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ORIGINAL RESEARCH

Drug Resistance Patterns and Pathogen Distribution in Patients with Urinary Tract Infection in Suzhou, China: A Five-Year Retrospective Study (2020–2024)

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Objective: To investigate the distribution of pathogens and their antimicrobial resistance profiles in urine cultures from patients with urinary tract infections (UTIs) in Suzhou, China, and to guide empirical treatment decisions.

Methods: We analyzed 9,249 non-duplicate, positive midstream urine cultures collected from January 2020 to December 2024. Bacterial and fungal identification was performed using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS). Antimicrobial susceptibility testing (AST) was conducted following Clinical and Laboratory Standards Institute (CLSI) guidelines.

Results: Female patients (60.1%) and those aged >65 years (64.3%) accounted for the majority of cases. *Escherichia coli* (33.3%) was the predominant pathogen followed by *Enterococcus faecalis* (8.6%), *Klebsiella pneumoniae* (8.4%), and *Enterococcus faecium* (8.0%). Its resistance to third/fourth-generation cephalosporins (eg, cefotaxime from 50.4% to 38.8%) decreased significantly ($P < 0.05$), while resistance to fluoroquinolones remained high (>60%). Carbapenem resistance in *Klebsiella pneumoniae* exhibited alarming fluctuations, peaking at 40.6% in 2023. The prevalence of extended-spectrum β-lactamase (ESBL)-producing *Escherichia coli* decreased significantly. *Enterococcus faecium* displayed extreme resistance to ampicillin and fluoroquinolones (>94%), whereas *Enterococcus faecalis* was more susceptible. Azole resistance in *Candida albicans* markedly declined but remained high in *Candida tropicalis*.

Conclusion: *Escherichia coli* was the main bacterial urinary pathogen in the Suzhou region. The dynamically high carbapenem resistance in *Klebsiella pneumoniae* and the severe, species-specific resistance profile of *Enterococcus faecium* critically limited treatment options. Significant temporal changes in pathogen distribution and resistance patterns underscored the necessity for ongoing local surveillance, tailored empirical therapy, and reinforced antimicrobial stewardship programs to guide effective UTI management in the region.

Keywords: urinary tract infection, pathogen distribution, antimicrobial resistance, carbapenem-resistant *Klebsiella pneumoniae*, empirical therapy

Introduction

Urinary tract infection (UTI) is one of the most common infections encountered in clinical practice worldwide, imposing a substantial burden on healthcare systems.[1,2] Its recurrent nature significantly impacts patients' quality of life.[3] Common uropathogens include *Escherichia coli, Klebsiella pneumoniae, Enterococcus faecalis, Enterococcus faecium, Streptococcus agalactiae, Proteus mirabilis*, and fungal species such as *Candida* spp.[4] Timely and appropriate antimicrobial therapy is crucial for the effective management of UTIs.[5] However, recent epidemiological shifts have revealed

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an increasing prevalence of multidrug-resistant (MDR) bacteria, such as extended-spectrum β-lactamase (ESBL)-producing Enterobacteriaceae, carbapenem-resistant *Klebsiella pneumoniae* (CRKP) and vancomycin-resistant enterococci (VRE), which markedly complicate empirical therapeutic strategies.[6–9]

Previous studies have indicated considerable variation in the prevalence of uropathogens across different geographical regions and investigations.[10] Therefore, data from other countries or regions can only serve as a reference. Furthermore, the prevalence of UTIs increases with age, affecting up to 20% of women over 65 years.[11] Notably, antimicrobial resistance trends are dynamic and continuously evolve under influences including antimicrobial selection pressure, the emergence and spread of resistant clones, and changes in healthcare practices.[12] Consequently, proactive and regular surveillance of local uropathogen distribution and associated resistance patterns is essential for promoting rational antimicrobial use and curbing the emergence of resistant strains.

Comprehensive longitudinal studies on uropathogen prevalence and the dynamic evolution of drug resistance profiles in the Suzhou region are currently lacking. While valuable, existing national or provincial surveillance data often lack the granularity required to provide precise, evidence-based guidance for empirical therapy across diverse healthcare settings.[13] This need for actionable, local clinical data persists even as research frontiers expand. For instance, a recent systematic review by Palumbo et al synthesized advances in understanding the urobiome and innovative molecular diagnostics for urinary disorders.[14] While such work is crucial for future diagnostic and therapeutic strategies, it also underscores the importance of local epidemiological surveillance. Data on pathogens and their antibiotic resistance profiles continued to provide the evidence required for empirical treatment decisions in current clinical practice. To address this gap, this study retrospectively analyzed clinical data from UTI patients in the Suzhou region from 2020 to 2024. We aimed to elucidate local pathogen distribution and changing trends in antimicrobial resistance, thereby providing valuable evidence-based insights to inform local UTI prevention, control strategies, and rational antibiotic utilization.

Materials and Methods

Study Design and Data Collection

This retrospective study was conducted at a Grade A tertiary general hospital with six campuses in Eastern China from January 2020 to December 2024. Patients who had received antimicrobial agents within two weeks prior to sample collection were excluded from this study. According to the standard clinical protocol, all urine samples (midstream clean catch, nappy pad, catheter aspirated) had been collected in sterile containers, properly labeled, and promptly transported to the clinical microbiology laboratory within two hours. To minimize contamination, a clean catch midstream method was employed wherever possible. In neonates and early infants, nappy pad method, described by Liaw et al was used.[15] In case of catheterized patients, urine specimen were collected either through the catheter collection port or through puncture of the tubing with a sterile needle.[16] For this analysis, only the first positive urine culture from each patient was included for analysis to avoid duplication. Demographic data (age, sex, ward) and collection dates were retrieved anonymously from the laboratory information system. The study was approved by the Ethics Committee of The Affiliated Suzhou Hospital of Nanjing Medical University (Approval No. K-2024-144-K01). The requirement for informed consent was waived due to the retrospective nature of the study.

