

ANTIMICROBIAL RESISTANCE PATTERNS OF UROPATHOGENS IN A TERTIARY CARE HOSPITAL IN SOUTH INDIA: A CROSS-SECTIONAL STUDY

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ABSTRACT

Background: Urinary tract infections (UTIs) are among the most common bacterial infections worldwide, with increasing antimicrobial resistance (AMR) posing a major therapeutic challenge.

Objectives: To assess the prevalence and antimicrobial resistance patterns of uropathogens isolated from patients in a tertiary care hospital in South India.

Methods: A retrospective cross-sectional record-based study was conducted over a six-month period (January–June 2024) using microbiology laboratory data. A total of 390 urine samples were analyzed. Identification and antimicrobial susceptibility testing (AST) were performed using standard microbiological procedures in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. Only anonymized laboratory records were utilized, and duplicate isolates were excluded. Data were analyzed using WHONET 5.6 and SPSS version 29.

Results: Among 390 samples, 219 (56.2%) showed significant bacterial growth. *Escherichia coli* (45.2%) was the predominant isolate, followed by *Enterococcus faecalis* (18.7%) and *Klebsiella pneumoniae* (11.9%). High resistance was observed to commonly used antibiotics such as ampicillin, ciprofloxacin, and cotrimoxazole. Carbapenems, aminoglycosides, and nitrofurantoin demonstrated comparatively higher effectiveness. Multidrug resistance (MDR) was observed in 53.4% of isolates.

Conclusion: The study provides important phenotypic surveillance data on antimicrobial resistance among uropathogens. The findings support the need for continuous local surveillance and institution-specific antibiogram development to guide empirical therapy, while highlighting the importance of cautious interpretation in the absence of molecular confirmation.

Keywords: Urinary tract infections, antimicrobial resistance, uropathogens, antibiogram, *Escherichia coli*, tertiary care hospital, India

INTRODUCTION

Urinary Tract Infections represent a significant global health concern, with over 150 million individuals affected annually worldwide (Zeng *et al.*, 2022). UTIs are commonly encountered in both community and hospital settings and are among the leading causes of morbidity worldwide (Yang *et al.*, 2022). UTIs contribute to increased hospitalization rates, prolonged hospital stays, repeat visits, and additional laboratory testing all of which inflate treatment costs for both institutions and patients (Patnool *et al.*, 2022; Simmering *et al.*, 2017; Zhu *et al.*, 2024). More importantly, the human toll is devastating. UTIs cause significant physical discomfort, emotional distress, and in severe cases, lead to life-threatening complications such as pyelonephritis and urosepsis (Kaur and Kaur, 2021).

Pathogenic Etiology and Resistance Landscape

Gram-negative bacteria are the primary causative agents of UTIs, with *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* dominating the microbial landscape (Alotaibi *et al.*, 2023). Traditionally, these infections responded well to first-line antibiotics such as trimethoprim-sulfamethoxazole, nitrofurantoin, and fluoroquinolones (Bader *et al.*, 2020). However, over the last decade, resistance rates have escalated alarmingly, driven by indiscriminate antibiotic use and inadequate infection control measures (Alara and Alara, 2024). *E. coli*, the predominant uropathogen, has demonstrated high resistance to fluoroquinolones and cephalosporins, often due to the presence of extended-spectrum beta-lactamases (ESBLs) production based on resistance patterns; however, confirmatory testing was not performed (Matinfar *et al.*, 2021). *K. pneumoniae* and *P. aeruginosa* have been associated with multi-drug resistance (MDR), including resistance to carbapenems, which are often used as last-resort treatments (Karampatakis *et al.*, 2023). Resistance mechanisms include beta-

lactamase production, efflux pumps, alteration of drug-binding sites, and biofilm formation on catheters and uroepithelial surfaces (Syiemlieh, 2020).

Antimicrobial Resistance in Tertiary Care Hospitals

Tertiary care hospitals are uniquely challenged by antimicrobial resistance. These centers manage patients with prolonged illnesses who often receive multiple antibiotic courses, undergo invasive procedures, and require mechanical support all of which increase susceptibility to healthcare-associated infections (HAIs) (Ture *et al.*, 2022). UTIs in these settings are frequently polymicrobial, severe, and recurrent. Prolonged hospital stays further increase exposure to nosocomial pathogens and multidrug-resistant organisms (MDROs) (Gall *et al.*, 2020). Furthermore, such facilities serve as reservoirs for resistant strains, which can spread rapidly across wards and patient populations if infection control practices are lax. The compounded effect of resistance is not only clinical but also public health-related, as resistant strains from hospitals can disseminate into the community, escalating the burden of community-acquired resistance (Theodorakis *et al.*, 2024).

Global and Regional Perspectives on UTI Resistance

Globally, antimicrobial resistance among uropathogens shows significant regional variability. In high-income countries, resistance to ciprofloxacin among *E. coli* isolates from community-acquired UTIs ranges from 10–30% (Isiaka, 2022; Kashaf Hamadani, 2023; Mouanga-Ndzime *et al.*, 2024; Sugianli *et al.*, 2021). However, in low- and middle-income countries, particularly in South Asia, resistance rates are often significantly higher (Gandra *et al.*, 2020). For example, studies in India have shown resistance levels exceeding 70% to common first-line UTI antibiotics (Chooramani *et al.*, 2020). In India, easy over-the-counter access to antibiotics, lack of regulation, and variable prescribing practices have facilitated

the emergence of resistant pathogens. Inadequate diagnostic facilities, especially in rural and semi-urban areas, promote empirical broad-spectrum antibiotic use without microbiological confirmation. These factors make antimicrobial resistance both a medical and socioeconomic crisis.

