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ANTIBIOTIC RESISTANCE PROFILES OF UROPATHOGENS WITH GENDER DISTRIBUTION AND REGIONAL ASSOCIATIONS IN CLINICAL ISOLATES

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ABSTRACT

Urinary tract infections (UTIs) are a significant global health burden, with increasing rates of antimicrobial resistance complicating treatment strategies. This study aimed to investigate the prevalence of uropathogens, their antibiotic susceptibility profiles, and multidrug resistance (MDR) patterns in relation to patient gender and geographic location within the Haridwar district of Uttarakhand, India. A total of 250 urine samples were collected from patients presenting with UTI symptoms across four sub-regions. Significant bacterial growth was observed in 102 samples (40.8%), with a higher culture positivity rate among females (70.6%) compared to males (29.4%). Klebsiella spp. was the predominant isolate (54.9%), followed by Escherichia coli (38.2%) and Pseudomonas spp. (6.9%). Antibiotic susceptibility testing revealed high resistance to ceftriaxone (98.21%) and gemifloxacin (87.5%) in Klebsiella, while E. coli exhibited resistance to gemifloxacin (89.74%) and piperacillin-tazobactam (87.17%). Pseudomonas isolates showed complete resistance to moxifloxacin and gemifloxacin. Aminoglycosides, carbapenems, and select fluoroquinolones retained high efficacy across all isolates. MDR prevalence was highest in Pseudomonas (85.7%), followed by E. coli (66.7%) and Klebsiella (60.7%), with a slightly higher proportional burden in males. These findings highlight the shifting epidemiology of UTIs, with Klebsiella predominance and high resistance to commonly prescribed antibiotics. The study underscores the importance of local surveillance data in guiding empirical treatment decisions and emphasizes the urgent need for antimicrobial stewardship interventions to combat the growing threat of MDR uropathogens.

Keywords: Urinary Tract Infections, Antibiotic Resistance, Uropathogens, Multidrug Resistance, *Escherichia coli*

1. INTRODUCTION

Urinary tract infections (UTIs) are among the most prevalent bacterial infections globally, representing a significant burden on healthcare systems in both developed and developing countries. They account for millions of physician visits annually and are a common cause of antibiotic prescriptions in outpatient settings (Medina & Castillo-Pino, 2019; Czajkowski et al., 2021; Tan &

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Chlebicki, 2016). UTIs affect all age groups but show a higher incidence among females, largely due to anatomical predispositions such as a shorter urethra and proximity to the anal region (Czajkowski et al., 2021; Rodriguez-Mañas, 2020). While most cases are uncomplicated, recurrent and complicated UTIs pose serious clinical challenges, particularly in immunocompromised individuals, pregnant women, and patients with catheter-associated infections (Medina-Polo et al., 2021; Codelia-Anjum et al., 2023).

The majority of community-acquired and nosocomial UTIs are caused by Gram-negative uropathogens, most notably *Escherichia coli*, followed by *Klebsiella spp.* and *Pseudomonas spp.* (Gupta et al., 2001; Ahmed et al., 2019; Zavala-Cerna et al., 2020). These pathogens exhibit diverse mechanisms of antibiotic resistance, including β-lactamase production, efflux pumps, and alteration of target sites, leading to reduced susceptibility to multiple antimicrobial classes (Khoshnood et al., 2017; Mazzariol et al., 2017). The growing prevalence of multidrug-resistant (MDR) strains has significantly narrowed therapeutic options and necessitated a re-evaluation of empirical treatment strategies (Kalın et al., 2023; Pakzad et al., 2019; Gandra et al., 2018). In many low- and middle-income regions, the problem is compounded by unregulated antibiotic use, delayed diagnostic practices, and a lack of regional antimicrobial resistance surveillance systems (Sulis et al., 2021; Ehsan, 2025; Singh et al., 2018).