Bacterial Culture and Identification

Urine samples were inoculated onto 5% sheep blood agar and MacConkey agar (Autobio, China) using a calibrated 10-μL pipette and inoculating loop. Plates were incubated at 35°C under 5% CO_2 for 24–48 hours. Significant growth was defined as $\geq 10^5$ CFU/mL for gram-negative bacteria and $\geq 10^4$ CFU/mL for gram-positive bacteria.[17] Contaminated samples (containing >3 bacterial species) were excluded. Bacterial identification was performed using matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS, Bruker Daltonics, Germany).

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing (AST) was performed using the Phoenix automated system (BD, USA), the VITEK-2 compact system (bioMérieux, France), or the Kirby-Bauer disk diffusion method, following Clinical and Laboratory Standards Institute (CLSI) guidelines.[18] The antibiotics tested included penicillin, ampicillin, piperacillin/tazobactam, ceftazidime, cefotaxime, cefuroxime, cefazolin, cefepime, cefoxitin, imipenem, meropenem, aztreonam, cefoperazone/sulbactam, ampicillin/sulbactam, nitrofurantoin, minocycline, tetracycline, ciprofloxacin, levofloxacin, amikacin, gentamicin, sulfamethoxazole/trimethoprim, vancomycin, teicoplanin, tigecycline, linezolid. Considering the use of multiple AST platforms, quality control was performed using reference strains: *Escherichia coli* ATCC25922, *Klebsiella pneumoniae* ATCC 700603, *Pseudomonas aeruginosa* ATCC 27853, *Staphylococcus aureus* ATCC 29213, *Staphylococcus aureus* ATCC 25923, and *Enterococcus faecalis* ATCC 29212. Results were interpreted as "susceptible" (S), "intermediate" (I), or "resistant" (R) according to CLSI breakpoints.

Antifungal Susceptibility Testing

Antifungal susceptibility testing for *Candida* isolates against flucytosine, amphotericin B, fluconazole, itraconazole, and voriconazole was performed using the ATB FUNGUS 3 kit (bioMérieux, France), with minimum inhibitory concentrations (MICs) determined according to the manufacturer's instructions. Quality control was ensured using *Candida parapsilosis* ATCC 22019 and *Candida krusei* ATCC 6258. Susceptibility was interpreted according to CLSI M60 guidelines.[19]

Statistical Analysis

Data analysis was conducted using WHONET 5.6 (WHO, Switzerland) and SPSS Statistics 27.0 (IBMCorp., USA). Categorical variables (demographic characteristics, pathogen distribution, resistance rates) were presented as frequencies and percentages. The chi-square test was used to compare categorical variables between groups. To assess significant temporal trends over the five-year study period (2020–2024) for key outcomes such as pathogen distribution and antimicrobial resistance rates, the chi-square test for trend (Cochran-Armitage test) was employed. A two-tailed P-value of <0.05 was considered statistically significant.

Results

Demographic Characteristics of Patients

A total of 9,249 non-duplicate urine samples were included. Females consistently accounted for the majority (60.1%, 5,560/9,249), which was significantly higher than males (39.9%, 3,689/9,249). The gender distribution remained stable across the study years ($Z = 0.867$, $P = 0.386$). Patients aged over 65 years constituted the largest group (64.3%, 5,948/9,249), with their proportion increasing from 62.1% to 65.9% ($Z = 2.659$, $P = 0.008$). The age distribution varied significantly over the study period ($\chi^2 = 84.799$, $P < 0.001$). The age group of 45–65 years represented a stable second largest group (23.4%, 2,164/9,249) of the total. Younger age groups (15–44 years and <15 years) were less represented, constituting 10.3% and 2.0% of the cohort, respectively (Table 1).

Pathogens Distribution

A total of 9,249 non-duplicate pathogenic strains were isolated from urine samples from 2020 to 2024. Their distribution was shown in Table 2. *Escherichia coli* was the predominant pathogen, accounting for 33.3% of isolates, followed by *Enterococcus faecalis* (8.6%), *Klebsiella pneumoniae* (8.4%), and *Enterococcus faecium* (8.0%). The isolation rate of *Escherichia coli* increased significantly over time (from 32.4% to 38.1%; $Z = 4.544$, $P < 0.001$). In contrast, *Enterococcus faecium* showed a significant declining trend (from 10.4% to 6.5%; $Z = -4.120$, $P < 0.001$). Additionally, the isolation frequencies of *Candida albicans* also exhibited a significant change over time (from 2.1% to 5.2%; $Z = 1.966$, $P = 0.049$). No significant temporal variation was observed for *Klebsiella pneumoniae* ($Z = 1.250$, $P = 0.211$) or *Enterococcus faecalis* ($Z = -0.664$, $P = 0.506$). Other organisms, including *Staphylococcus aureus* and *Citrobacter freundii*, were less frequently isolated.

Table 1 The Characteristics of Patients According to Their Age and Gender

Characteristics	2020 (n = 1560)		2021 (n = 1838)		2022 (n = 1937)		2023 (n = 1928)		2024 (n = 1986)		Total (n = 9249)		*Z*	*P*
	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)		
Sex														
Male	611	39.2	765	41.6	787	40.6	746	38.7	780	39.3	3689	39.9	−0.867	0.386
Female	949	60.8	1073	58.4	1150	59.4	1182	61.3	1206	60.7	5560	60.1	0.867	0.386
Age in years														
< 15	70	4.5	51	2.8	30	1.5	11	0.6	25	1.3	187	2.0	−7.925	<0.001
15–44	157	10.1	186	10.1	203	10.5	191	9.9	213	10.7	950	10.3	0.499	0.618
45–65	364	23.3	443	24.1	454	23.4	456	23.7	447	22.5	2164	23.4	−0.732	0.464
> 65	969	62.1	1158	63.0	1250	64.5	1270	65.9	1301	65.5	5948	64.3	2.659	0.008

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Table 2 Distribution of Main Pathogens Causing UTIs Among Patients

