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ORIGINAL RESEARCH

Analysis of Antimicrobial Use and Bacterial Susceptibility in Patients with Urinary Tract Infections at a Certain Hospital From 2021 to 2023: A Retrospective Cohort Study

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Objective: This study aimed to investigate the distribution of pathogens, the usage of antimicrobial agents, and the sensitivity analysis of antimicrobial agents in patients with urinary tract infections (UTIs) in a certain hospital from 2021 to 2023, so as to provide clinical evidence for the selection of antimicrobial agents in clinical patients with UTIs.

Methods: A retrospective review was conducted on medical records of patients diagnosed with UTI during 2021–2023. Demographic characteristics (gender, age), urine sample data, pathogen distribution, and antimicrobial prescription patterns were collected. Midstream urine specimens submitted to the microbiology laboratory were processed for bacterial culture, identification, and antibiotic susceptibility testing. Differences in resistance rates to various antimicrobials were compared among pathogens from different clinical categories.

Results: From 2021 to 2023, 623 cases of positive urine culture samples were detected. Gram-negative organisms predominated (489 isolates), particularly *Escherichia coli* (*E. coli*, 61.80%, 385 isolates). Gram-positive isolates were mainly *Enterococcus faecalis* (6.10%, 38 isolates) and *Enterococcus faecium* (*E. faecalis*, 4.01%, 25 isolates). Gender distribution revealed that *E. coli* was more frequent in females (69.87%), while other principal pathogens were more common in males. Age analysis showed higher prevalence in females at young and middle age, whereas elderly males predominated (68.60%). Susceptibility testing indicated marked interspecies differences: *E. coli* showed 81.56% resistance to ampicillin; *Proteus mirabilis* exhibited 72.73% resistance to levofloxacin; *E. faecalis* demonstrated 94.74% resistance to tetracycline. Conversely, cefotaxime/clavulanic acid and vancomycin retained good activity against most isolates.

Conclusion: From 2021 to 2023, *E. coli* was the leading UTI pathogen. There were significant differences in the susceptibility of various pathogens to antimicrobial agents. It is necessary to regularly monitor the distribution of pathogens causing UTIs and their sensitivity to antimicrobial agents to provide a scientific reference for the rational use of antimicrobial agents during treatment.

Keywords: urinary tract infection, pathogen distribution, antibacterial agents, drug susceptibility

Introduction

Urinary tract infections (UTIs) are among the most common bacterial infections worldwide, displaying marked variability in etiology, clinical presentation, and severity. They range from mild conditions such as urethritis and cystitis to severe, potentially life-threatening complications including pyelonephritis, bacteremia, and septic shock. The causative pathogens differ across time periods and geographic regions.[1] However, Gram-negative bacteria—particularly *Escherichia coli* (*E. coli), Klebsiella pneumoniae* (*K. pneumoniae*), and *Proteus mirabilis* (*P. mirabilis*)—remain dominant, alongside Gram-positive species such as *Enterococcus faecalis* (*E. faecalis*) and *Staphylococcus saprophyticus* (*S. saprophyticus*). *E. coli* is consistently

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identified as the leading etiological agent across all UTI categories.[2] Common symptoms include urinary frequency, urgency, and dysuria, while severe infections may result in permanent renal damage.[3] Epidemiologically, the global burden of UTIs has risen sharply. From 1990 to 2021, incident cases increased by 66.45%, reaching 4.49 billion, with an age-standardized incidence rate of 5,531.88 per 100,000. Women and elderly men are disproportionately affected, and substantial differences exist across geographic regions, age groups, and socioeconomic strata.[4] This growing burden underscores the importance of effective clinical management and evidence-based public health strategies.

