



Original Article

Antimicrobial Resistance Pattern Among Patients with Complicated Urinary Tract Infection.

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ABSTRACT

Background: Complicated urinary tract infection (cUTI) is a common cause of hospital admissions and is associated with significant morbidity, particularly in patients with diabetes mellitus, urinary tract abnormalities, catheterization, and other comorbid conditions. The rapid emergence of antimicrobial resistance among uropathogens has limited the effectiveness of commonly used antibiotics, resulting in increased treatment failure, prolonged hospitalization, and healthcare costs. Continuous surveillance of antimicrobial susceptibility patterns is essential for guiding empirical therapy and strengthening antimicrobial stewardship.

Objectives: To determine the antimicrobial resistance pattern among patients with complicated urinary tract infection, identify the predominant uropathogens, and evaluate factors associated with multidrug-resistant infections.

Materials and Methods: A hospital-based cross-sectional observational study was conducted over 18 months in the Department of General Medicine. A total of **120 adult patients** with clinically diagnosed complicated urinary tract infection were enrolled using consecutive sampling. Demographic details, clinical characteristics, urine culture findings, and antimicrobial susceptibility profiles were recorded. Bacterial identification and antimicrobial susceptibility testing were performed according to Clinical and Laboratory Standards Institute (CLSI) guidelines using standard microbiological techniques. Statistical analysis was carried out using SPSS version 26.0. Continuous variables were expressed as mean $\pm$ standard deviation, while categorical variables were expressed as frequencies and percentages. A p-value <0.05 was considered statistically significant.

Results: *Escherichia coli* was the most frequently isolated organism (45.0%), followed by *Klebsiella pneumoniae* (23.3%) and *Pseudomonas aeruginosa* (11.7%). High resistance rates were observed against ampicillin (85.0%), ciprofloxacin (70.0%), and ceftriaxone (65.0%). Meropenem (91.7%), amikacin (81.7%), and nitrofurantoin (76.7%) demonstrated the highest susceptibility. Multidrug-resistant organisms were identified in **46.7%** of isolates and were significantly associated with diabetes mellitus, previous antibiotic exposure, urinary catheterization, recurrent urinary tract infection, chronic kidney disease, and prolonged hospital stay ($p < 0.05$).

Conclusion: Antimicrobial resistance among patients with complicated urinary tract infection is alarmingly high, with multidrug-resistant Gram-negative organisms predominating. Routine urine culture with antimicrobial susceptibility testing, continuous local resistance surveillance, and implementation of antimicrobial stewardship programs are essential for optimizing empirical antibiotic therapy, improving clinical outcomes, and limiting the spread of resistant pathogens.

INTRODUCTION

Urinary tract infection (UTI) is one of the most common bacterial infections encountered in clinical practice and remains a major cause of morbidity and healthcare utilization worldwide. Complicated urinary tract infection (cUTI) refers to infection occurring in the presence of structural or functional abnormalities of the urinary tract, urinary obstruction, indwelling catheters, renal calculi, neurogenic bladder, diabetes mellitus, chronic kidney disease, immunosuppression, or other conditions that increase the risk of treatment failure and recurrent infection. Compared with uncomplicated UTIs, cUTIs is associated with greater clinical severity, prolonged hospitalization, recurrent infections, increased healthcare costs, and a higher risk of progression to pyelonephritis, urosepsis, septic shock, and death. Consequently, prompt diagnosis and appropriate antimicrobial therapy are essential for improving patient outcomes and minimizing complications. (1,2).

The microbial spectrum of complicated urinary tract infections is broader than that of uncomplicated infections because affected patients frequently have repeated healthcare exposure and prior antibiotic use. Although *Escherichia coli* remains the predominant uropathogen, other Gram-negative organisms such as *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Proteus mirabilis*, *Enterobacter* species, and *Acinetobacter* species are increasingly encountered, particularly in hospitalized patients. Gram-positive organisms including *Enterococcus* species also contribute to a significant proportion of infections, especially among catheterized individuals. The distribution of pathogens varies according to geographical region, patient characteristics, healthcare practices, and local antimicrobial prescribing patterns. (3-6)

One of the greatest challenges in the management of complicated urinary tract infections is the rapid emergence of antimicrobial resistance (AMR). Extensive and often inappropriate use of antibiotics has accelerated the development of multidrug-resistant (MDR) organisms, including extended-spectrum β -lactamase (ESBL)-producing Enterobacterales, carbapenem-resistant Enterobacterales (CRE), and resistant *Pseudomonas aeruginosa*. These pathogens substantially reduce available treatment options and are associated with increased treatment failure, prolonged hospitalization, greater healthcare expenditure, and higher mortality. Early studies describing the microbiology of UTIs emphasized the changing spectrum of causative organisms and the growing importance of resistant pathogens in both community and hospital settings. (7,8)