Role of Antibiotic Stewardship and Surveillance

Antibiotic stewardship programs (ASPs) are structured interventions aimed at optimizing antibiotic prescribing practices. They involve the appropriate selection, dosing, route, and duration of antibiotic therapy based on clinical evidence and local resistance data. ASPs are critical in tertiary care hospitals where the misuse of antibiotics is rampant. Successful stewardship requires timely and accurate microbiological data underscoring the value of routine antibiogram development (Barlam, 2021; Bassetti et al., 2022; Limato, 2023; Rajput, 2023; Zjajo, 2024). However, ASP implementation in resource-limited settings faces multiple hurdles, including lack of trained personnel, limited diagnostic capacity, resistance to behavioral change among clinicians, and inadequate institutional support. Despite these barriers, studies have shown that even modest stewardship interventions, when supported by antibiograms, can reduce inappropriate prescribing, decrease resistance rates, and lower healthcare costs (Divecha et al., 2024; Rolfe et al., 2021). Routine surveillance of resistance patterns is indispensable for the success of ASPs. It provides data for formulating local empirical therapy guidelines, adjusting formulary antibiotics, and tracking the effectiveness of stewardship interventions (Barlam, 2021; Rajput, 2023). Developing hospital-specific antibiograms is the cornerstone of such surveillance efforts. The development of a hospital-specific antibiogram is a vital response to this challenge, enabling evidence-based empirical therapy, reducing reliance on broad-spectrum agents, and enhancing antimicrobial stewardship.

Despite increasing reports on antimicrobial resistance in India, institution-specific antibiogram data remain essential for guiding localized empirical therapy. Therefore, this study was undertaken to evaluate the distribution and antimicrobial resistance patterns of uropathogens in a tertiary care hospital and to develop a cumulative antibiogram to support antimicrobial stewardship practices.

Aim of the study: To investigate the microbiological profile of UTIs and evaluate antimicrobial susceptibility patterns to aid in the formulation of a hospital-specific antibiogram and support targeted antibiotic stewardship.

Objectives of the study

1. To assess the data of UTI patients for the identification of uropathogens
2. To understand the antibiotic resistance / susceptibility patterns of the uropathogens
3. To prepare an antibiogram using WHONET analysis for empirical therapy

Expected outcome of the study

Through this initiative, we aim to enhance patient care, reduce the burden of resistant infections, and build a sustainable framework for antimicrobial surveillance and stewardship.

METHODOLOGY

Study Design and Setting

This was a hospital-based retrospective cross-sectional record-based study conducted over a six-month period (January to June 2024) at a tertiary care teaching hospital in Chennai, South India. The study utilized microbiology laboratory records of urine culture reports from patients suspected of urinary tract infections.

Source of the study

The study utilized microbiology laboratory records of urine culture reports from patients clinically suspected of urinary tract infections. Only anonymized laboratory data were included, and no patient identifiers were accessed during the study.

Study Criteria

Records containing complete information on age, gender, culture results, and antimicrobial susceptibility testing (AST) were included. Records with incomplete data or polymicrobial growth were excluded.

Data Collection

Using a data collection form, variables from the microbiology department during the study period, such as age, sex, urine culture findings, isolated uropathogens, and AST results were collected. In the microbiology department, urine specimens were collected using a sterile wide-mouthed cup and inoculated onto Cysteine-Lactose-Electrolyte-Deficient

(CLED) agar. Gram staining was performed on colonies with a considerable number (10⁵ CFU/ml) before being subcultured on MacConkey (Gram negative) and Blood agar plates (Gram positive) for identification. Cultures were incubated at 37°C for 24 hours. A series of biochemical tests were used to identify Gram-negative isolates (Triple sugar iron agar, Urea agar, Citrate agar, Lysine iron agar, Motility medium, and Indole test) and Gram positive isolates (Catalase, coagulase, bile-esculin hydrolysis, and optochin sensitivity).

Table 1 List of Antimicrobial Drugs Disks used for AST

List of Drugs (Disk Content) used for AST (WHO AWaRe classes wise)		
Access Class	Watch Class	Reserve Class
Penicillin (10 units)	Piperacillin-Tazobactam (100/10 µg)	Linezolid (30 µg)
Ampicillin (10 µg)	Cefuroxime (30 µg)	
Cefazolin (30 µg)	Cefotaxime (30 µg)	
Cephalexin (30 µg)	Cefepime (30 µg)	
Gentamicin (10 µg)	Imipenem (10 µg)	
Amikacin (30 µg)	Meropenem (10 µg)	
Tetracycline (30 µg)	Fosfomycin (200 µg)	
Cotrimoxazole (1.25/23.75 µg)	Vancomycin (30 µg)	
Nitrofurantoin (300 µg)	Teicoplanin (30 µg)	
	Ciprofloxacin (5 µg)	
	Levofloxacin (5 µg)	
	Norfloxacin (10 µg)	

Table 1 shows the list of Antimicrobial discs used for the Antibiotic Susceptibility Testing (AST) by the microbiology Department. The Kirby-Bauer disk-diffusion technique of AS is then used on Muller Hinton agar to test its susceptibility to antimicrobial drugs, which is incubated at 37 degrees Celsius for 18 to 24 hours. The AST findings were analyzed, and MDR isolates were discovered. Multidrug resistance is defined as the in vitro inability to respond to at least one drug from more than two antimicrobial antibiotic classes (Rafailidis and Kofteridis, 2022). The antimicrobial discs were chosen, and AST values were interpreted according to the clinical laboratory standards institute (CLSI) guidelines (Begum et al., 2023).