Pathogen	2020 (n = 1560)		2021 (n = 1838)		2022 (n = 1937)		2023 (n = 1928)		2024 (n = 1986)		Total (n = 9249)		*Z*	*P*
	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)	Strain (n)	Percentage (%)		
Escherichia coli	506	32.4	557	30.3	605	31.2	657	34.1	756	38.1	3081	33.3	4.544	<0.001
Enterococcus faecalis	151	9.7	140	7.6	174	9.0	160	8.3	169	8.5	794	8.6	−0.664	0.506
Klebsiella pneumoniae	124	7.9	139	7.6	168	8.7	187	9.7	163	8.2	781	8.4	1.250	0.211
Enterococcus faecium	162	10.4	155	8.4	147	7.6	145	7.5	130	6.5	739	8.0	−4.120	<0.001
Pseudomonas aeruginosa	88	5.6	87	4.7	79	4.1	77	4.0	69	3.5	400	4.3	−3.265	0.001
Candida albicans	33	2.1	95	5.2	100	5.2	87	4.5	84	4.2	399	4.3	1.966	0.049
Proteus mirabilis	68	4.4	86	4.7	89	4.6	76	3.9	75	3.8	394	4.3	−1.339	0.181
Streptococcus agalactiae	61	3.9	72	3.9	83	4.3	72	3.7	81	4.1	369	4.0	0.092	0.926
Acinetobacter baumannii	35	2.2	56	3.0	44	2.3	42	2.2	27	1.4	204	2.2	−2.587	0.010
Enterobacter cloacae	30	1.9	42	2.3	42	2.2	32	1.7	25	1.3	171	1.8	−2.079	0.038
Corynebacterium striatum	29	1.9	26	1.4	27	1.4	26	1.3	43	2.2	151	1.6	0.745	0.456
Morgan morganella	29	1.9	28	1.5	28	1.4	28	1.5	35	1.8	148	1.6	−0.183	0.855
Candida tropicalis	14	0.9	33	1.8	33	1.7	38	2.0	29	1.5	147	1.6	1.198	0.231
Candida glabrata	12	0.8	29	1.6	25	1.3	47	2.4	20	1.0	133	1.4	1.286	0.199
Klebsiella aerogenes	16	1.0	34	1.8	32	1.7	14	0.7	19	1.0	115	1.2	−1.737	0.082
Staphylococcus epidermidis	14	0.9	20	1.1	29	1.5	21	1.1	25	1.3	109	1.2	0.825	0.409
Streptococcus anginosus	16	1.0	27	1.5	23	1.2	11	0.6	29	1.5	106	1.1	−0.056	0.955
Staphylococcus aureus	24	1.5	18	1.0	22	1.1	25	1.3	15	0.8	104	1.1	−1.533	0.125
Citrobacter freundii	6	0.4	10	0.5	22	1.1	19	1.0	17	0.9	74	0.8	1.971	0.049
Others	142	9.1	184	10.0	165	8.5	164	8.5	175	8.8	830	9.0	−1.009	0.313

Abbreviation: UTIs, urinary tract infections.

Drug Resistance Patterns

Resistance of *Escherichia coli* to Common Antibiotics

Escherichia coli isolates exhibited significant temporal variations in resistance to several antibiotics (Table 3). Consistently high resistance was observed to ampicillin (75.8% overall), with no significant annual variation (P = 0.577). High resistance was also noted for fluoroquinolones: ciprofloxacin (63.2% overall) and levofloxacin (60.2% overall). Significant decreasing trends were observed for ceftazidime (from 22.5% to 14.4%, P = 0.001), cefotaxime (from 50.4% to 38.8%, P = 0.001), cefuroxime (from 52.6% to 41.7%, P = 0.025), cefepime (from 37.2% to 27.9%, P = 0.005), and cefoxitin (from 13.8% to 7.3%, P = 0.002). Resistance to sulfamethoxazole/trimethoprim remained high (43.8% overall). In contrast, carbapenems (imipenem 1.2%, meropenem 1.0%) maintained excellent activity, with both showing decreasing trends (P = 0.009 and P = 0.029, respectively). Similarly, amikacin (1.9% overall) and β-lactam/β-lactamase inhibitor combinations such as cefoperazone/sulbactam (3.9% overall) and piperacillin/tazobactam (3.7% overall) proved highly effective.

Resistance of *Klebsiella pneumoniae* to Common Antibiotics

Klebsiella pneumoniae exhibited significant temporal variations in resistance to some antibiotics (Table 4). Alarmingly, carbapenem resistance showed marked fluctuations. Imipenem resistance rose from 20.2% in 2020 to a peak of 40.6% in 2023 before declining to 22.1% in 2024 (Z = 1.754, P = 0.079); meropenem resistance followed a nearly similar pattern (Z = 1.872, P = 0.061). Resistance to third- and fourth-generation cephalosporins was consistently high and variable: ceftazidime (39.7% overall), cefepime (41.4% overall), and cefotaxime (46.0% overall). High resistance was also noted