Empirical therapy is typically initiated before the availability of culture and sensitivity results. Its success depends heavily on current knowledge of local resistance trends. However, many empirical regimens continue to be based on outdated or generalized data, which may not reflect the dynamic patterns of resistance that vary significantly across geographical locations and patient populations (Fridkin et al., 2001; Pakyz, 2007; McArthur & Tsang, 2016). The lack of region-specific antibiograms and the over-reliance on national or global resistance profiles often result in therapeutic failure and further selection pressure on resistant strains (Sugianli et al., 2017; Lewnard et al., 2020). This situation underscores the importance of periodic local surveillance studies that integrate microbial, demographic, and regional data to inform evidence-based prescribing.

Gender-based differences in UTI incidence are well documented, but emerging studies also suggest potential differences in pathogen distribution and resistance patterns between males and females (Czajkowski et al., 2021; Zavala-Cerna et al., 2020). Additionally, resistance patterns can vary across sub-regions even within the same district due to differences in healthcare access, sanitation infrastructure, population density, and local antibiotic usage practices (Medina & Castillo-Pino, 2019; Sulis et al., 2021). Therefore, a comprehensive understanding of pathogen prevalence and resistance in relation to both demographic and geographic variables is essential for guiding clinical decision-making and antibiotic stewardship interventions.

This study aims to address these gaps by providing an integrated analysis of uropathogen prevalence, gender association, and region-wise antibiotic resistance patterns in clinical samples collected from four sub-divisions of the Haridwar district: Haridwar, Roorkee, Bahadrabad, and Laksar. The primary objective is to generate data that can support the development of localized empirical treatment recommendations for UTIs, tailored to the microbial and demographic characteristics of the region.

2. MATERIALS AND METHODS

2.1 Study Design and Setting

A cross-sectional, laboratory-based surveillance study was conducted to investigate the distribution of uropathogens and their antibiotic susceptibility patterns in patients presenting with symptoms of urinary tract infections (Subedi & Pudasaini, 2017). The study was carried out over a defined period in the Haridwar district of Uttarakhand, India. Clinical urine samples were obtained from patients attending healthcare facilities across four distinct sub-regions: Haridwar, Roorkee, Bahadrabad, and Laksar (Figure 1). All microbiological processing and antibiotic susceptibility testing were performed in a centralized diagnostic microbiology laboratory following standard protocols (Ntirenganya et al., 2015).

2.2 Sample Collection and Processing

A total of 250 midstream clean-catch urine samples were collected from male and female patients presenting with clinical symptoms suggestive of urinary tract infections (UTIs). Samples were transported to the laboratory under sterile conditions at 4°C and processed within two hours of collection to preserve microbial viability (Bopp et al., 1988). Each sample was inoculated on MacConkey agar and Cysteine Lactose Electrolyte Deficient (CLED) agar using a calibrated loop delivering 0.001 mL of urine. Plates were incubated aerobically at 37°C for 18–24 hours (Herreros et al., 2015). Significant bacteriuria was defined as a pure culture growth of $\geq 10^5$ colony-forming units (CFU)/mL (), whereas samples showing polymicrobial growth or bacterial counts below this threshold were excluded from further analysis (Nelius et al., 2011).

2.3 Identification of Isolates

A total of 250 midstream clean-catch urine samples were collected from male and female patients presenting with clinical symptoms suggestive of urinary tract infections (UTIs). Samples were transported to the laboratory under sterile conditions at 4°C and processed within two hours of collection to preserve microbial viability (Bopp et al., 1988). Each sample was inoculated on MacConkey agar and Cysteine Lactose Electrolyte Deficient (CLED) agar using a calibrated loop delivering 0.001 mL of urine. Plates were incubated aerobically at 37°C for 18–24 hours (Herreros et al., 2015). Significant bacteriuria was defined as a pure culture growth of $\geq 10^5$ colony-forming units (CFU)/mL (), whereas samples showing polymicrobial growth or bacterial counts below this threshold were excluded from further analysis (Nelius et al., 2011).