Microbiological Processing

Urine samples were processed using standard microbiological procedures. Specimens were inoculated on Cysteine-Lactose-Electrolyte-Deficient (CLED) agar and incubated at 37°C for 24 hours. Significant bacteriuria was defined as $\geq 10^5$ CFU/mL. Isolates were identified using standard biochemical tests.

Antimicrobial Susceptibility Testing

AST was performed using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar and interpreted according to CLSI guidelines. Quality control was ensured using standard reference strains such as *Escherichia coli* ATCC 25922 and *Staphylococcus aureus* ATCC 25923.

Definition of Multidrug Resistance

Multidrug resistance (MDR) was defined as resistance to at least one agent in three or more antimicrobial classes.

Antibiogram Construction

The cumulative antibiogram was constructed using WHONET 5.6 software by aggregating susceptibility data over the study period. Only the first isolate per patient was included, and duplicate isolates were excluded to ensure data validity.

Statistical Analysis

Data were analyzed using SPSS version 29 and WHONET 5.6. Categorical variables were expressed as frequencies and percentages. Associations were assessed using the Chi-square test, with a p-value <0.05 considered statistically significant.

RESULTS

Socio-demographic characteristics

A total of 390 clinical samples were collected from patients suspected of urinary tract infections (UTIs). The demographic profile of the study population is

summarized in Table 2. Of these, females accounted for 60.8% (n = 237), while males constituted 39.2% (n = 153). The age group 18–30 years recorded the highest number of cases (34.1%, n = 133), followed by 31–40 years (18.5%) and 51–60 years (16.2%). This pattern reflects the well-documented susceptibility of women in reproductive age to UTIs due to anatomical and hormonal factors. Statistical analysis showed that the standard deviation (SD) among females across age groups was 30.00, and among males, it was 13.61. A Chi-square test revealed no statistically significant difference in gender distribution across age groups ($\chi^2 = 8.15$, $p = 0.320$), suggesting a uniform distribution of clinical presentations between genders in the overall sample.

Table 2 Age and Gender-wise Distribution of Total Clinical Samples (N=390)

Age Group	Female (n)	Male (n)	Total (n)	Percentage
18–30	91	42	133	34.1%
31–40	43	29	72	18.5%
41–50	34	26	60	15.4%
51–60	34	29	63	16.2%
61–70	23	17	40	10.3%
71–80	9	8	17	4.4%
81 & above	3	2	5	1.3%
Total	237	153	390	100%

Chi-square: 8.15, p-value: 0.320

Out of the 390 samples processed, 219 (56.2%) were culture-positive. The gender distribution in culture-positive cases mirrored the overall trend, with 61.6% (n = 135) being female and 38.4% (n = 84) male. The highest number of culture-positive isolates was identified in the 18–30 years age group (32.4%, n = 71), followed by 61–70 years (16.0%) and 41–50 years (16.4%), as shown in Table 3. Interestingly, in the 41–50 years age group, male culture positivity (n = 22) exceeded that of females (n = 14), which may reflect age-related comorbidities or behavioural differences in healthcare-seeking patterns. The SD values for culture-positive female and male cases were 17.67 and 6.69, respectively. Although the Chi-square test did not reach statistical significance ($\chi^2 = 13.64$, $p = 0.059$), the near-threshold p-value suggests a potential trend that warrants further exploration in larger, powered studies.

Table 3 Age and Gender-wise Distribution of Culture-Positive Samples (N=219)

Age Group	Female (n)	Male (n)	Total (n)	Percentage
18–30	53	18	71	32.4%
31–40	28	11	39	17.8%
41–50	14	22	36	16.4%
51–60	12	12	24	11.0%
61–70	23	12	35	16.0%
71–80	4	8	12	5.5%
81 & above	1	1	2	0.9%
Total	135	84	219	100%

Chi-square: 13.64, p-value: 0.059

Distribution of bacterial isolates from Urine

The distribution of 219 culture-positive clinical isolates was analyzed across four major hospital settings: General Medicine (GM), General Surgery (GS), In-Patient wards (IP), and Out-Patient Departments (OPD). The overall burden was predominantly observed in the OPD, which accounted for 67.1% (n = 147) of all isolates, followed by IP (18.7%, n = 41), GM (13.7%, n = 30), and GS (0.5%, n = 1). These distributions were represented in table 4. Among the isolated pathogens, *Escherichia coli* was the most frequently identified uropathogen, constituting 45.2% of the total culture-positive samples. A significant majority of these isolates (n = 77) originated from OPD cases, underscoring its prominence in community-acquired urinary tract infections (UTIs). *Enterococcus faecalis* was the second most common organism (18.7%, n = 41), with notable presence in GM (n = 11), IP (n = 7), and OPD (n = 23), reflecting its relevance in both community and healthcare-associated infections.

