al. (2021). High prevalence of multidrug-resistant uropathogens in Iran: A systematic review. Iranian Journal of Microbiology, 13(2), 141–152. https://doi.org/10.18502/ijm.v13i2.6091

Farshad S, Ranjbar R, Japoni A, Hosseini M, Anvarinejad M, Mohammadzadegan R. Microbial susceptibility, virulence

factor, and plasmid profiles of uropathogenic Escherichia coli strains isolated from children in Jahrom. Arch Iran Med. 2012; 15(5):312-316. http://www.ams.ac.ir/AIM/NEWPUB/12/15/5/004.pdf

Flores-Mireles AL, Walker JN, Caparon M, Hultgren SJ. Urinary tract infections: epidemiology, mechanisms of infection and treatment options. Nat Rev Microbiol. 2015; 13(5):269-284. https://doi.org/10.1038/nrmicro3432

Flores-Mireles, A. L., Walker, J. N., Caparon, M., & Hultgren, S. J. (2015). Urinary tract infections: Epidemiology, mechanisms of infection and treatment options. Nature Reviews Microbiology, 13(5), 269–284. https://doi.org/10.1038/nrmicro3432

Foxman B. Epidemiology of urinary tract infections: incidence, morbidity, and economic costs. Dis Mon. 2003; 49(2):53-70. https://doi.org/10.1067/mda.2003.7

Foxman, B. (2014). Urinary tract infection syndromes: Occurrence, recurrence, bacteriology, risk factors, and disease burden. Infectious Disease Clinics of North America, 28(1), 1–13. https://doi.org/10.1016/j.idc.2013.09.003

Garau J, Xercavins M, Rodriguez-Carballeira M, Gomez-Vera JR, Coll I, Vidal D, et al. Emergence and dissemination of quinolone-resistant Escherichia coli in the community. Antimicrob Agents Chemother. 1999; 43(11):2736-41. https://doi.org/10.1128/AAC.43.11.2736

Ghaffar I, Imran M, Perveen S, Kanwal T, Saifullah S, Bertino MF, Shah MR. Synthesis of chitosan coated metal organic frameworks (MOFs) for increasing vancomycin bactericidal potentials against resistant S. aureus strain. Mater Sci Eng C. 2019; 105:110111. https://doi.org/10.1016/j.msec.2019.110111

Gupta K, Hooton TM, Stamm WE. Increasing antimicrobial resistance and the management of uncomplicated community-acquired urinary tract infections. Ann Intern Med. 2001; 135(1):41-50. https://doi.org/10.7326/0003-4819-135-1-200107030-00012

Huebner J, Goldmann DA. Coagulase-negative staphylococci: role as pathogens. Annu Rev Med. 1999; 50:223-36. https://doi.org/10.1146/annurev.med.50.1.223

Humphries, R., Bobenchik, A. M., Hindler, J. A. & Schuetz, A. N. (2021).Overview of changes to the clinical and laboratory standards institute performance standards for antimicrobial susceptibility testing, M100. J. Clin. Microbiol. 59, 12. http s : / /doi. org / 1 0. 1 1 2 8 / jcm .0 0 2 1 3 - 2 1.

Huppert JS, Biro FM, Mehrabi J, Slap GB. J Pediatr Adolesc Gynecol. 2003; 16:133-7.

Hvidberg, H., Struve, C., Krogfelt, K. A., Christensen, N., Rasmussen, S. N., & Frimodt-Møller, N. (2000). Development of a long-term ascending urinary tract infection model in mice. Infection and Immunity, 68(6), 3550–3560.https://doi.org/10.1128/IAI.68.6.3550-3560.2000

Ihsan A, Kumar N, Ahmed S, Iqbal J. Antibiotic resistance in uropathogenic Escherichia coli strains isolated from non-hospitalized patients in Pakistan. J Clin Diagn Res. 2014; 8(9):DC01–DC04.https://doi.org/10.7860/JCDR/2014/9937.4780

Iqbal, S., et al. (2022). Rising antimicrobial resistance among uropathogens: A global concern. Journal of Global Antimicrobial Resistance, 29, 197–205. https://doi.org/10.1016/j.jgar.2022.03.011

Jabrodini A, Heidari F, Taghavi S, Shokouh M. The investigation of frequency and antibiotic resistance pattern of Escherichia coli and Klebsiella pneumoniae Isolated from urinary tract infection in outpatients referred to Amiralmomenin Ali hospital in Gerash city in 2017: a short report. J Rafsanjan Univ Med Sci. 2018; 17(1):75-84.