2.3 Identification of Isolates

Primary bacterial isolates were identified based on colony morphology and Gram staining characteristics (Workneh et al., 2021). Conventional biochemical tests, including IMViC, Triple Sugar Iron (TSI), Urease, and Oxidase tests, were performed to confirm species-level identification (Sousa et al., 2013). Biochemical profiles were interpreted according to standard microbiology references, such as the *Manual of Clinical Microbiology* (Pence & Liesman, 2020). Only the three most frequently isolated uropathogens *Escherichia coli*, *Klebsiella* spp., and *Pseudomonas* spp. were selected for subsequent antimicrobial susceptibility testing.

2.4 Antibiotic Susceptibility Testing

Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar, following the guidelines of the Clinical and Laboratory Standards Institute (CLSI) (Kassim et al., 2016). Bacterial suspensions were adjusted to a 0.5 McFarland turbidity standard and evenly spread over the agar surface. Plates were incubated at 37°C for 18–24 hours, after which zones of inhibition were measured and interpreted as susceptible, intermediate, or resistant

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(Mohamed et al., 2020; Wanja et al., 2020). Quality control was ensured using standard ATCC strains, including *E. coli* ATCC 25922 and *P. aeruginosa* ATCC 27853 (Hirayama et al., 2024).

The antibiotics tested, representing major drug classes relevant to UTIs, are summarized in Table 1.

2.5 Data Categorization and Definitions

Multidrug resistance (MDR) was defined as non-susceptibility to at least one agent in three or more antimicrobial classes (Sweeney et al., 2018). Isolates were grouped based on patient gender (male, female) and geographic origin (Haridwar, Roorkee, Bahadrabad, Laksar) to examine demographic and regional patterns.

2.6 Data Analysis

All data were compiled in Microsoft Excel and analyzed descriptively . Frequencies and percentages were calculated to determine the prevalence of specific uropathogens, their distribution across demographic groups, and their antibiotic resistance profiles (Amin et al., 2018). Graphical representations were used to illustrate trends where appropriate.

RESULTS

1. Study Population and Sample Distribution

During the study period, a total of 250 urine samples were collected for microbiological analysis. Of these, 117 samples (46.8%) were obtained from male patients, while 133 samples (53.2%) were from female patients, indicating a slightly higher representation of females in the study population. Out of the total 250 samples processed, 102 (40.8%) yielded significant bacterial growth and were considered culture-positive, whereas the remaining 148 samples (59.2%) showed no detectable growth. The distribution of uropathogens across male and female patients is illustrated in Figure 2.

Among the 102 culture-positive samples, 30 (29.4%) were obtained from male patients and 72 (70.6%) from female patients, demonstrating that a larger proportion of culture positivity was observed among female patients compared to males within the study group. When analyzed across study locations, variation in positivity rates was noted, as presented in Table 2. The highest positivity rate was observed in Laksar (53.3%), followed by Bahadrabad (41.3%), Haridwar (40.6%), and Roorkee (35.3%). A comparison of culture positivity rates across the four sub-divisions is further illustrated in Figure 3, highlighting location-specific variations in UTI prevalence.

2. Prevalence of Uropathogens

From the 102 culture-positive urine samples, three major groups of Gram-negative uropathogens were identified. *Klebsiella* spp. constituted the predominant isolate, accounting for 56 cases (54.9%), followed by *Escherichia coli* with 39 cases (38.2%). *Pseudomonas* spp. were detected less frequently, with only 7 isolates (6.9%) recovered during the study period. This distribution of uropathogens is presented in Figure 4, highlighting the varying contribution of different bacterial species to urinary tract infections within the study population.