Table 3 Resistance of *Escherichia coli* to Common Antibiotics

Antibiotics	2020 (n = 506)		2021 (n = 557)		2022 (n = 605)		2023 (n = 657)		2024 (n = 756)		2020–2024 (n = 3081)		*Z*	*P*
	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)		
Amikacin	9	1.8	6	1.1	12	2.0	18	2.7	15	2.0	60	1.9	1.137	0.256
Ampicillin	396	78.3	421	75.6	444	73.4	499	76.0	575	76.1	2335	75.8	−0.557	0.577
Aztreonam	155	30.6	150	26.9	146	24.1	175	26.6	174	23.0	800	26.0	−2.699	0.007
Ceftazidime	114	22.5	107	19.2	87	14.4	118	18.0	109	14.4	535	17.4	−3.474	0.001
Ciprofloxacin	320	63.2	350	62.8	363	60.0	441	67.1	474	62.7	1948	63.2	0.520	0.603
Cefoperazone/sulbactam	33	6.5	22	3.9	13	2.1	26	4.0	26	3.4	120	3.9	−2.200	0.028
Cefotaxime	255	50.4	250	44.9	239	39.5	255	38.8	315	41.7	1314	42.6	−3.376	0.001
Cefuroxime	266	52.6	253	45.4	252	41.7	295	44.9	338	44.7	1404	45.6	−2.239	0.025
Cefazolin	276	54.5	256	46.0	266	44.0	328	49.9	349	46.2	1475	47.9	−1.768	0.077
Cefepime	188	37.2	156	28.0	169	27.9	186	28.3	211	27.9	910	29.5	−2.830	0.005
Cefoxitin	70	13.8	71	12.7	44	7.3	72	11.0	64	8.5	321	10.4	−3.069	0.002
Gentamicin	160	31.6	174	31.2	177	29.3	206	31.4	231	30.6	948	30.8	−0.293	0.769
Imipenem	14	2.8	6	1.1	4	0.7	5	0.8	7	0.9	36	1.2	−2.612	0.009
Levofloxacin	298	58.9	337	60.5	349	57.7	416	63.3	455	60.2	1855	60.2	0.827	0.408
Meropenem	12	2.4	5	0.9	3	0.5	4	0.6	7	0.9	31	1.0	−2.177	0.029
Ampicillin/sulbactam	126	24.9	117	21.0	106	17.5	133	20.2	134	17.7	616	20.0	−2.805	0.005
Sulfamethoxazole/trimethoprim	241	47.6	261	46.9	247	40.8	257	39.1	342	45.2	1348	43.8	−1.659	0.097
Piperacillin/tazobactam	25	4.9	12	2.2	15	2.5	35	5.3	27	3.6	114	3.7	0.324	0.746

Notes: The specific concentrations tested for each antibiotic are defined by the manufacturer's panel configuration (for automated systems) or standard disk content (for Kirby-Bauer), in full compliance with the referenced Clinical and Laboratory Standards Institute (CLSI) guidelines.

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Table 4 Resistance of *Klebsiella pneumoniae* to Common Antibiotics

Antibiotics	2020 (n = 124)		2021 (n = 139)		2022 (n = 168)		2023 (n = 187)		2024 (n = 163)		2020–2024 (n = 781)		*Z*	*P*
	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)		
Amikacin	21	16.9	27	19.4	47	28.0	65	34.8	34	20.9	194	24.8	1.984	0.047
Aztreonam	46	37.1	44	31.7	85	50.6	98	52.4	63	38.7	336	43.0	1.789	0.074
Ceftazidime	42	33.9	42	30.2	79	47.0	93	49.7	54	33.1	310	39.7	1.339	0.181
Ciprofloxacin	59	47.6	55	39.6	90	53.6	112	59.9	70	42.9	386	49.4	0.877	0.381
Cefoperazone/sulbactam	35	28.2	35	25.2	64	38.1	77	41.2	41	25.2	252	32.3	0.748	0.454
Cefotaxime	55	44.4	46	33.1	93	55.4	100	53.5	65	39.9	359	46.0	0.846	0.398
Cefuroxime	61	49.2	53	38.1	97	57.7	108	57.8	74	45.4	393	50.3	0.923	0.356
Cefazolin	61	49.2	56	40.3	99	58.9	114	61.0	72	44.2	402	51.5	0.794	0.427
Cefepime	45	36.3	41	29.5	85	50.6	92	49.2	60	36.8	323	41.4	1.538	0.124
Cefoxitin	37	29.8	39	28.1	74	44.0	91	48.7	52	31.9	293	37.5	1.880	0.060
Gentamicin	41	33.1	38	27.3	66	39.3	83	44.4	51	31.3	279	35.7	1.093	0.274
Imipenem	25	20.2	32	23.0	53	31.5	76	40.6	36	22.1	222	28.4	1.754	0.079
Levofloxacin	48	38.7	45	32.4	82	48.8	103	55.1	62	38.0	340	43.5	1.647	0.100
Meropenem	24	19.4	31	22.3	52	31.0	74	39.6	36	22.1	217	27.8	1.872	0.061
Ampicillin/sulbactam	56	45.2	49	35.3	91	54.2	106	56.7	63	38.7	365	46.7	0.636	0.525
Sulfamethoxazole/trimethoprim	40	32.3	36	25.9	83	49.4	77	41.2	50	30.7	286	36.6	0.808	0.419
Piperacillin/tazobactam	32	25.8	38	27.3	70	41.7	89	47.6	48	29.4	277	35.5	2.099	0.036

Notes: The specific concentrations tested for each antibiotic are defined by the manufacturer's panel configuration (for automated systems) or standard disk content (for Kirby-Bauer), in full compliance with the referenced Clinical and Laboratory Standards Institute (CLSI) guidelines.

for fluoroquinolones (ciprofloxacin 49.4%; levofloxacin 43.5%) and ampicillin/sulbactam (46.7% overall). Although lower, amikacin resistance (24.8% overall) showed a significant increasing trend ($Z = 1.984$, $P = 0.047$), peaking at 34.8% in 2023. Similarly, resistance to piperacillin/tazobactam also rose from 25.8% to 47.6% ($Z = 2.099$, $P = 0.036$). Resistance to β-lactam/β-lactamase inhibitor combinations, cefoperazone/sulbactam, was 32.3%, with no significant annual variation ($P = 0.454$).

ESBL and CRE Prevalence in Common Pathogens

From 2020 to 2024, the prevalence of ESBL-producing *Escherichia coli* significantly declined from 50.4% to 38.8% ($Z = -3.376$, $P = 0.001$). Carbapenem-resistant *Escherichia coli* showed a decreasing trend (from 2.8% to 0.7%; $Z = -2.612$, $P = 0.009$). ESBL rates in *Klebsiella pneumoniae* fluctuated between 33.1% and 55.4% ($Z = 0.846$, $P = 0.398$), peaking at 55.4% in 2022 before falling to 39.9% in 2024. The prevalence of CRKP also showed a fluctuation ($Z = 1.754$, $P = 0.079$), rising from 20.2% in 2020 to a peak of 40.6% in 2023, then declining to 22.1% in 2024 (Table 5).