Antimicrobial agents have consistently served as the primary treatment for UTI. The therapeutic decisions regarding antibiotic selection, route of administration, and treatment duration are guided by several factors: the patient's individual risk profile, the anatomical site of infection (whether lower or upper tract), and their hemodynamic stability. These decisions are then refined with the results of microbiological culture and susceptibility testing.[5] International guidelines recommend nitrofurantoin, trimethoprim-sulfamethoxazole, fosfomycin, pivmecillinam, fluoroquinolones, and β-lactams.[6] However, recurrent and chronic infections are common, often requiring repeated antibiotic courses.[7] In many low- and middle-income settings, limited laboratory capacity for pathogen identification and susceptibility testing, coupled with inappropriate antimicrobial use, accelerates resistance development.[8,9] Antimicrobial resistance (AMR) among uropathogens is an escalating global threat. Extended-spectrum β-lactamase (ESBL)-producing *Enterobacteriaceae* hydrolyze broad-spectrum β-lactams, conferring resistance to penicillins and cephalosporins, leaving carbapenems as the last viable option. The prevalence of these multidrug-resistant strains is rising worldwide.[10,11] Resistance mechanisms—including β-lactamase production, efflux pumps, biofilm formation, horizontal gene transfer, and immune evasion—enable bacterial persistence despite treatment.[12] As a result, therapeutic efficacy is diminished, and the widespread annual use of antibiotics further drives resistance selection.[13]

Despite the global recognition of AMR as a public health crisis, recent region-specific data on UTI pathogen distribution, antimicrobial use patterns, and resistance profiles—particularly at the hospital level in China—remain scarce. Existing studies are often constrained to single time points, specific pathogens, or limited antibiotic classes, leaving important gaps in understanding temporal trends and the relationship between prescribing practices and resistance development. Based on the aforementioned background, we hypothesize that significant changes have occurred in the resistance patterns of major pathogens among UTI cases in the hospital from 2021 to 2023, and that these changes are associated with the patterns of clinical antimicrobial use. To verify this hypothesis, this study aims to achieve the following specific objectives through a retrospective cohort analysis: (1) to clarify the distribution and evolutionary trends of major pathogens during this period; (2) to analyze the patterns of clinical antimicrobial use; (3) to evaluate the antimicrobial susceptibility profiles and resistance rates of major pathogens and compare their differences among key populations. We aim to provide empirical evidence for optimizing the clinical application and management strategies of antimicrobials in our hospital.

Materials and Methods

Ethics Statement

The research obtained the approval from the Ethic Committee of Xian Yang Central Hospital . All participants provided written informed consent prior to enrollment. This study was conducted in accordance with the ethical principles outlined in the Declaration of Helsinki.

Study Design and Study Subjects

This study adopted a retrospective cohort study design and retrospectively analyzed the clinical data of 623 patients with UTIs (who underwent urine culture and had positive results) hospitalized in the Pharmacy department of Xian Yang Central Hospital from January 1, 2021, to December 31, 2023.

Inclusion and Exclusion Criteria

Case selection criteria strictly followed the internationally recognized diagnostic guidelines[14] Eligible patients were required to meet all of the following: (1) age ≥ 18 years; (2) a confirmed clinical diagnosis of UTI, characterized by classic bladder irritation symptoms such as frequency, urgency, and dysuria, with or without fever or flank pain; (3) urinalysis revealing > 10 white blood cells per high-power field; (4) midstream urine culture yielding ≥ 10^5 CFU/mL; and (5) availability of complete medical records. Exclusion criteria comprised: (1) pregnancy or lactation; (2) coexisting severe hepatic or renal dysfunction (Child-Pugh class C or eGFR < 30 mL/min/1.73 m^2); (3) asymptomatic bacteriuria associated with an indwelling catheter; (4) concurrent active infection in another organ system; and (5) absence of more than 20% of essential clinical data in the medical record.

Urine Sample Collection

For all subjects, the first clean mid-stream urine sample in the morning was collected before the use of antimicrobial agents and placed in a sterile cup. Before collection, all patients were required to clean their external genitalia as instructed. Female patients should avoid the menstrual period to prevent contamination of the urine sample. The collected urine specimens should be immediately sent to the clinical laboratory for testing and inoculated onto the culture medium using a sterile inoculating loop (10 μL) within 2 hours.[15]