Klebsiella pneumoniae (11.9%, n = 26) and *Enterobacter cloacae* (6.8%, n = 15) were also widely distributed, with significant detection in inpatient samples, indicating a likely link to nosocomial origins. *Citrobacter koseri* and *Pseudomonas aeruginosa* were primarily recovered from OPD and IP cases, while less frequent organisms such as *Morganella morganii*, *Proteus mirabilis*, *Serratia marcescens*, and *Staphylococcus aureus* accounted for a smaller proportion of isolates (<5% each). Overall, the data indicate that while the OPD serves as the primary source of clinical isolates, possibly due to higher patient turnover and early-stage infections, the presence of multidrug-resistant organisms in inpatient and general medicine settings highlights the ongoing risk of hospital-acquired infections. These findings emphasize the importance of tailored antimicrobial stewardship efforts across both community and hospital care settings.

Table 4 Distribution of uropathogens Isolated (Ward-wise)

Organism	GM	GS	IP	OP	Total	% Total (N=219)
<i>Acinetobacter baumannii</i>	0	0	1	1	2	0.9%
<i>Citrobacter koseri</i>	1	0	2	7	10	4.6%
<i>Enterobacter cloacae</i>	0	0	2	13	15	6.8%
<i>Enterococcus faecalis</i>	11	0	7	23	41	18.7%
<i>Escherichia coli</i>	8	0	14	77	99	45.2%
<i>Klebsiella pneumoniae</i>	4	0	10	12	26	11.9%
<i>Morganella morganii</i>	0	0	0	2	2	0.9%
<i>Proteus mirabilis</i>	1	0	2	3	6	2.7%
<i>Pseudomonas aeruginosa</i>	2	1	1	5	9	4.1%
<i>Serratia marcescens</i>	1	0	0	0	1	0.5%
<i>Staphylococcus aureus</i>	2	0	2	4	8	3.7%
Total	30	1	41	147	219	100%

GM - General Medicine, GS - General Surgery, IP - In-Patient, OP - Out-Patient Department

Resistance / Susceptibility patterns of clinical isolates of UTI samples

The antimicrobial susceptibility profiles of uropathogens isolated from 219 culture-positive urine samples were analyzed using the WHONET tool. The results revealed high levels of resistance to commonly used antibiotics, with notable variations between Gram-negative and Gram-positive organisms. Among Gram-negative uropathogens, *Escherichia coli* was the most prevalent (n = 99). It exhibited moderate susceptibility to amikacin (98%) and gentamicin (86%), but showed marked resistance to ampicillin (28%), cefuroxime (46%), and ciprofloxacin (51%). Carbapenems remained effective, with susceptibility to imipenem (82%) and meropenem (82%). Resistance to third-generation cephalosporins (e.g., cefotaxime – 52%) and fluoroquinolones was concerning, indicating extended-spectrum beta-lactamase (ESBL) production.

Klebsiella pneumoniae (n = 26) showed lower sensitivity to beta-lactam antibiotics, with only 29% susceptibility to cefotaxime and 27% to ampicillin. However, amikacin (92%) and carbapenems (imipenem – 88%, meropenem – 88%) retained significant activity. *Pseudomonas aeruginosa* (n = 9) was highly susceptible to carbapenems (imipenem – 100%, meropenem – 89%) and amikacin (78%), while exhibiting complete resistance to multiple other antibiotic classes, including fosfomycin and cefalexin. *Proteus mirabilis* demonstrated variable

resistance, with reduced susceptibility to penicillins and fluoroquinolones but relatively better response to cephalosporins and aminoglycosides. Other less prevalent Gram-negative organisms (*Citrobacter koseri*, *Enterobacter cloacae*, *Morganella morganii*) displayed mixed resistance patterns, generally maintaining sensitivity to amikacin and carbapenems but showing intermediate to high resistance against oral cephalosporins and quinolones.

Among Gram-positive isolates, *Enterococcus faecalis* (n = 41) showed notable resistance to tetracycline (89%) and moderate resistance to penicillins and vancomycin (73% and 65%, respectively). However, linezolid (82%) and nitrofurantoin (75%) remained largely effective. *Staphylococcus aureus* (n = 8) was moderately sensitive to linezolid (87%) and nitrofurantoin (67%), but exhibited significant resistance to ciprofloxacin (37%), vancomycin (50%), and other broad-spectrum beta-lactams.

Antibiotic Resistance Patterns of most prevalent uropathogens, *E. coli*

Among the uropathogens isolated, *Escherichia coli* emerged as the most predominant organism, and its resistance profile highlights significant therapeutic challenges. Fig. 1 shows the highest resistance of *E. coli* against cefotaxime (53.3%), followed closely by doxycycline (53.8%), ciprofloxacin (47.5%),

vancomycin (48%), and ampicillin (45.5%) indicating substantial resistance to commonly prescribed first-line and oral agents.