Resistance of *Enterococcus faecalis* to Common Antibiotics

Enterococcus faecalis showed significant temporal variations in resistance to several antibiotics (Table 6). Resistance to ciprofloxacin increased significantly from 28.7% to 50.3% ($Z = 2.861$, $P = 0.004$). Levofloxacin resistance also showed an increasing trend (from 28.2% to 46.9%; $Z = 2.258$, $P = 0.024$). Although high, the resistance to tetracycline (from 89.4% to 78.7%; $Z = -2.452$, $P = 0.014$) and minocycline (from 84.8% to 65.0%; $Z = -4.737$, $P < 0.001$) showed a decreasing trend. However, no resistance was detected to high-level gentamicin, teicoplanin, or vancomycin during the study period. Notably, linezolid resistance showed a significant increasing trend (from 2.6% to 8.1%; $Z = 2.401$, $P = 0.016$). Resistance to ampicillin, nitrofurantoin, and penicillin showed no significant temporal variations.

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Table 5 ESBL and CRE Prevalence in Common Pathogens

Year	*Escherichia coli*				*Klebsiella pneumoniae*			
	n	ESBLs (%)	n	CRE (%)	n	ESBLs (%)	n	CRE (%)
2020	255	50.4	14	2.8	55	44.4	25	20.2
2021	250	44.9	6	1.1	46	33.1	32	23.0
2022	239	39.5	4	0.7	93	55.4	53	31.6
2023	255	38.8	5	0.8	100	53.5	76	40.6
2024	315	41.7	7	0.9	65	39.9	36	22.1
Z	−3.376		−2.612		0.846		1.754	
P	0.001		0.009		0.398		0.079	

Abbreviations: ESBL, Extended-spectrum beta-lactamases; CRE, Carbapenem-resistant Enterobacteriaceae.

Table 6 Resistance of *Enterococcus faecalis* to Common Antibiotics

Antibiotics	2020 (n = 151)		2021 (n = 140)		2022 (n = 174)		2023 (n = 160)		2024 (n = 169)		2020–2024 (n = 794)		*Z*	*P*
	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)		
Ampicillin	2	1.3	3	2.1	2	1.1	0	0.0	1	0.6	8	1.0	−1.403	0.161
Ciprofloxacin	57	37.7	56	40.0	50	28.7	79	49.4	85	50.3	327	41.2	2.861	0.004
Nitrofurantoin	5	3.3	1	0.7	2	1.1	2	1.3	1	0.6	11	1.4	−1.675	0.094
High concentration of Gentamicin	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	/	/
Linezolid	4	2.6	5	3.6	7	4.0	13	8.1	12	7.1	41	5.2	2.401	0.016
Levofloxacin	56	37.1	55	39.3	49	28.2	75	46.9	79	46.7	314	39.5	2.258	0.024
Minocycline	128	84.8	120	85.7	116	66.7	104	65.0	115	68.0	583	73.4	−4.737	<0.001
Penicillin	10	6.6	12	8.6	13	7.5	13	8.1	10	5.9	58	7.3	−0.299	0.765
Tetracycline	135	89.4	124	88.6	147	84.5	142	88.8	133	78.7	681	85.8	−2.452	0.014
Teicoplanin	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	/	/
Tigecycline	1	0.7	0	0.0	0	0.0	0	0.0	0	0.0	1	0.1	/	/
Vancomycin	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	/	/

Notes: The specific concentrations tested for each antibiotic are defined by the manufacturer's panel configuration (for automated systems) or standard disk content (for Kirby-Bauer), in full compliance with the referenced Clinical and Laboratory Standards Institute (CLSI) guidelines. "/" represents not applicable.

Resistance of *Enterococcus faecium* to Common Antibiotics

Enterococcus faecium exhibited very high resistance to ciprofloxacin (97.3%), penicillin (97.2%), ampicillin (96.5%), and levofloxacin (94.5%) over the five-year period (Table 7). Significant temporal variations were observed in resistance to nitrofurantoin (70.2% overall, $Z = 5.088$, $P < 0.001$) and tetracycline (39.5% overall, $Z = 3.329$, $P = 0.001$). In contrast, resistance remained low for high-level of gentamicin, tigecycline, teicoplanin, vancomycin, and linezolid, suggesting their potential efficacy (Table 7).

Resistance of *Candida albicans* to Common Antifungal Agents

As shown in Table 8, *Candida albicans* demonstrated consistently high susceptibility to amphotericin B, with no resistant isolates detected. Significant decreases in resistance were observed for fluconazole (from 33.3% to 5.7%, $Z = -5.616$, $P <$

Table 7 Resistance of *Enterococcus faecium* to Common Antibiotics

Antibiotics	2020 (n = 162)		2021 (n = 155)		2022 (n = 147)		2023 (n = 145)		2024 (n = 130)		2020–2024 (n = 739)		*Z*	*P*
	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)		
Ampicillin	154	95.1	147	94.8	142	96.6	144	99.3	126	96.9	713	96.5	1.759	0.079
Ciprofloxacin	153	94.4	148	95.5	143	97.3	145	100.0	130	100.0	719	97.3	3.706	<0.001
Nitrofurantoin	102	63.0	96	61.9	89	60.5	127	87.6	105	80.8	519	70.2	5.088	<0.001
High concentration of Gentamicin	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	/	/
Linezolid	2	1.2	0	0.0	0	0.0	2	1.4	0	0.0	4	0.5	/	/
Levofloxacin	148	91.4	141	91.0	142	96.6	142	97.9	125	96.2	698	94.5	2.844	0.004
Minocycline	58	35.8	51	32.9	27	18.4	45	31.0	58	44.6	239	32.3	1.002	0.316
Penicillin	156	96.3	148	95.5	144	98.0	144	99.3	126	96.9	718	97.2	1.243	0.214
Tetracycline	65	40.1	50	32.3	39	26.5	63	43.4	75	57.7	292	39.5	3.329	0.001
Teicoplanin	0	0.0	1	0.6	0	0.0	0	0.0	1	0.8	2	0.3	/	/
Tigecycline	0	0.0	0	0.0	0	0.0	0	0.0	1	0.8	1	0.1	/	/
Vancomycin	0	0.0	1	0.6	0	0.0	0	0.0	1	0.8	2	0.3	/	/

Notes: The specific concentrations tested for each antibiotic are defined by the manufacturer's panel configuration (for automated systems) or standard disk content (for Kirby-Bauer), in full compliance with the referenced Clinical and Laboratory Standards Institute (CLSI) guidelines. "/" represents not applicable.