Pathogen Culture and Identification, and Antimicrobial Susceptibility Testing

Pathogen culture, isolation and identification were performed in strict accordance with the laboratory's standard operating procedures and established guidelines for bacterial and fungal diagnostics.[15] Urine samples were inoculated onto Columbia blood agar plates and MacConkey agar plates, respectively, and incubated at 35°C for 18–24 hours (if there was no bacterial growth after 18–24 hours, the incubation time was extended to 48 hours). Meanwhile, the size and shape of the colonies were observed. If only a single bacterial colony with a concentration reaching 105 CFU/mL was detected in the urine sample, it was considered as a pathogen, and further identification and drug susceptibility testing were carried out. Additionally, findings involving more than three pathogens were also disregarded. Bacterial identification of suspicious colonies was conducted using a German Siemens fully automatic identification instrument and its accompanying reagents (for fungal identification, instruments and reagents provided by bioMérieux, France, were utilized). Drug sensitivity response cards (VITEK 2 XL® BioMérieux) in conjunction with the Kirby-Bauer disk diffusion method were employed to evaluate the antimicrobial susceptibility of the organisms. These data were interpreted based on the CLSI 2020 criteria (Clinical and Laboratory Standards Institute). The quality control strains, including *E. coli* ATCC 25922, *Pseudomonas aeruginosa* (*P. aeruginosa*) ATCC 27853, *Staphylococcus aureus* ATCC 25923 and ATCC 29213, *E. faecalis* ATCC 29912, and *K. pneumoniae* ATCC 700324, were all procured from the Clinical Laboratory Center of the National Health Commission.

Data Collection

Patient data were retrieved from the hospital's electronic medical records, laboratory information system, and antimicrobial resistance surveillance platform. Collected variables included demographic characteristics (age, gender, comorbidities), and microbiological findings (urine culture results, pathogen identification reports, and antimicrobial susceptibility profiles).

Statistical Analysis

Statistical analysis was performed using SPSS 25.0 software (Chicago, Illinois, USA). Categorical data such as patient characteristics (gender, age, comorbidities) were expressed as constituent ratios or rates (%). The drug resistance of different pathogens to antimicrobial agents was expressed as percentages. The susceptibility test findings were examined using WHONET 5.6 software (WHO, Geneva, Switzerland). GraphPad Prism 9 software (La Jolla, California, USA) was used for plotting, and the chi-square test was used for comparison between groups. The significance level of each statistical test was set as $P < 0.05$.

Results

Analysis of Baseline Data

Between 2021 and 2023, a total of 623 strains of pathogenic bacteria were isolated from 2021 to 2023 (the pathogens tested positive in microbial growth tests, with a significant pathogen count > 1.0×10^5 CFU/mL). Baseline demographic and clinical characteristics of the corresponding patients were analyzed. Females accounted for 365 cases (58.59%), slightly exceeding the proportion of males (258 cases, 41.41%). The majority of infections occurred in middle-aged and older adults, with 176 cases (28.25%) aged 41–60 years, 314 cases (50.40%) aged > 60 years, and 125 cases (20.06%) aged 21–40 years; only 8 cases (1.28%) involved individuals aged 18–20 years. Regarding comorbidities, the largest subgroup had no significant underlying disease (n = 241, 38.68%), followed by diabetes mellitus (n = 176, 28.25%), urolithiasis (n = 149, 23.92%), and benign prostatic hyperplasia (n = 57, 9.15%) (Table 1).

Distribution of Major Bacteria

Among UTI cases, Gram-negative bacteria predominated, accounting for 491 isolates. *E. coli* was the leading pathogen (n = 385, 61.80%), followed by *K. pneumoniae* (n = 54, 8.67%), *P. mirabilis* (n = 22, 3.53%), and *P. aeruginosa* (n = 22, 3.53%); other Gram-negative species each represented <1% of isolates. Gram-positive bacteria comprised 79 isolates, mainly *E. faecalis* (n = 38, 6.10%) and *Enterococcus faecium* (*E. faecalis*) (n = 25, 4.01%). Fungal pathogens totaled 28 isolates, primarily *Candida albicans* (*C. albicans*) (n = 25, 4.01%). An additional 25 isolates (0.40%) were classified as other pathogens (Table 2 and Figure 1).

Gender Distribution Characteristics of Pathogenic Bacteria Causing UTIs

There were differences in the distribution of major pathogens causing UTIs between different genders. A total of 385 strains of *E. coli* were isolated, including 116 strains (30.13%) from males and 269 strains (69.87%) from females. The number of female patients infected with *E. coli* was higher than that of males ($P < 0.05$). However, except for *E. coli*, the number of male patients with other major pathogens (such as *K. pneumoniae, P. aeruginosa, E. faecalis, C. albicans*, etc.) was higher than that of females ($P < 0.05$) (Table 3 and Figure 2).