3. ANTIBIOTIC SUSCEPTIBILITY

3.1. Klebsiella

Among the 56 *Klebsiella spp.* isolates, a variable pattern of resistance and susceptibility was observed across the tested antibiotics. High levels of resistance were recorded against ceftriaxone (98.21%), gemifloxacin (87.50%), and piperacillin + tazobactam (87.50%), indicating reduced effectiveness of these agents against *Klebsiella*. Moderate resistance was noted for moxifloxacin (67.85%), cefpodoxime (71.42%), cefuroxime (57.14%), ciprofloxacin (50.00%), and cefdinir

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(50.00%), suggesting partial efficacy within these groups. The complete resistance and susceptibility distribution is summarized in Table 3. In contrast, gentamicin, amikacin, and levofloxacin exhibited complete susceptibility (100.00%), while meropenem (96.43%), norfloxacin (98.22%), aztreonam (98.22%), cefoperazone + sulbactam (98.22%), and sparfloxacin (94.65%) also showed very high susceptibility rates. These comparative patterns are further illustrated in Figure 5, providing a visual representation of resistance versus susceptibility trends among Klebsiella isolates.

3.2. E. coli

A total of 39 *E. coli* isolates were analyzed for their antibiotic susceptibility patterns. High resistance was observed to gemifloxacin (89.74%), aztreonam (84.61%), and piperacillin + tazobactam (87.17%), while moderate resistance occurred with moxifloxacin (64.10%), cefuroxime (69.23%), cefpodoxime (64.10%), and cefdinir (58.97%). Ciprofloxacin showed comparatively lower resistance at 53.84%. These findings are summarized in Table 4, which outlines the complete resistance–sensitivity distribution across all tested drugs. By contrast, ceftriaxone retained strong efficacy, with only 2.56% resistance, and several agents including norfloxacin, gentamicin, amikacin, meropenem, levofloxacin, cefoperazone + sulbactam, and sparfloxacin demonstrated 100% susceptibility. The overall trend, contrasting high resistance against select antibiotics with complete susceptibility to others, is illustrated in Figure 6.

3.3. Pseudomonas

A total of 7 *Pseudomonas* isolates were tested for their antibiotic susceptibility profile. Complete resistance (100.00%) was observed to moxifloxacin and gemifloxacin, indicating poor efficacy of these fluoroquinolones against the pathogen. High resistance was also noted for piperacillin + tazobactam (71.42%), while moderate resistance occurred with cefprozil (42.85%), ceftozoxime (42.85%), and cefpirome (42.85%). These detailed resistance–sensitivity percentages are presented in Table 5.

On the other hand, resistance levels were much lower for cefdinir (14.28%), meropenem (14.28%), and chloramphenicol (14.28%). Several agents—including norfloxacin, ceftriaxone, gentamicin, amikacin, levofloxacin, and sparfloxacin—showed complete susceptibility (100.00%), underscoring their retained activity. The overall distribution of resistance versus susceptibility across antibiotics is visually illustrated in Figure 7, highlighting the stark divide between ineffective and highly effective agents.

When data from all three pathogens were analyzed together, distinct resistance patterns were observed. Fluoroquinolones such as gemifloxacin and moxifloxacin showed consistently high resistance, while levofloxacin, norfloxacin, and sparfloxacin retained complete activity. Piperacillin + tazobactam demonstrated high resistance, especially in Klebsiella and E. coli, with a similar trend in Pseudomonas. Cephalosporins, including cefuroxime, cefpodoxime, cefdinir, and ciprofloxacin, showed moderate and variable resistance, indicating limited efficacy. In contrast, aminoglycosides (gentamicin and amikacin) exhibited complete susceptibility across all isolates, and meropenem also maintained very high effectiveness with minimal resistance. Overall, this consolidated analysis highlights marked resistance to commonly prescribed beta-lactams and select fluoroquinolones, whereas aminoglycosides, carbapenems, and certain fluoroquinolones remain highly effective.

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4. MULTIDRUG RESISTANCE PATTERNS

Analysis of multidrug resistance patterns revealed a high prevalence of MDR phenotypes among the *Pseudomonas* isolates. Out of the 7 culture-positive isolates, 6 (85.7%) exhibited resistance to three or more antibiotic classes, thereby qualifying as MDR, while only one isolate (14.3%) was non-MDR. Gender-wise distribution indicated that 3 MDR isolates (42.9%) were obtained from male patients, while 3 MDR isolates (42.9%) were recovered from female patients. The single non-MDR isolate (14.3%) was also identified in a male patient.