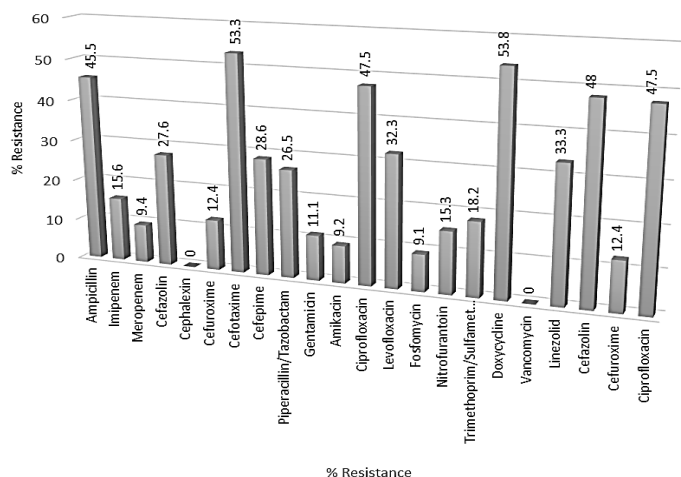


Figure 1 Resistance patterns of highly prevalent uropathogens, *E. coli*

Moderate resistance levels were noted for cefepime (28.6%), cefuroxime (12.4%), levofloxacin (32.3%), and trimethoprim-sulfamethoxazole (18.2%). Notably, carbapenems like imipenem (15.6%) and meropenem (9.4%) maintained relatively low resistance rates, suggesting preserved efficacy. Similarly, amikacin (9.2%) and gentamicin (11.1%) remained effective, indicating that aminoglycosides continue to be viable treatment options for complicated cases. Resistance to nitrofurantoin (15.3%), a common choice for uncomplicated UTIs, was also comparatively low. The high resistance to beta-lactams and fluoroquinolones observed in this study underscores the growing challenge posed by extended-spectrum beta-lactamase (ESBL) producing *E. coli* and supports the need for ongoing surveillance and antibiotic stewardship in both hospital and community settings.

Resistance patterns of second most prevalent isolate, *Enterococcus faecalis*

Enterococcus faecalis was the second most frequently isolated uropathogen in this study, accounting for 18.7% (41/219) of the total culture-positive urine samples. Its resistance pattern revealed a particularly alarming trend, with 88.9% resistance to vancomycin, indicating a significant presence of vancomycin-resistant enterococci (VRE) a major concern in clinical management due to limited therapeutic alternatives. Fig. 2 shows the resistance patterns of *Enterococcus* spp. where moderate resistance was observed to ampicillin (29.3%), cefotaxime (50%), and cefepime (20%), while resistance to aminoglycosides such as gentamicin (7.3%) and amikacin (14.6%) remained comparatively low.

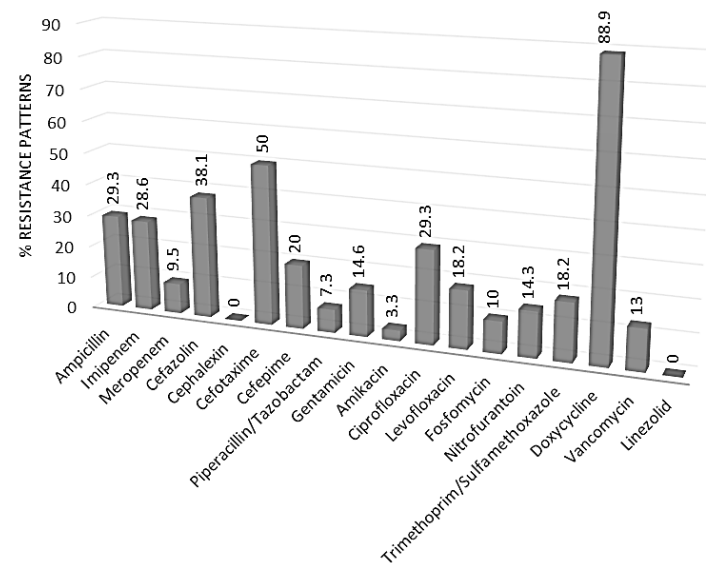


Figure 2 Resistance patterns of *Enterococcus faecalis*

Fluoroquinolone resistance showed a marked difference between ciprofloxacin (3.3%), which retained good efficacy, and levofloxacin (29.3%), which showed reduced sensitivity. Oral treatment options such as nitrofurantoin (10%), trimethoprim/sulfamethoxazole (14.3%), and doxycycline (18.2%) showed moderate susceptibility, indicating potential utility in outpatient care. Crucially, linezolid exhibited 0% resistance, preserving its role as a reliable therapeutic option against multidrug-resistant *Enterococcus* spp. Overall, the resistance profile

of *E. faecalis* underscores the need for routine susceptibility testing and targeted antimicrobial strategies, particularly in healthcare-associated settings where VRE poses a critical threat.

Distribution and Burden of Multidrug-Resistant (MDR) Uropathogens

Multidrug resistance (MDR), defined as non-susceptibility to at least one agent in three or more antimicrobial categories (Rafailidis and Kofteridis, 2022) was observed at a concerning frequency among the 219 uropathogenic isolates in this study. An organism-specific MDR analysis is summarized in Table 5, which highlights both the isolate count and the MDR rate per species. Out of 219 clinical uropathogenic isolates a total of 117 isolates (53.42%) were identified as multidrug-resistant (MDR). The distribution of MDR organisms varied across species and is detailed below (Table 5)

Among the most prevalent isolates, *Escherichia coli* accounted for 99 cases, of which 53 (53.54%) were identified as MDR. Similarly, *Enterococcus faecalis* (n = 41) showed 19 MDR isolates (46.34%), and *Klebsiella pneumoniae* (n = 26) had 17 MDR strains (65.38%), indicating a high level of resistance in common uropathogens. *Enterobacter cloacae* (n = 15) and *Citrobacter koseri* (n = 10) showed MDR rates of 53.33% and 50.00%, respectively. Notably, *Pseudomonas aeruginosa* exhibited a high MDR rate of 66.67% (6 out of 9 isolates), while *Acinetobacter baumannii* and *Serratia marcescens*, though isolated in small numbers (n = 2 and n = 1, respectively), showed MDR in all observed isolates; however, this finding should be interpreted with caution due to the small number of isolates, emphasizing their critical clinical importance despite low occurrence. Other species such as *Proteus mirabilis* (33.33%), *Morganella morganii* (50.00%), and *Staphylococcus aureus* (37.50%) also contributed to the overall MDR burden.