Table 8 Resistance of *Candida albicans* to Common Antifungal Agents

Antifungal Agents	2020 (n = 33)		2021 (n = 95)		2022 (n = 100)		2023 (n = 87)		2024 (n = 84)		2020–2024 (n = 399)		*Z*	*P*
	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)		
Amphotericin B	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	/	/
Flucytosine	0	0.0	0	0.0	1	1.0	0	0.0	2	2.4	3	0.8	/	/
Fluconazole	11	33.3	29	30.5	8	8.0	5	5.7	5	6.0	58	14.5	−5.616	<0.001
Itraconazole	9	27.3	27	28.4	7	7.0	2	2.3	3	3.6	48	12.0	−5.919	<0.001
Voriconazole	16	48.5	29	30.5	8	8.0	4	4.6	6	7.1	63	15.8	−6.541	<0.001

Notes: The specific concentrations tested for each antifungal agent are defined by the manufacturer of ATB FUNGUS 3 kit in full compliance with the referenced Clinical and Laboratory Standards Institute (CLSI) guidelines. "/" represents not applicable.

0.001), itraconazole (from 28.4% to 2.3%, $Z = -5.919$, $P < 0.001$), and voriconazole (from 48.5% to 4.6%, $Z = -6.541$, $P < 0.001$). These trends suggested improved antifungal stewardship and possibly more appropriate triazole usage in recent years.

Resistance of *Candida tropicalis* to Common Antifungal Agents

In contrast, *Candida tropicalis* exhibited persistently higher resistance to azole antifungals (Table 9). Amphotericin B and flucytosine remained effective. Fluconazole resistance remained high (44.9% overall) and did not exhibit a statistically significant temporal trend over the study period ($Z = -1.401$, $P = 0.161$). Itraconazole resistance averaged 34.0% with fluctuations ($Z = -0.536$, $P = 0.592$). A non-significant numerical decrease in voriconazole resistance was observed ($Z = -1.110$, $P = 0.267$).

Table 9 Resistance of *Candida tropicalis* to Common Antifungal Agents

Antifungal Agents	2020 (n = 14)		2021 (n = 33)		2022 (n = 33)		2023 (n = 38)		2024 (n = 29)		2020–2024 (n = 147)		*Z*	*P*
	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)	n	R (%)		
Amphotericin B	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	0	0.0	/	/
Flucytosine	0	0.0	0	0.0	0	0.0	1	2.6	0	0.0	1	0.7	/	/
Fluconazole	8	57.1	13	39.4	20	60.6	16	42.1	9	31.0	66	44.9	−1.401	0.161
Itraconazole	5	35.7	11	33.3	15	45.5	9	23.7	10	34.5	50	34.0	−0.536	0.592
Voriconazole	7	50.0	14	42.4	18	54.5	17	44.7	9	31.0	65	44.2	−1.110	0.267

Notes: The specific concentrations tested for each antifungal agent are defined by the manufacturer of ATB FUNGUS 3 kit in full compliance with the referenced Clinical and Laboratory Standards Institute (CLSI) guidelines. "/" represents not applicable.

Discussion

UTIs represent a major clinical and public health challenge due to their high incidence, recurrence rate, and the growing threat of antimicrobial resistance.[20,21] Empirical treatment of UTIs requires a thorough understanding of local pathogen epidemiology and resistance data.[22] Our study provides a detailed five-year analysis of uropathogen distribution and evolving resistance patterns in a tertiary hospital with six campuses in Suzhou, China, revealing several notable trends with direct clinical implications.

The study found that female patients accounted for 60.1% of cases, significantly outnumbering males (39.9%). This finding was consistent with the observations of Herbawi A et al, who reported a higher proportion of UTIs in females (59.1%) compared to males (40.9%).[23] In Romania, the proportion of UTIs in females was 73%, considerably higher than that of males (27%).[24] Numerous factors, including female anatomical and physiological characteristics, menopause, pregnancy, and pelvic organ prolapse, contribute to their higher risk of UTIs.[25] Previous studies have indicated that the incidence of UTIs increases with patient age.[26] The majority of cases occurred in individuals aged >65 years (64.3%), a finding aligned with other studies and likely reflecting age-associated factors such as comorbidities, urinary incontinence, catheter use, prolonged antimicrobial exposure, and declined immune function.[27,28] However, the proportion of pediatric cases (<15 years) declined significantly across the study period ($Z = -7.925$, $P < 0.001$). This trend could be attributed to improvements in community hygiene education, early intervention for congenital urological anomalies, and reduced unnecessary antimicrobial use in pediatric settings. Such targeted interventions highlighted the potential impact of public health strategies on reducing UTI burden in vulnerable pediatric populations, a point that warranted further prospective evaluation.

Escherichia coli (33.3%) was the predominant uropathogen in this study, confirming its leading role in both community and healthcare settings worldwide.[29] Its remarkable adaptability in the urinary tract environment is facilitated by various virulence factors, including adhesins, toxins, and iron acquisition systems.[30] *Enterococcus faecalis* was the second most frequently isolated bacterial pathogen, followed by *Klebsiella pneumoniae, Enterococcus faecium, Pseudomonas aeruginosa*, and *Candida albicans*. However, some studies have ranked *Klebsiella pneumoniae* as the second most common uropathogen.[31] A survey in India reported that *Escherichia coli* accounted for 39.7% of isolates, while *Klebsiella pneumoniae* constituted 20.7%.[32] This discrepancy might stem from differences in patient demographics and local antimicrobial use policies. Nevertheless, the most prevalent uropathogens remain consistent, albeit with regional variations in their rankings.