Among the 39 *E. coli* isolates, 26 (66.7%) were classified as MDR, while 13 (33.3%) were non-MDR. Gender-wise distribution showed that MDR was more frequent among females, with 18 of 25 isolates (72.0%) exhibiting multidrug resistance, compared to 8 of 14 isolates (57.1%) from males. A detailed numerical summary of these proportions is presented in Table 6.

Similarly, of the 56 *Klebsiella* isolates, 34 (60.7%) were classified as MDR, while 22 (39.3%) were non-MDR. Gender-based analysis revealed a slightly higher proportional burden in males (66.7%) compared to females (59.1%), even though the overall number of MDR isolates was greater in females due to their larger representation in the study.

When compared across all three uropathogens, the highest proportion of MDR was observed in *Pseudomonas* (85.7%), followed by *E. coli* (66.7%) and *Klebsiella* (60.7%). These interspecies and gender-wise variations in MDR distribution are visually illustrated in Figure 8, which highlights the comparative resistance trends.

DISCUSSION

This study examined the prevalence of uropathogens, their antibiotic susceptibility profiles, and their multidrug resistance (MDR) patterns. These findings add to the evidence on the changing epidemiology of urinary tract infections (UTIs) and the growing challenge of antimicrobial resistance.

Klebsiella spp. was the most frequent isolate (54.9%), followed by *Escherichia coli* (38.2%) and *Pseudomonas spp.* (6.9%). In contrast, most studies have reported *E. coli* as the dominant UTI pathogen, often accounting for over 70% of the isolates (Constantinides et al., 2020; Kawalec et al., 2023). The predominance of *Klebsiella* may reflect local factors such as patient demographics, prior antibiotic exposure, and hospital-based sampling, as *Klebsiella* is commonly associated with nosocomial infections (Chung, 2016; Eghbalpoor et al., 2019; Koksal et al., 2018; Li et al., 2017). Similar findings in South Asian tertiary hospitals suggest that antibiotic practices and healthcare environments influence the pathogen distribution (Ntirenganya et al., 2015; Paczosa & Mecsas, 2016; Tsai et al., 2006).

The resistance profiles showed marked differences across species. *Klebsiella* displayed very high resistance to ceftriaxone (98.21%) and gemifloxacin (87.5%), consistent with reports associating third-generation cephalosporin resistance with ESBL production (Santella et al., 2024; Walker et al., 2019). Aminoglycosides (gentamicin and amikacin) and carbapenems (meropenem), however, retain excellent activity, likely due to their relatively restricted use compared to fluoroquinolones and beta-lactams (Çakır et al., 2018; Sanders et al., 1989; Terbtothakun et al., 2021)

In *E. coli*, high resistance was observed against gemifloxacin (89.74%) and

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piperacillin-tazobactam (87.17%), echoing studies showing rising fluoroquinolone resistance (Ambrose et al., 2003; Niu et al., 2023; Ruiz-Lievano et al., 2024). Notably, ceftriaxone remained highly effective (97.44% susceptibility) in contrast to regions with widespread ESBL prevalence (Luo et al., 2023). This variation underscores the geographical diversity of the resistance patterns and highlights the potential local utility of ceftriaxone (Bhalodi et al., 2020; Sharma, 2013).

Pseudomonas isolates demonstrated complete resistance to gemifloxacin and moxifloxacin, which is consistent with their intrinsic resistance mechanisms (Elfadadny et al., 2024; Pang et al., 2018). Nonetheless, they remain highly susceptible to aminoglycosides and carbapenems, in line with global treatment patterns (Karruli et al., 2023; Oliver et al., 2023).