Distribution Characteristics of the Incidence of UTIs Among Different Genders and Age Groups

The data from this study show that the incidence of UTIs increases with age. In the 18–20-year age group, incidence was similar between genders, with 2 male cases (0.76%) and 6 female cases (1.64%). There was no significant difference in the incidence of UTIs between different genders in this age group ($P > 0.05$). However, in the 21–40, 41–60, and > 60

Table 1 Baseline Data of the Subjects

Characteristics	Categories	Number of Cases	Proportion (%)
Gender	Male	258	41.41
	Female	365	58.59
Age distribution (years)	18-20	8	1.28
	21-40	125	20.06
	41-60	176	28.25
	> 60	314	50.40
Infection type	Uncomplicated lower urinary tract infection	287	46.07
	Complicated urinary tract infection	285	45.75
	Acute pyelonephritis	51	8.19
Comorbidities	Diabetes mellitus	176	28.25
	Urolithiasis	149	23.92
	Benign prostatic hyperplasia	57	9.15
	No significant comorbidities	241	38.68

Table 2 Distribution of Pathogens in Patients with UTI

Pathogens	Type	Number of Strains	Proportion (%)
Gram-negative bacteria (n = 491)	*Escherichia coli*	385	61.80
	Klebsiella pneumoniae	54	8.67
	Proteus mirabilis	22	3.53
	Pseudomonas aeruginosa	22	3.53
	Proteus species	5	0.80
	Enterobacter agglomerans	3	0.48
Gram-positive bacteria (n = 79)	*Enterococcus faecalis*	38	6.10
	Enterococcus faecium	25	4.01
	Streptococcus agalactiae (Group B)	9	1.44
	Staphylococcus epidermidis	5	0.80
	Staphylococcus haemolyticus	2	0.32
Fungi (n = 28)	*Candida albicans*	25	4.01
	Candida tropicalis	3	0.48
Others		25	0.40

age groups, the differences in the incidence of UTIs between different genders were statistically significant ($P < 0.05$). For ages 21–40 and 41–60, incidence was higher in females (26.03% and 34.79%, respectively) than in males (11.63% and 18.99%, respectively). In contrast, for patients >60 years, males exhibited a markedly higher incidence (68.60%) compared with females (37.53%) (Table 4 and Figure 3).

Susceptibility Analysis of Common Pathogens in Patients with UTIs to Antimicrobial Agents

Among Gram-negative bacteria, *E. coli* exhibited very high resistance to ampicillin (81.56%), with notable resistance rates to ceftriaxone (48.83%) and cefuroxime (47.79%). Resistance to cefotaxime/clavulanate and meropenem was

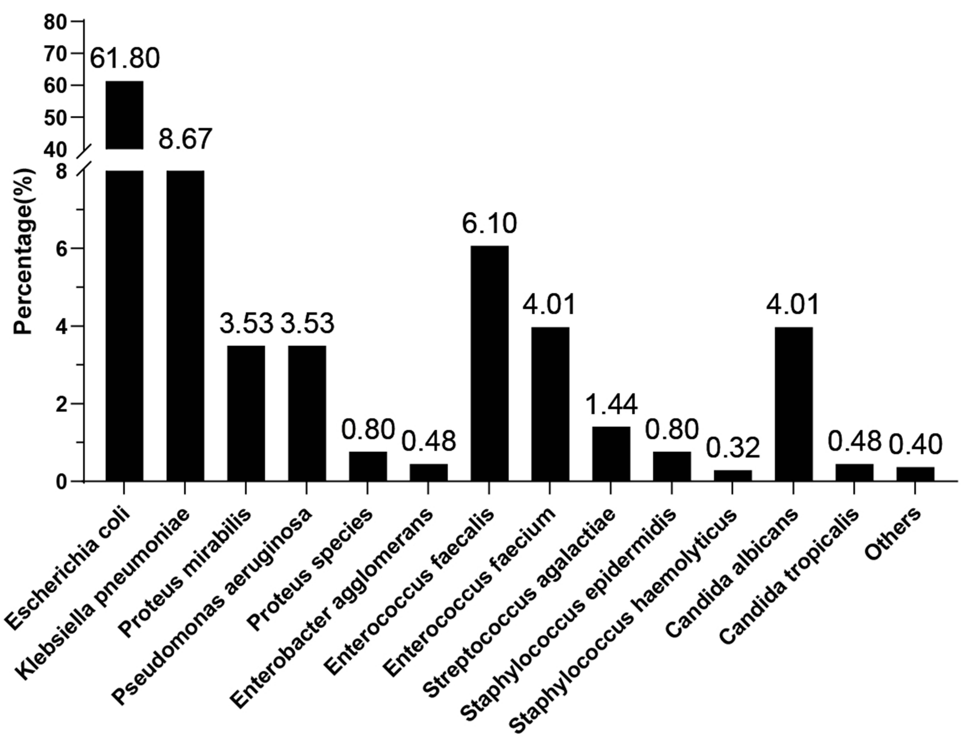

Figure 1 Distribution of pathogens isolated from urine cultures of patients with urinary tract infections in our hospital from 2021 to 2023.