In recent years, antimicrobial resistance has evolved into a major global public health crisis. Comprehensive global analyses have demonstrated that bacterial AMR is responsible for millions of deaths and disability-adjusted life years annually, making it one of the leading infectious causes of mortality worldwide. Resistant urinary pathogens contribute significantly to this burden because UTIs are among the most common bacterial infections requiring antimicrobial therapy. The increasing prevalence of resistant organisms has highlighted the importance of antimicrobial stewardship, surveillance of local susceptibility patterns, and evidence-based empirical antibiotic selection. (9,10)

The selection of empirical antimicrobial therapy for complicated UTIs should therefore be guided by local microbiological epidemiology and antimicrobial susceptibility data rather than relying solely on standard treatment recommendations. Routine urine culture and antimicrobial susceptibility testing remain the cornerstone of appropriate management, enabling clinicians to tailor antibiotic therapy based on the identified pathogen and its resistance profile. Continuous monitoring of institutional antibiograms also assists in updating empirical treatment protocols and reducing unnecessary use of broad-spectrum antibiotics.

In developing countries, including India, the burden of complicated urinary tract infections is increasing because of rising rates of diabetes mellitus, population ageing, frequent urinary catheterization, recurrent hospital admissions, and widespread empirical antibiotic use. Regional variations in antimicrobial susceptibility further emphasize the need for institution-specific surveillance studies. Understanding the antimicrobial resistance patterns of uropathogens and identifying factors associated with multidrug-resistant infections are essential for optimizing treatment strategies and strengthening antimicrobial stewardship programs.

Therefore, the present study was undertaken to determine the antimicrobial resistance pattern among patients with complicated urinary tract infection, identify the predominant bacterial pathogens, and evaluate factors associated with multidrug-resistant infections. The findings are expected to provide valuable local epidemiological data that will support rational empirical antibiotic selection, improve clinical outcomes, and contribute to strategies aimed at limiting the spread of antimicrobial resistance.

MATERIALS AND METHODS

Study Design

A hospital-based cross-sectional observational study was conducted to evaluate the antimicrobial resistance pattern among patients with complicated urinary tract infection and to identify the predominant bacterial pathogens and factors associated with multidrug-resistant infections.

Study Setting

The study was carried out in a tertiary care teaching hospital. Patients were recruited from both outpatient and inpatient services.

Study Duration

The study was conducted over a period of 18 months after obtaining approval from the Institutional Ethics Committee.

Study Population

The study included adult patients clinically diagnosed with complicated urinary tract infection attending or admitted to the Department of General Medicine during the study period.

Sample Size

A total of **120 patients** were enrolled.

The sample size was calculated using the formula:

$$n = Z^2pq/d^2$$

where:

- **Z = 1.96** (95% confidence interval)
- **p = 50%** (expected prevalence of antimicrobial resistance)
- **q = 50%**
- **d = 10%**

The minimum calculated sample size was approximately **96**, which was increased to **120** to improve statistical power and compensate for incomplete microbiological data.

Sampling Technique

Consecutive sampling was used, and all eligible patients fulfilling the inclusion criteria were recruited until the required sample size was achieved.

Inclusion Criteria

- Patients aged **18 years or older**.
- Clinically diagnosed complicated urinary tract infection.
- Positive urine culture with significant bacteriuria.
- Patients willing to provide written informed consent.

Exclusion Criteria

- Patients receiving antibiotics for more than 72 hours before urine culture.
- Contaminated or inadequate urine specimens.
- Asymptomatic bacteriuria.
- Pregnancy.
- Patients unwilling to participate.

Data Collection

Information was collected using a structured case record form including:

- Demographic characteristics.
- Clinical presentation.
- Comorbidities.
- Previous antibiotic exposure.
- Previous hospitalization.
- Catheterization history.
- Recurrent UTI.
- Laboratory findings.
- Urine culture and antimicrobial susceptibility reports.

Sample Collection and Microbiological Processing

Midstream clean-catch urine specimens were collected under aseptic precautions. Catheterized patients provided urine samples through freshly replaced sterile catheters whenever indicated. Samples were transported promptly to the

microbiology laboratory and cultured on **Cysteine Lactose Electrolyte Deficient (CLED)** agar and **MacConkey agar** using calibrated loops.

Bacterial identification was performed using standard microbiological methods including colony morphology, Gram staining, biochemical reactions, and automated identification systems where available.