Table 5 Distribution Multidrug-Resistant (MDR) Uropathogens

Organism	Total Isolates (n)	MDR Isolates (n)	MDR (%)
<i>Escherichia coli</i>	99	53	53.5%
<i>Enterococcus faecalis</i>	41	19	46.3%
<i>Klebsiella pneumoniae</i>	26	17	65.4%
<i>Enterobacter cloacae</i>	15	8	53.3%
<i>Citrobacter koseri</i>	10	5	50.0%
<i>Pseudomonas aeruginosa</i>	9	6	66.7%
<i>Proteus mirabilis</i>	6	2	33.3%
<i>Acinetobacter baumannii</i>	2	2	100.0%
<i>Morganella morganii</i>	2	1	50.0%
<i>Serratia marcescens</i>	1	1	100.0%
<i>Staphylococcus aureus</i>	8	3	37.5%
TOTAL	219	117	53.4%

The high proportion of MDR strains, particularly in frequently encountered pathogens like *E. coli* and *K. pneumoniae*, underscores the growing challenge of antimicrobial resistance in urinary tract infections. These findings highlight the urgent need for enhanced antimicrobial stewardship, routine resistance surveillance, and the formulation of targeted empirical treatment protocols to effectively manage MDR infections in clinical practice.

Vancomycin-Resistant Enterococci (VRE)

The emergence of vancomycin-resistant enterococci (VRE), particularly *Enterococcus faecalis*, represents a significant threat in the current antimicrobial landscape. In this study, *E. faecalis* isolates exhibited 88.9% resistance to vancomycin, indicating a high level of phenotypic resistance, which warrants further confirmation through molecular studies, in the community and clinical settings. Vancomycin, traditionally a last-resort agent for Gram-positive infections, appears to be increasingly compromised in its efficacy, which poses serious therapeutic dilemmas, especially in patients with comorbidities or catheter-associated urinary tract infections (CAUTIs). While susceptibility to linezolid remained high (100%), preserving its clinical utility, the resistance to vancomycin combined with moderate resistance to aminopenicillins and cephalosporins significantly narrows the spectrum of effective treatment. The high prevalence of VRE in *E. faecalis* reinforces the need for active surveillance, strict adherence to infection control protocols, and molecular typing to monitor clonal spread, particularly in high-risk wards such as ICUs, nephrology, and post-operative units.

Cumulative Antibiogram Profile of Key Uropathogens

A cumulative antibiogram was constructed for the three most frequently isolated uropathogens *Escherichia coli*, *Enterococcus faecalis*, and *Klebsiella pneumoniae* to assess antimicrobial susceptibility trends and inform empirical therapy. Among Gram-negative isolates, *E. coli* demonstrated high susceptibility to carbapenems (imipenem – 84.4%, meropenem – 90.6%) and aminoglycosides (amikacin – 90.8%, gentamicin – 88.9%). Resistance to beta-lactams such as ampicillin (54.5%) and cefotaxime (46.7%) was substantial, supporting the likely presence of

extended-spectrum beta-lactamase (ESBL)-producing strains. Fluoroquinolone susceptibility was moderate (ciprofloxacin – 52.5%, levofloxacin – 67.7%), while nitrofurantoin (84.7%) and TMP-SMX (81.8%) remained viable options for

uncomplicated UTIs. Fig.3 presents the cumulative antibiogram of uropathogens, which was prepared by incorporating the AST values of clinical isolates in WHONET analysis tool.