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Table 3 Gender Distribution Characteristics of Pathogens Causing UTI

Pathogens	Number of Strains	Males (n = 258)		Females (n = 365)		χ^2	*P*
		Number of Strains	Proportion (%)	Number of Strains	Proportion (%)		
Escherichia coli	385	116	30.13	269	69.87	121.600	<0.001
Klebsiella pneumoniae	54	36	66.67	18	33.33	12.000	0.001
Proteus mirabilis	22	12	54.54	10	45.45	0.364	0.547
Pseudomonas aeruginosa	22	16	72.73	6	27.27	9.091	0.003
Enterococcus faecalis	38	29	76.32	9	23.68	21.050	< 0.001
Enterococcus faecium	25	13	52.00	12	48.00	0.080	0.777
Candida albicans	25	17	68.00	8	32.00	6.480	0.011

negligible, at 0.00% and 0.08%, respectively. *K. pneumoniae* showed the highest resistance to trimethoprim-sulfamethoxazole (44.44%) and moderate resistance to cefepime (31.48%) and ciprofloxacin (35.19%), while resistance to cefoxitin, ceftriaxone, and several other agents remained low (all ≤3.70%). *P. mirabilis* displayed high resistance to levofloxacin (72.73%) and ampicillin (50.00%), but no resistance (0.00%) to piperacillin/tazobactam or meropenem. *P. aeruginosa* maintained low resistance rates overall, with slightly higher resistance to ciprofloxacin (18.18%) and ceftazidime (18.18%), and complete susceptibility (0.00%) to cefuroxime and trimethoprim-sulfamethoxazole (Table 5).

Among Gram-positive bacteria, *E. faecalis* demonstrated extremely high resistance to tetracycline (94.74%) and moderate resistance to levofloxacin (34.21%), rifampin (34.21%), and ciprofloxacin (39.47%), while showing complete susceptibility (0.00%) to vancomycin, ampicillin, and penicillin. *E. faecalis* exhibited markedly high resistance to ampicillin (68.00%), penicillin (60.00%), levofloxacin (72.00%), tetracycline (64.00%), and ciprofloxacin (64.00%), with lower resistance to nitrofurantoin (20.00%), minocycline (32.00%), and rifampin (24.00%), and full susceptibility (0.00%) to vancomycin, linezolid, and teicoplanin (Table 6).