In this study, *Escherichia coli* exhibited high resistance rates to several commonly used antibiotics. Resistance to first- and second-generation cephalosporins and sulfamethoxazole/trimethoprim reached 40–50%, while resistance to ampicillin, ciprofloxacin, and levofloxacin was as high as 60–76%. These resistance rates significantly compromise the effectiveness of empirical therapeutic regimens. Similar findings were reported by Niu X et al, who noted resistance rates exceeding 50% to ampicillin and quinolones in *Escherichia coli*.[33] This trend, consistent with observations in other countries,[34] was primarily driven by plasmid-mediated quinolone resistance (PMQR) genes and chromosomal mutations in target enzymes.[35] Notably, we observed a significant decline in *Escherichia coli* resistance to third-generation

cephalosporins (ceftazidime: 22.5% to 14.4%, $P = 0.001$; cefotaxime: 50.4% to 38.8%, $P = 0.001$) over the study period. This reduction correlates with the implementation of our hospital's antimicrobial stewardship program (ASP), which restricted the empirical use of third-generation cephalosporins for uncomplicated UTIs and mandated pre-prescription culture testing for complicated cases. The ASP also promoted the use of narrow-spectrum agents, which likely reduced selection pressure on cephalosporin-resistant strains. In contrast, *Escherichia coli* demonstrated low resistance to aminoglycosides (amikacin, 1.9%) and β-lactam/β-lactamase inhibitor combinations (piperacillin/tazobactam, 3.7%; cefoperazone/sulbactam, 3.9%), providing valuable options for targeted therapy. The low resistance to aminoglycosides and β-lactam/β-lactamase inhibitors was comparable to the reports by Siriphap A et al.[36] However, a study from Malawi reported a resistance rate of 88.1% to sulfamethoxazole/trimethoprim in *Escherichia coli*, indicating considerable regional and national variation in antibiotic resistance patterns.[37] Furthermore, carbapenems (imipenem, 1.2%; meropenem, 1.0%) maintained excellent and consistent activity against *Escherichia coli* isolates throughout the study period, a finding largely consistent with Bayaba S et al.[38] This sustained susceptibility made carbapenems reliable alternatives for treating multidrug-resistant *Escherichia coli* infections. However, the use of carbapenems should remain restricted to confirmed MDR infections to prevent resistance emergence.

The resistance profile of *Klebsiella pneumoniae* was particularly concerning. The high and fluctuating resistance to cephalosporins, fluoroquinolones, and especially carbapenems (peaking at 40.6% in 2023) drastically limited treatment options. Maraki S et al reported high resistance rates in *Klebsiella pneumoniae* to ciprofloxacin (47.8%), amoxicillin/clavulanic acid (34.2%), and sulfamethoxazole-trimethoprim (42.8%).[31] Another study indicated resistance rates of 4% to amikacin, 21% to meropenem, and 36% to cefuroxime axetil.[39] The disparities in resistance rates among uropathogenic bacteria across these studies may be attributed to various factors, such as differences in study populations and geographic regions. The most striking finding was the sharp increase in carbapenem resistance in *Klebsiella pneumoniae*, rising from 20.2% in 2020 to 40.6% in 2023 before declining to 22.1% in 2024. While the precise cause remained to be fully elucidated, this peak was highly suggestive of a localized clonal outbreak within our hospital network, potentially exacerbated by high antimicrobial selection pressure. The subsequent decline in 2024 likely reflected the effectiveness of intensified infection control measures, including enhanced hand hygiene monitoring, contact precautions for CRKP-positive patients, and environmental decontamination of high-touch surfaces in urology and geriatric wards. This trend underscored the volatile and rapidly evolving nature of carbapenem resistance and the critical need for real-time surveillance to trigger immediate intervention strategies.[40] For empirical therapy, this trend also implied that carbapenems should no longer be considered first-line agents for Klebsiella pneumoniae UTIs in our region, especially in high-risk settings. Instead, newer β-lactam/β-lactamase inhibitor combinations (eg, ceftazidime/avibactam) or polymyxins might be more appropriate, though their use requires careful consideration of local susceptibility data.

ESBL-producing Enterobacteriaceae often exhibit cross-resistance to multiple antibiotics, severely limiting treatment options.[41] From 2020 to 2024, the rate of MDR in ESBL-positive *Escherichia coli* declined (from 50.4% to 38.8%), while the proportion of ESBL-positive *Klebsiella pneumoniae* fluctuated (peaking at 55.4% in 2022). This regional variation likely reflects differences in antimicrobial use intensity. The five-year ESBL-positive detection rate was similar to previous findings.[42] However, the Yartey SN reported a lower ESBL-positive rate (16.8%).[43] The high proportions of ESBL-producing strains among *Escherichia coli* (42.6%) and *Klebsiella pneumoniae* (46.0%) isolates meant that first-line use of cephalosporins was no longer justified; instead, β-lactam/β-lactamase inhibitor combinations (eg, piperacillin/tazobactam) should be prioritized, especially in patients with risk factors for ESBL infection. Fluctuations in the annual prevalence of ESBL-producing strains suggested complex dynamics involving clonal dissemination, infection control measures, and antibiotic selective pressure.