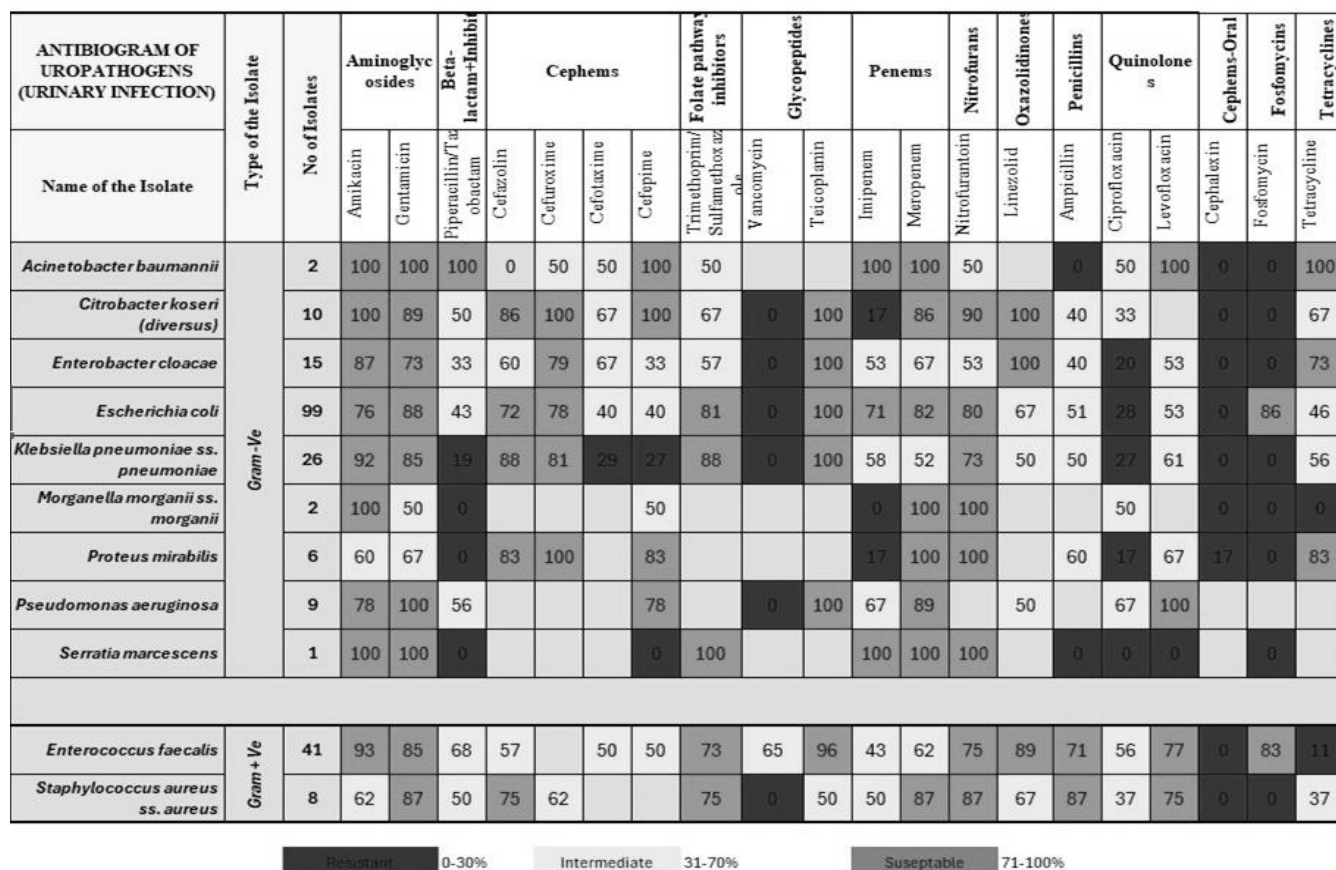


Figure 3 Cumulative Antibiogram of isolated clinical uropathogens

Klebsiella pneumoniae showed a similar profile with notable resistance to ampicillin (10%) and third-generation cephalosporins (cefotaxime – 29%). However, susceptibility to carbapenems (88%), amikacin (92%), and gentamicin (86%) remained encouraging, highlighting their role in treating severe infections. For Gram-positive *Enterococcus faecalis*, linezolid demonstrated complete susceptibility (100%), while gentamicin (92.7%), amikacin (85.4%), and nitrofurantoin (90%) also showed strong activity. Alarming, vancomycin susceptibility was only 11.1%, indicating a high prevalence of vancomycin-resistant enterococci (VRE). Resistance to ampicillin (29.3%) and doxycycline (18.2%) was moderate, whereas fluoroquinolones retained higher efficacy (ciprofloxacin – 96.7%).

This antibiogram underscores the limited utility of conventional oral agents and the continued effectiveness of carbapenems, aminoglycosides, and linezolid. The observed resistance trends support the need for locally tailored empirical treatment protocols, regular antibiogram updates, and strict antibiotic stewardship initiatives.

DISCUSSION

This study analyzed a total of 390 clinical cases, with 219 bacterial isolates identified, aiming to evaluate the distribution and antimicrobial resistance patterns of uropathogens in a tertiary care setting. The findings offer insights into the epidemiological trends, organism prevalence, and growing challenge of antimicrobial resistance (AMR), including multidrug resistance (MDR). The study population was predominantly female (60.8%), a trend consistent with existing literature (Medina & Castillo-Pino, 2019) that highlights a higher incidence of urinary tract infections (UTIs) among females due to anatomical and physiological factors (Medina and Castillo-Pino, 2019). The 18–30 year age group recorded the highest number of cases (34.1%), supporting earlier observations (Foxman, 2014). that sexually active young women are particularly vulnerable to UTIs (Foxman, 2014).

Outpatient departments accounted for the majority of sample contributions (69%), followed by General Medicine (18%) and Inpatients (7%). This reflects the typical clinical presentation of UTIs as non-complicated, community-acquired infections. Similar patterns (Kothari & Sagar, 2008) have been reported in urban hospital settings across India (Kothari and Sagar, 2008). Among the 219 isolates, *Escherichia coli* was the most prevalent pathogen (45.2%), aligning with global data that positions it as the leading cause of community and hospital-acquired UTIs (Flores-Mireles et al., 2015). Other notable pathogens included *Enterococcus*

faecalis (18.7%), *Klebsiella pneumoniae* (11.9%), and *Enterobacter cloacae* (6.8%). Rare organisms like *Acinetobacter baumannii* and *Serratia marcescens* were also identified, reflecting the diversity and potential severity of nosocomial infections.