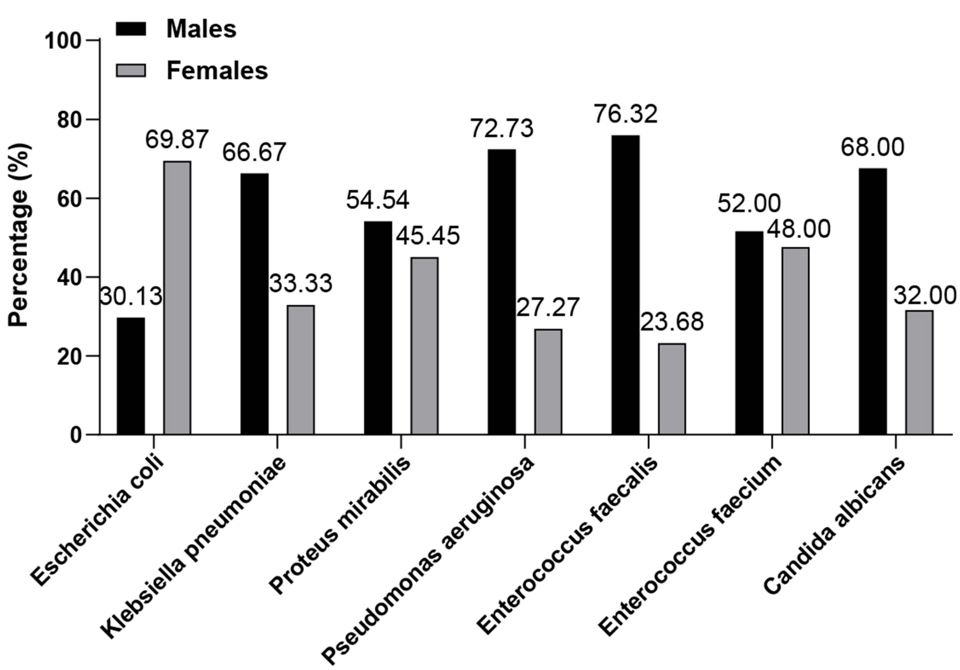

Figure 2 Gender distribution characteristics of pathogens in patients with urinary tract infections in our hospital from 2021 to 2023.

Table 4 Distribution Characteristics of UTI Incidence in Different Genders and Age Groups

Age (years)	Males (n = 258)		Females (n = 365)		χ^2	*P*
	Number	Proportion (%)	Number	Proportion (%)		
18-20	2	0.78	6	1.64	0.900	0.343
21-40	30	11.63	95	26.03	19.540	< 0.001
41-60	49	18.99	127	34.79	18.620	< 0.001
> 60	177	68.60	137	37.53	58.370	< 0.001

Discussion

This study retrospectively analyzed the etiological distribution, antimicrobial use, and antimicrobial susceptibility data of 623 patients with UTIs in our hospital from 2021 to 2023. The results showed that the predominant pathogens causing UTIs in our hospital during 2021–2023 were Gram-negative bacteria, primarily *E. coli*, with significant variations in antimicrobial susceptibility among different pathogens.

A total of 623 urine culture-positive samples were included in this study, revealing that Gram-negative bacteria were the predominant pathogens, consistent with the general understanding that Gram-negative bacilli are the main pathogens of UTIs,[16–18] confirming the dominant role of Gram-negative bacteria in the etiology of UTIs. Among them, *E. coli* (accounting for 61.80%) was the most prevalent isolate. Benjamin et al reported that uropathogenic *E. coli* accounts for approximately 80% of community-acquired UTIs in healthy populations.[19] Based on this, the importance of *E. coli* as a core pathogen of UTIs is highlighted.

In terms of population distribution, the distribution of major pathogens causing UTIs varied among different genders. This study found that, except for *E. coli*, other major pathogens (such as *K. pneumoniae, E. faecalis*, and *E. faecalis*) were more prevalent in male patients. This finding aligns with known epidemiological characteristics, indicating that the pathogen spectrum of UTIs in males, especially those with prostate diseases or indwelling urinary catheters, tends to be more diverse and more likely to include Gram-positive bacteria such as *Enterococcus*.[20,21] As reported in studies, the pathogenic microorganisms causing UTIs in males are more diverse than those observed in females, with *E. coli* being

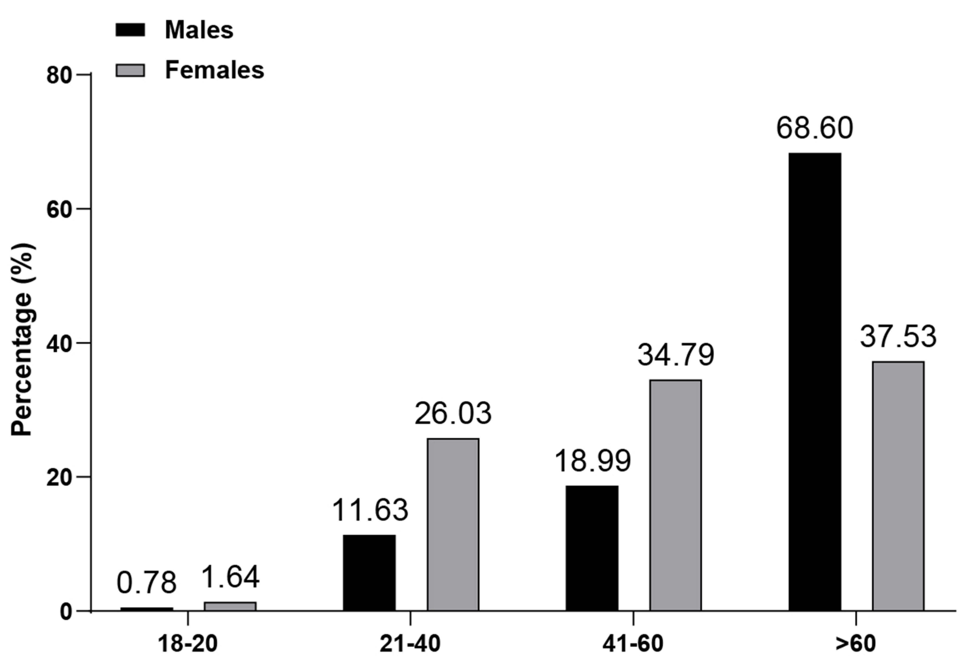

Figure 3 Distribution characteristics of the incidence of urinary tract infections among different genders and age groups.