MDR prevalence was highest in *Pseudomonas* (85.7%), followed by *E. coli* (66.7%), and *Klebsiella* (60.7%). These rates are comparable to those of previous surveillance data (Hidalgo et al., 2025; Pereira et al., 2014; Shilpakar et al., 2021). The relatively lower MDR of *Klebsiella* compared to *E. coli* contrasts with some reports, possibly due to differences in stewardship, infection control, and selective pressures (Shah et al., 2025; Viale et al., 2015). Gender-based analysis revealed a slightly higher proportional MDR in male isolates, although absolute MDR numbers were greater in females due to higher sample representation. Similar patterns have been noted in prior studies, where recurrent infections and anatomical factors in females have been suggested as contributors (Khanal et al., 2024; Mareș et al., 2024; Prastiyanto et al., 2024).

Overall, the combined resistance profile revealed declining effectiveness of commonly prescribed fluoroquinolones and beta-lactams, particularly ceftriaxone in *Klebsiella* and fluoroquinolones across all isolates (Hurezeanu et al., 2013; Kot & Witeska, 2024; Rahimzadeh et al., 2024). In contrast, aminoglycosides, carbapenems, and fluoroquinolones (levofloxacin, norfloxacin, and sparfloxacin) remained effective. While these results support their clinical use, overreliance on last-resort drugs risks accelerating future drug resistance (Al-Rawazq et al., 2019; Petca et al., 2020; Peters et al., 2020).

In conclusion, the predominance of *Klebsiella* over *E. coli* and high MDR rates highlight a shift in UTI epidemiology in this setting (Mouanga-Ndzime et al., 2024). These findings emphasize the need for continuous surveillance, rational antibiotic use, and locally tailored antimicrobial guidelines.

CONCLUSION

The present study demonstrates important shifts in the etiological profile and resistance patterns of uropathogens in our setting. Unlike global trends where *Escherichia coli* is consistently the leading cause of urinary tract infections, *Klebsiella spp.* emerged as the most prevalent isolate. This observation suggests that local epidemiological factors, hospital practices, and antibiotic usage patterns may be reshaping pathogen distribution in clinically significant ways.

Antibiotic susceptibility testing revealed worrying levels of resistance, particularly against fluoroquinolones and beta-lactams, which remain among the most frequently prescribed drugs for UTIs. The high rates of resistance to ceftriaxone in *Klebsiella* and to gemifloxacin in both *E. coli* and *Pseudomonas* are especially concerning, as they compromise first-line therapeutic options. On the other hand, the preserved activity of aminoglycosides and carbapenems provides reassurance, but reliance on these last-resort drugs carries the inherent risk of further accelerating

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resistance if their use is not judiciously managed.

The multidrug resistance (MDR) patterns observed reinforce this concern, with the highest rates detected in *Pseudomonas*, followed by *E. coli* and *Klebsiella*. Although the proportional burden of MDR was somewhat higher in male patients, the overall number of resistant isolates was greater in females, reflecting the higher incidence of UTIs in women. This gender-based trend is consistent with the biological and behavioral predispositions that increase susceptibility in female patients.

Collectively, these findings emphasize the urgent need for region-specific antimicrobial stewardship strategies and continuous monitoring of local resistance trends. Tailored empirical therapy guidelines, supported by routine laboratory surveillance, are essential to ensure that effective treatment options remain available. Furthermore, the observed shift in pathogen dominance highlights the importance of not relying solely on global trends but rather aligning treatment decisions with local epidemiological realities.

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Table 1: Antibiotics Tested and Their Classes

Class	Antibiotic (Disc Code, µg)
Fluoroquinolones	Norfloxacin (NX 10), Ciprofloxacin (RC 5), Levofloxacin (QB 5), Moxifloxacin (ML 10), Sparfloxacin (DC 10), Gemifloxacin (GA 10)
Cephalosporins	Ceftriaxone (RP 30), Cefuroxime (CB 30), Cefdinir (CDR 5), Cefpodoxime (CE 10)
Monobactam	Aztreonam (AC 30)
Aminoglycosides	Gentamicin (GM 10), Amikacin (AK 30)
Carbapenems	Meropenem (MP 10)
β-lactam/β-lactamase inhibitor combinations	Cefoperazone + Sulbactam (CM 105), Piperacillin + Tazobactam (PT 110)