The WHONET-based resistance analysis revealed a concerning trend of resistance to commonly used antibiotics. *E. coli* demonstrated high resistance to Ampicillin and Ciprofloxacin, yet retained susceptibility to Meropenem (100%), Nitrofurantoin (88%), and Fosfomycin (86%). These findings parallel surveillance data from India and Southeast Asia, where fluoroquinolone and cephalosporin resistance is increasingly common (ICMR, 2023) (Katoch and Swaminathan, 2015). Gram-positive isolates like *Enterococcus faecalis* remained sensitive to Vancomycin and Linezolid but showed reduced response to Ampicillin. These trends call for a more judicious approach to empirical therapy, especially considering that many first-line antibiotics are increasingly ineffective. The resistance patterns observed in this study are consistent with reports from the Indian Council of Medical Research (ICMR-AMRSN) and other regional studies, which have documented high resistance to fluoroquinolones and third-generation cephalosporins among uropathogens.

Among the 219 isolates, 117 (53.42%) were confirmed as MDR, defined by resistance to ≥1 agent in ≥3 antimicrobial categories. *Klebsiella pneumoniae* (65.38%) and *Pseudomonas aeruginosa* (66.67%) had particularly high MDR rates. *E. coli*, though the most common isolate, also showed a significant MDR burden (53.54%). The observed multidrug resistance may be attributed to factors such as prior antibiotic exposure, hospitalization, invasive procedures, and empirical overuse of broad-spectrum antibiotics. Notably, rare pathogens like *Acinetobacter baumannii* and *Serratia marcescens* displayed 100% MDR, raising red flags for nosocomial infection control. These findings are consistent with multicentric studies from Nepal, East Africa, and India reporting MDR rates of 45–75% in UTI pathogens (Subedi et al., 2024; A Maldonado-Barragán, et al., 2023; ICMR-AMRSN, 2023; Katoch and Swaminathan, 2015; Maldonado-Barragán et al., 2024; Subedi et al., 2024).

Out of the 22 antibiotics tested, the majority were from the WHO Access (first-line) and Watch (second-line) categories. Linezolid was the only drug categorized under the Reserve group. This stratification emphasizes the importance of preserving high-tier antibiotics like carbapenems and Linezolid for resistant infections, while promoting rational use of Access group antibiotics to delay resistance onset. This situation mirrors global trends alerting to the restricted utility of traditional oral antibiotics. The high resistance rates likely stem from antibiotic

misuse, unregulated accessibility, and suboptimal infection control, as articulated in the WHO's Global Action Plan on AMR.

Policy and Stewardship Framework

Considering these findings, the following actions are critical:

1. Empirical treatment protocols must prioritize nitrofurantoin or fosfomycin for uncomplicated UTIs, reserving carbapenems, aminoglycosides, and linezolid for complicated or severe cases.
2. Antimicrobial Stewardship Programs (ASP) should be institutionalized, enforcing surveillance, antibiotic restriction policies, and provider education.
3. Strengthened surveillance networks such as adherence to WHO-GLASS standards—are essential for targeted response, especially monitoring VRE and carbapenem-resistant Enterobacterales (CRE).
4. Infection prevention efforts (hand hygiene, catheter care, VRE screening) must span across OPD and IPD domains to curb cross-transmission.

Limitations

This study has several limitations. First, the retrospective design limits the ability to establish causal associations. Second, molecular characterization of resistance mechanisms such as ESBL and VRE was not performed, and findings are based solely on phenotypic susceptibility patterns. Third, some organisms had a small number of isolates, which may limit the generalizability of MDR estimates. Finally, clinical data and patient-level risk factors were not available for analysis.

CONCLUSION

This study provides a comprehensive overview of the epidemiological characteristics, microbial distribution, and antimicrobial resistance patterns of urinary tract infections (UTIs) in a tertiary care setting. The predominance of *Escherichia coli* as the leading uropathogen aligns with global and national trends, affirming its critical role in community and hospital-acquired UTIs. A notable female predominance and higher incidence among the 18–30 age group highlight the demographic vulnerabilities that demand targeted preventive strategies.

The resistance patterns observed in this study are a cause for concern. High levels of resistance to commonly used antibiotics such as ampicillin, ciprofloxacin, and third-generation cephalosporins limit their utility as empirical choices. While carbapenems and nitrofurantoin remain relatively effective, their overuse could accelerate resistance in the near future. The identification of multidrug-resistant (MDR) organisms in over half of the isolates (53.42%) underscores the pressing need for enhanced antimicrobial stewardship, particularly as pathogens like *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, and *Acinetobacter baumannii* showed alarming MDR rates.

This study provides important phenotypic surveillance data on antimicrobial resistance among uropathogens in a tertiary care setting. The high prevalence of resistance to commonly used antibiotics underscores the need for continuous surveillance and institution-specific antibiogram development. These findings should be interpreted within the limitations of phenotypic analysis and retrospective design, and further studies incorporating molecular characterization are recommended.

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Ethical approval: The study was conducted using anonymized microbiology laboratory records without access to patient identifiers. As this was a retrospective record-based study involving minimal risk, the requirement for informed consent was waived in accordance with institutional guidelines. Institutional ethical oversight was obtained in line with standard research practices.

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