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Table 5 Drug Resistance Rates of Major Gram-Negative Bacteria to Common Antibacterial Drugs (%)

Antibacterial Drugs	*Escherichia coli* (n = 385)		*Klebsiella pneumoniae* (n = 54)		*Proteus mirabilis* (n = 22)		*Pseudomonas aeruginosa* (n = 22)	
	Number of strains	Proportion (%)	Number of Strains	Proportion (%)	Number of Strains	Proportion (%)	Number of Strains	Proportion (%)
Gentamicin	146	37.92	11	20.37	6	27.27	1	4.55
Cefoxitin	11	2.86	2	3.70	1	4.55	1	4.55
Cefepime	154	40.00	17	31.48	5	22.73	3	13.64
Ceftriaxone	188	48.83	2	3.70	7	31.82	1	4.55
Piperacillin/Tazobactam Sodium	8	0.78	1	1.85	0	0.00	2	9.09
Cefuroxime	184	47.79	16	29.63	8	36.36	0	0.00
Cefotaxime	9	2.33	2	3.70	0	0.00	1	4.55
Ampicillin	314	81.56	2	3.70	11	50.00	1	4.55
Levofloxacin	147	38.18	15	27.78	16	72.73	3	13.64
Meropenem	3	0.08	4	7.41	0	0.00	1	4.55
Cotrimoxazole	165	42.86	24	44.44	10	45.45	0	0.00
Ciprofloxacin	157	40.78	19	35.19	7	31.82	4	18.18
Ceftazidime	77	20.00	11	20.37	0	0.00	4	18.18
Cefotaxime/Clavulanate Potassium	0	0.00	0	0.00	0	0.00	0	0.00

Table 6 Drug Resistance Rates of Major Gram-Positive Bacteria to Common Antibacterial Drugs (%)

Antibacterial Drugs	*Enterococcus Faecalis* (n = 38)		*Enterococcus Faecium* (n = 25)	
	Number of Strains	Proportion (%)	Number of Strains	Proportion (%)
Vancomycin	0	0.00	0	0.00
Ampicillin	0	0.00	17	68.00
Penicillin	0	0.00	15	60.00
Nitrofurantoin	0	0.00	5	20.00
Minocycline	6	15.79	8	32.00
Linezolid	0	0.00	0	0.00
Levofloxacin	13	34.21	18	72.00
Teicoplanin	0	0.00	0	0.00
Tetracycline	36	94.74	16	64.00
Rifampicin	13	34.21	6	24.00
Ciprofloxacin	15	39.47	16	64.00

clearly dominant. Their urinary pathogens exhibit greater diversity, including other *Enterobacteriaceae* (*K. pneumoniae, P. mirabilis), E. faecalis*, and *P. aeruginosa*.[21,22]

Regarding age distribution, the data showed that the incidence rate was higher among young and middle-aged women, while the proportion of male patients significantly increased to 68.60% in the elderly group (as suggested by the data in this study, >65 years old). This confirms that elderly males are a high-risk group for complicated UTIs.[20,23] This shift in older men may be linked to benign prostatic hyperplasia, incomplete bladder emptying, recurrent catheterization, and higher rates of asymptomatic bacteriuria.[1,24] Therefore, these findings emphasize the necessity of targeted prevention strategies, such as hygiene education for young women; prevention, etiological monitoring, and initial treatment plans for UTIs in elderly males should differ from those for other populations. Ferdous et al reported that UTIs are most common in women aged 16–35, with up to 10% of women experiencing an infection each year and 40–60% of women being infected at some point in their lives.[23] Additionally, their data also revealed a sudden increase in infection rates among males aged 50–70, possibly because this is typically the age when the male prostate begins to grow. After the age of 70, the infection rate in males gradually decreases but remains higher than that in females.[23]