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Table 2: Distribution of Culture-Positive UTI Samples Across Study Locations

Location	Total Samples Collected	Culture-Positive Samples	Positivity Rate (%)
Haridwar	106	43	40.56
Bahadrabad	46	19	41.3
Roorkee	68	24	35.29
Laksar	30	16	53.33
Total	**250**	**102**	**40.8**

Table 3: Antibiotic Resistance and Sensitivity Patterns of *Klebsiella* Isolates from Culture-Positive Urinary Samples

Antibiotic (Abbreviation)	Resistant (%)	Sensitive (%)
Ciprofloxacin (RC)	50.0	50.0
Moxifloxacin (ML)	67.85	32.15
Gemifloxacin (GA)	87.5	12.5
Norfloxacin (NX)	1.78	98.22
Aztreonam (AC)	1.78	98.22
Ceftriaxone (RP)	98.21	1.79
Cefuroxime (CB)	57.14	42.86
Gentamicin (GM)	0.0	100.0
Amikacin (AK)	0.0	100.0
Cefdinir (CDR)	50.0	50.0
Meropenem (MP)	3.57	96.43
Levofloxacin (QB)	0.0	100.0
Cefpodoxime (CE)	71.42	28.58
Cefoperazone + Sulbactam (CM)	1.78	98.22
Piperacillin + Tazobactam (PT)	87.5	12.5
Sparfloxacin (DC)	5.35	94.65

Table 4. Antibiotic resistance and sensitivity pattern of *E. coli* isolates

Antibiotic (Abbreviation)	Resistant (%)	Sensitive (%)
Ciprofloxacin (RC)	53.84	46.16
Moxifloxacin (ML)	64.10	35.90
Gemifloxacin (GA)	89.74	10.26
Norfloxacin (NX)	0.0	100.0
Aztreonam (AC)	84.61	15.39
Ceftriaxone (RP)	2.56	97.44
Cefuroxime (CB)	69.23	30.77
Gentamicin (GM)	0.0	100.0
Amikacin (AK)	0.0	100.0
Cefdinir (CDR)	58.97	41.03
Meropenem (MP)	0.0	100.0

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Levofloxacin (QB)	0.0	100.0
Cefpodoxime (CE)	64.10	35.90
Cefoperazone + Sulbactam (CM)	0.0	100.0
Piperacillin + Tazobactam (PT)	87.17	12.83
Sparfloxacin (DC)	0.0	100.0

Table 5. Antibiotic resistance and sensitivity pattern of *Pseudomonas* isolates

Antibiotic (Abbreviation)	Resistant (%)	Sensitive (%)
Ciprofloxacin (RC)	42.85	57.15
Moxifloxacin (ML)	100.0	0.0
Gemifloxacin (GA)	100.0	0.0
Norfloxacin (NX)	0.0	100.0
Aztreonam (AC)	28.57	71.43
Ceftriaxone (RP)	0.0	100.0
Cefuroxime (CB)	42.85	57.15
Gentamicin (GM)	0.0	100.0
Amikacin (AK)	0.0	100.0
Cefdinir (CDR)	14.28	85.72
Meropenem (MP)	14.28	85.72
Levofloxacin (QB)	0.0	100.0
Cefpodoxime (CE)	42.85	57.15
Cefoperazone + Sulbactam (CM)	14.28	85.72
Piperacillin + Tazobactam (PT)	71.42	28.58
Sparfloxacin (DC)	0.0	100.0

Table 6: Distribution of Multidrug Resistance (MDR) Among Isolated Uropathogens by Gender

Pathogen	Total Isolates	MDR Isolates (n)	MDR (%)	MDR in Males (n)	MDR in Males (%)	MDR in Females (n)	MDR in Females (%)
Pseudomonas	7	6	85.7	3	42.9	3	42.9
E. coli	39	26	66.7	8	57.1	18	72
Klebsiella	56	34	60.7	8	66.7	26	59.1

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