Carbapenems are often used as first-line drugs for infections caused by MDR bacteria such as *Klebsiella pneumoniae*.[44] The molecular mechanisms typically involve the production of carbapenemases, such as *Klebsiella pneumoniae* carbapenemases (KPC) and new delhi metallo-β-lactamase (NDM), along with porin mutations and efflux pump overexpression.[45] In this study, the resistance rate to imipenem in *Klebsiella pneumoniae* rose from 20.2% in 2020 to a peak of 40.6% in 2023, representing one of the most significant threats to effective UTI treatment in this region. This trend necessitated a critical re-evaluation of empirical carbapenem use for severe UTIs in our hospital, using them in combination with rapid diagnostic tests when CRKP risk was high. This trend also mirrored the spread of CRE, often

facilitated by healthcare transmission.[46] This alarming rise in CRKP might warrant the use of newer β-lactam/β-lactamase inhibitor combinations as preferred empirical choices in high-risk settings.[47] Furthermore, while tracking dominant pathogens is vital, the emergence of rare, MDR organisms, as illustrated by a recent case of *Cedecea lapagei* UTI, reminded us that continuous laboratory vigilance and tailored susceptibility testing remain irreplaceable for optimal patient management, especially among the elderly and immunocompromised.[48]

Enterococcus faecium isolates exhibited extremely high resistance rates to ampicillin (96.5%), penicillin (97.2%), ciprofloxacin (97.3%), and levofloxacin (94.5%), rendering these traditional anti-enterococcal agents largely ineffective. Fluoroquinolones are a critical class of antibiotics, as they have traditionally been highly effective against complicated UTIs.[49] The increasing rate of resistance to these drugs should be a cause for concern. In contrast, *Enterococcus faecalis* demonstrated significantly lower resistance to the aforementioned drugs, underscoring the importance of species identification in guiding appropriate therapy. The difference in resistance patterns between the two enterococcal species reflects their distinct inherent and acquired resistance mechanisms. Conversely, glycopeptides (vancomycin, 0.3%; teicoplanin, 0.3%) as well as agents such as tigecycline (0.1%) and linezolid (0.5%) remained highly active against *Enterococcus faecium*, providing reliable options for severe infections. The absence of high-level aminoglycoside resistance (HLAR) suggests that combination synergistic therapy remains viable. It is noteworthy that linezolid resistance in enterococci is typically associated with mutations in the 23S rRNA gene or acquisition of the transferable *cfr* gene.[50] Although the proportion of linezolid-resistant enterococci was low in this study (*Enterococcus faecalis*, 5.2%; *Enterococcus faecium*, 0.5%), its emergence warranted vigilant monitoring and further investigation through molecular characterization of resistance mechanisms.

Candida albicans was the predominant fungal isolate, consistent with its status as the most common cause of fungal UTIs globally.[51] Antifungal susceptibility analysis revealed a significant declining trend in azole resistance among *Candida albicans* isolates, with fluconazole resistance decreasing from 33.3% to 5.7% over the study period. This encouraging trend coincided with broader institutional efforts in antifungal stewardship and might reflect improved adherence to appropriate dosing regimens. In contrast, *Candida tropicalis* maintained high fluconazole resistance (44.9% overall), emphasizing the need for species-specific testing. Consistent with other reports, the susceptibility to amphotericin B remained nearly universal.[52,53] It is important to note that the smaller sample size for some Candida species may contribute to variation in resistance rates when compared to larger studies. A key limitation of our analysis was the lack of detailed clinical data on prior azole exposure, diabetes mellitus status, or immunosuppressive therapy, which restricted our ability to investigate specific risk factors for azole-resistant candiduria. Future prospective studies incorporating these variables were needed. Collectively, these fluctuating and species-dependent patterns underscore the dynamic nature of antifungal resistance and reinforce the imperative for continuous local surveillance to inform empirical therapy decisions.

Study Limitations

This study has several limitations. First, as a single-center study, its findings may not be fully generalizable to other regions. Second, the retrospective design limited the availability of detailed clinical data (eg, prior antibiotics, catheter use, outcomes) for risk factor analysis and further stratification of the patient population. Third, by including only symptomatic patients with positive urine cultures, the true UTI prevalence, particularly in outpatients or culture-negative cases, may be underestimated. Future multicenter prospective studies should integrate clinical and molecular data to address these limitations and provide more actionable insights for empirical therapy.

Conclusion

Our study highlighted dynamic trends in UTI pathogens and resistance in Suzhou, with key implications for clinical practice. *Escherichia coli*, while predominant, showed high resistance to fluoroquinolones, advising against their empirical first-line use. The fluctuating but high carbapenem resistance in *Klebsiella pneumoniae* necessitated restricting empirical carbapenem use, especially in severe cases. The high rates of ESBL-production in *Escherichia coli* and *Klebsiella pneumoniae*, often associated with MDR profiles, severely limit therapeutic options. Furthermore, species-specific MDR patterns were evident among enterococci, with *Enterococcus faecium* demonstrating extremely high resistance to ampicillin and fluoroquinolones, unlike *Enterococcus faecalis*. The significant decline in ESBL-producing

Escherichia coli and azole resistance in *Candida albicans* reflected successful stewardship. These data, derived from a predominantly female and elderly (> 65 year) patient population, underscored the necessity of continuous local surveillance. The high and evolving MDR rates, particularly of CRKP and *Enterococcus faecium*, highlighted the urgent need for tailored empirical therapy and enhanced antimicrobial stewardship to guide effective UTI management.

Abbreviations

UTIs, Urinary tract infections; ESBL, Extended-spectrum beta-lactamases; CRE, Carbapenem-resistant Enterobacteriaceae; CRKP, Carbapenem-resistant *Klebsiella pneumoniae*; VRE, Vancomycin-resistant *enterococci*; MDR, Multidrug-resistant; MALDI-TOF MS, Matrix-assisted laser desorption/ionization time-of-flight mass spectrometry; AST, Antimicrobial susceptibility testing; CLSI, Clinical and Laboratory Standards Institute; MIC, Minimal inhibitory concentration; HLAR, High-level aminoglycoside resistance; KPC, *Klebsiella pneumoniae* carbapenemases; NDM, New Delhi metallo-β-lactamase; PMQR, Plasmid-mediated quinolone resistance; ASP, Antimicrobial stewardship program.

Ethics Approval

This study was approved by the Ethics Committee of The Affiliated Suzhou Hospital of Nanjing Medical University (Approval No. K-2024-144-K01). As a retrospective analysis, the requirement for obtaining informed consent was exempted by the same ethics committee. De-identified patient data were obtained from the hospital microbiology laboratory, where the bacterial strains were isolated. All procedures were carried out in strict conformity with the principles of the Declaration of Helsinki.

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Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work.

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Disclosure

The authors declare no conflicts of interest in this work.

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