Jalal and, F., et al. (2020). Uropathogenic Escherichia coli in Iran: Virulence traits and antimicrobial resistance. New Microbes and New Infections, 37, 100734.

https://doi.org/10.1016/j.nmni.2020.100734

Jalilian S, Farahani A, Mohajeri P. Antibiotic resistance in uropathogenic Escherichia coli isolated from urinary tract infections out-patients in Kermanshah. Int J Med Public Health. 2014; 4(1):75-7. https://doi.org/10.4103/2230-8598.127182

Khoshbakht R, Salimi A, Shirzad Aski H, Keshavarzi H. Antibiotic Susceptibility of Bacterial Strains Isolated From Urinary Tract Infections in Karaj, Iran. Jundishapur J Microbiol. 2012; 6(1):86–90

Khoshbakht R, Salimi A, Shirzad Aski H, Keshavarzi H. Antibiotic susceptibility of bacterial strains isolated from urinary tract infections in Karaj, Iran. Jundishapur J Microbiol. 2012; 6(1):86–90.https://sites.kowsarpub.com/jjm/articles/86751.html

Medina, M., & Castillo-Pino, E. (2019). An introduction to the epidemiology and burden of urinary tract infections. Therapeutic Advances in Urology, 11, 1756287219832172. https://doi.org/10.1177/1756287219832172

Michael OO, Adenike AV. Asymptomatic bacteriuria: occurrence and antibiotic susceptibility profiles among students of a tertiary institution in Ile-Ife, Nigeria. Afr J Microbiol Res. 2016; 10(15):505–10. https://doi.org/10.5897/AJMR2016.8085

Mohammadi S, Argha K, Akhzarifar N, Panahi Z, Pakzad I, Sayehmiri K. Analysis of antibiotic resistance in bacterial strains isolated from urine cultures of patients referred to clinical laboratories of Ilam City during 2012. J Ilam Univ Med Sci. 2016; 24(2):179-85.

Molaabaszadeh H, Hajisheikhzadeh B, Mollazadeh M, Eslami K, Mohammadzadeh-Gheshlaghi N. The study of sensibility and antimicrobial resistance in Escherichia coli isolated from urinary tract infection in Tabriz City. J Fasa Univ Med Sci. 2013; 3(2):149-54.

Molazade A, Gholami MS, Shahi A, Najafipour S, Mobasheri F, Ashraf-Mansuri J, et al. Evaluation of antibiotic resistance pattern of isolated gram-negative bacteria from urine culture of hospitalized patients in different wards of Vali-Asr Hospital in Fasa during the years 2012 and 2013. J Fasa Univ Med Sci. 2014; 4(3):275-83.

Moniri R, Khorshidi A, Akbari H. Emergence of multidrug resistant strains of Escherichia coli isolated from urinary tract infections. Iran J Public Health. 2003; 32(4):42-6.

Murray PR, Rosenthal KS, Pfaller MA. Medical Microbiology. 4th ed. St Louis: Elsevier Mosby; 2005.

Patra, J. K. et al. (2020). Isolation, culture, and biochemical characterization of microbes. Pract. Guide Environ. Biotechnol. 6, 83–133.

Paterson DL, Bonomo RA. Extended-spectrum beta-lactamases: a clinical update. Clin Microbiol Rev. 2005; 18(4):657-86. https://doi.org/10.1128/CMR.18.4.657-686.2005

Paterson, D. L., & Bonomo, R. A. (2005). Extended-spectrum β-lactamases: A clinical update. Clinical Microbiology Reviews, 18(4), 657–686. https://doi.org/10.1128/CMR.18.4.657-686.2005

Pizarro J, Cossart P. Bacterial adhesion and entry into host cells. J Cell Sci. 2006; 124(4):715-27. https://doi.org/10.1242/jcs.018119

Pourakbari, B., et al. (2021). Increase in antimicrobial resistance in urinary pathogens among Iranian children. Journal of Pediatric Urology 17(5), 636.e1–636.e8. https://doi.org/10.1016/j.jpurol.2021.07.017

Prais D, Straussberg R, Avitzur Y, Nussinovitch M, Harel L, Amir J. Bacterial susceptibility to oral antibiotics in community acquired urinary tract infection. Arch Dis Child. 2003; 88(3):215-8.