Antimicrobial susceptibility testing revealed high resistance rates of *E. coli* to ampicillin, ceftriaxone, and cefuroxime, and of *K. pneumoniae* to cotrimoxazole. Both species are known to harbor extended-spectrum β-lactamases (ESBLs), limiting the efficacy of β-lactam agents.[25] Conversely, low resistance rates to cefotaxime/clavulanate potassium and meropenem in *E. coli*, and to piperacillin/tazobactam and meropenem in *K. pneumoniae*, suggest these agents remain viable options for empirical therapy in severe infections. Among Gram-positive isolates, *E. faecalis* exhibited high tetracycline resistance (94.74%) but remained fully susceptible to vancomycin and penicillin, supporting their continued use as first-line agents. *E. faecium* showed high resistance to multiple drugs but preserved susceptibility to vancomycin and linezolid. These resistance patterns highlight the importance of antimicrobial stewardship, particularly in limiting unnecessary use of ampicillin, tetracyclines, and fluoroquinolones. Furthermore, prophylactic systemic antibiotics for catheterized patients should be avoided unless clinically indicated, as this practice is a known driver of resistance.[25] According to existing research data, *E. coli* exhibits high resistance rates to amoxicillin and ciprofloxacin but low resistance rates to nitrofurantoin; *P. mirabilis* shows high resistance rates to trimethoprim/sulfamethoxazole.[21,26] In comparison, the resistance spectrum of pathogens causing UTIs in our hospital exhibits distinct localized characteristics. These differences may reflect specific antimicrobial prescribing habits in our region (such as the historical intensity of fluoroquinolone and tetracycline use). The data from this study clearly indicate that ampicillin, levofloxacin, and tetracycline should no longer be considered as empirical treatment options for related UTIs in our hospital. Secondly, this study also confirms that drugs such as cefotaxime/clavulanic acid and vancomycin maintain good activity against most pathogens, providing reliable last-line options for treating multidrug-resistant infections.

This study has several limitations. First, it was conducted in a single hospital, which may limit generalizability to other regions or healthcare settings with different patient populations and antimicrobial prescribing patterns. Second, as a retrospective analysis, it relied on the completeness and accuracy of electronic medical records; missing data, including detailed prior antibiotic exposure history, could have biased susceptibility interpretations. Third, the study did not assess clinical outcomes or treatment effectiveness, preventing correlation between in vitro susceptibility and patient recovery. Finally, molecular characterization of resistance mechanisms (eg, ESBL or carbapenemase genes) was not performed, which could provide deeper insights into resistance epidemiology. To address the aforementioned limitations, it is recommended to conduct multicenter prospective studies in the future to systematically collect complete clinical, microbiological, and pharmacological data to establish more precise localized treatment and resistance early warning models. Simultaneously, conducting molecular epidemiological studies to track the spread of highly resistant clones will provide scientific evidence for controlling the diffusion of resistant bacteria at the source.

Conclusion

In conclusion, this study systematically depicted the pathogen distribution landscape and resistance status of UTIs in our hospital from 2021 to 2023, revealing severe challenges represented by ampicillin resistance and localized resistance patterns. The study results emphasize that continuous local-based microbiological monitoring, formulation of individualized empirical treatment plans, and implementation of strict antimicrobial stewardship are key measures to address antimicrobial resistance in UTIs and improve patient outcomes. Based on the aforementioned results, we propose the following specific recommendations: Empirical treatment: It is recommended to update the diagnosis and treatment pathway for UTIs in our hospital and exclude ampicillin from the empirical medication regimen. For suspected complicated infections or elderly male patients, initial treatment should prioritize coverage of *Enterococcus* and exercise caution in the use of fluoroquinolones. Antimicrobial stewardship: The hospital's antimicrobial stewardship team should focus on and restrict the unindicated use of ampicillin, levofloxacin, and tetracycline in UTIs. It is recommended to regularly publish the pathogen resistance spectrum based on our hospital's data and embed it into the electronic medical record system to provide real-time decision support for clinicians.

Ethical Statement

The research obtained the approval from the Ethic Committee of Xian Yang Central Hospital . The subjects participating in the study signed the written informed consent form.

Consent to Participate

Informed consent was obtained from all individual participants included in the study.

Consent for Publication

Patients signed informed consent regarding publishing their data and photographs.

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Disclosure

The authors declared that they have no conflicts of interest regarding this work.

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