Prais D, Straussberg R, Avitzur Y, Nussinovitch M, Harel L, Amir J. Bacterial susceptibility to oral antibiotics in community-acquired urinary tract infection. Arch Dis Child. 2003; 88(3):215-8. https://doi.org/10.1136/adc.88.3.215

Puca E. Urinary tract infection in adults. Clin Microbiol. 2014; 3:e120. https://doi.org/10.4172/2327-5073.1000120

Puca, E. (2014). Urinary tract infection: Etiology and antibiotic resistance patterns. International Journal of Infectious Diseases, 21, 218. https://doi.org /10.1016/j.ijid.2014.03.659

Ranjan Dash N, Albataineh MT, Alhourani N, Khoudeir AM, Ghanim M, Wasim M, Mahmoud I. Community-acquired urinary tract infections due to extended-spectrum β-lactamase-producing organisms in United Arab Emirates. Travel Med Infect Dis. 2018; 22:46–50. https://doi.org/10.1016/j.tmaid.2018.07.008

Ranjan Dash, H., et al. (2018). Frequency and antibiotic resistance of uropathogens: A global study. Microbial Pathogenesis, 115,357–361. https://doi.org/10.1016/ j.micpath.2017.12.054

Rossignol L, Vaux S, Maugat S, Blake A, Barlier R, Heym B, et al. Incidence of urinary tract infections and antibiotic resistance in the outpatient setting: a cross-sectional study. Infection. 2017; 45(1):33-40.https://doi.org/10.1007/ s15010 -016-0910-3

Saleh F, Soleiman Nejad S, Bahrami Chegeni F, Jafari S, Javanmard A, Rouhi S, et al. Determination of bacterial factors causing urinary infections and its antibiotic resistance patterns in patients referred to Khorramabad Hospital, Iran. Pajouhan Sci J. 2018; 16(4):1-5.

Salvatore S, Cattoni E, Siesto G, Serati M, Sorice P, Torella M. Urinary tract infections in women. Eur J Obstet Gynecol Reprod Biol. 2011; 156(2):131-6. https://doi.org/10.1016/j.ejogrb. 2011 .01.028

Shaikh, S., et al. (2022). Antibiotic resistance and biofilm formation in uropathogens. Frontiers in Cellular and Infection Microbiology, 12, 865028. https://doi.org/10.3389/fcimb.2022.865028.

Sheikholeslami Z, Hassanshahi G. The frequency of coagulase negative staphylococci urinary infections with antimicrobial resistance pattern in Rafsanjan. Pak J Med Sci. 2010; 26(1):107-10.

Shrestha, S., et al. (2022). Bacterial pathogens and antibiotic resistance profiles in urinary tract infections. Journal of Infection and Public Health, 15(5), 565–571.https://doi.org/10.1016/j.jiph.2022.04.005

Stamm WE. An epidemic of urinary tract infections? N Engl J Med. 2001; 345:1055-7. https://doi.org/10.1056/NEJMra012116

Stamm, W. E., & Norrby, S. R. (2001). Urinary tract infections: Disease panorama and challenges. The Journal of Infectious Diseases, 183(Suppl 1), S1–S4. https://doi.org/10.1086/318850.

Terlizzi ME, Gribaudo G, Maffei ME. Uropathogenic Escherichia coli (UPEC) infections: virulence factors, bladder responses, antibiotic, and non-antibiotic antimicrobial strategies. Front Microbiol. 2017; 8:1566. https://doi.org/ 10.3389/fmicb.2017.01566

Terlizzi, M. E., Gribaudo, G., & Maffei, M. E. (2017). Uropathogenic Escherichia coli (UPEC) infections: Virulence factors, bladder responses, antibiotic resistance, and new therapies. Pathogens, 6(2), 34. https://doi.org/10.3390/pathogens6020034

Ventola, C. L. (2015). The antibiotic resistance crisis. Pharmacy and Therapeutics, 40(4), 277–283. PMID: 25859123

WHO. (2023). Antimicrobial resistance. World Health Organization. Retrieved from https://www.who.int/news-room/fact-sheets/detail/antimicrobial-resistance

Zorc JJ, Kiddoo DA, Shaw KN. Diagnosis and management of pediatric urinary tract infections. Clin Microbiol Rev. 2005; 18(2):417-22. https://doi.org/10.1128/ CMR.18.2.417-422.200