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed using the **Kirby–Bauer disk diffusion method** according to **Clinical and Laboratory Standards Institute (CLSI)** guidelines. Antibiotics tested included:

- Ampicillin
- Amoxicillin-clavulanate
- Ceftriaxone
- Cefotaxime
- Ceftazidime
- Piperacillin-tazobactam
- Ciprofloxacin
- Levofloxacin
- Gentamicin
- Amikacin
- Nitrofurantoin
- Fosfomycin
- Imipenem
- Meropenem
- Colistin (when indicated)

Extended-spectrum β -lactamase (ESBL) production and carbapenem resistance were identified using CLSI-recommended phenotypic methods.

Outcome Measures

Primary Outcome

- Antimicrobial resistance pattern among bacterial isolates causing complicated urinary tract infection.

Secondary Outcomes

- Distribution of bacterial pathogens.
- Frequency of multidrug-resistant organisms.
- Antibiotic susceptibility profile.
- Risk factors associated with multidrug-resistant infections.

Statistical Analysis

Data was entered into Microsoft Excel and analyzed using **SPSS version 26.0**. Continuous variables were expressed as **mean $\pm$ standard deviation**, while categorical variables were summarized as frequencies and percentages. Independent Student's *t*-test or Mann–Whitney *U* test was used for continuous variables, whereas Chi-square test or Fisher's exact test was used for categorical variables. Variables significant on univariate analysis were entered into multivariable logistic regression to identify independent predictors of multidrug-resistant infection. Odds ratios with **95% confidence intervals** were calculated, and **$p < 0.05$** was considered statistically significant.

RESULTS

A total of **120 patients** with clinically diagnosed complicated urinary tract infection (cUTI) were included in the study. The mean age of the study population was **56.8 $\pm$ 15.2 years**, with ages ranging from 21 to 84 years. Females constituted **68 (56.7%)** of the participants, while **52 (43.3%)** were males. Diabetes mellitus (58.3%), urinary catheterization (32.5%), recurrent UTI (30.0%), and chronic kidney disease (18.3%) were the most common predisposing conditions. Urine culture yielded significant bacterial growth in all patients. Gram-negative bacilli accounted for the majority of isolates, with *Escherichia coli* being the predominant pathogen. High resistance rates were observed against ampicillin, ciprofloxacin, and third-generation cephalosporins, whereas carbapenems, nitrofurantoin, and amikacin retained good antimicrobial activity. Multidrug-resistant (MDR) isolates were detected in nearly half of the patients and were significantly associated with diabetes mellitus, previous antibiotic exposure, urinary catheterization, and recurrent infections.

Table 1. Distribution of bacterial isolates among patients with complicated urinary tract infection (n=120)

Bacterial isolate	Number (%)
<i>Escherichia coli</i>	54 (45.0)
<i>Klebsiella pneumoniae</i>	28 (23.3)
<i>Pseudomonas aeruginosa</i>	14 (11.7)
<i>Proteus mirabilis</i>	8 (6.7)
<i>Enterococcus faecalis</i>	7 (5.8)
<i>Acinetobacter baumannii</i>	5 (4.2)
Others	4 (3.3)
Total	120 (100)

Among the 120 culture-positive cases, *Escherichia coli* was the most frequently isolated pathogen, accounting for **45.0%** of all isolates, followed by *Klebsiella pneumoniae* (**23.3%**) and *Pseudomonas aeruginosa* (**11.7%**). Collectively, Gram-negative organisms constituted over **90%** of isolates, indicating their dominant role in complicated urinary tract infections. Gram-positive organisms were comparatively less common.

Table 2. Antimicrobial susceptibility pattern of predominant Gram-negative isolates

Antibiotic	Sensitive n (%)	Resistant n (%)
Ampicillin	18 (15.0)	102 (85.0)
Ceftriaxone	42 (35.0)	78 (65.0)
Ciprofloxacin	36 (30.0)	84 (70.0)
Piperacillin–Tazobactam	90 (75.0)	30 (25.0)
Gentamicin	78 (65.0)	42 (35.0)
Amikacin	98 (81.7)	22 (18.3)
Nitrofurantoin	92 (76.7)	28 (23.3)
Meropenem	110 (91.7)	10 (8.3)

Resistance to commonly prescribed antibiotics was substantial. Ampicillin demonstrated the highest resistance rate (**85.0%**), followed by ciprofloxacin (**70.0%**) and ceftriaxone (**65.0%**). In contrast, meropenem showed the greatest effectiveness with **91.7%** susceptibility, followed by amikacin (**81.7%**) and nitrofurantoin (**76.7%**). These findings suggest that empirical use of fluoroquinolones and third-generation cephalosporins may be inappropriate in many patients with complicated UTI because of high resistance rates.

Table 3. Association of multidrug-resistant infection with selected clinical risk factors

Variable	MDR Isolates (n=56)	Non-MDR Isolates (n=64)	p value
Diabetes mellitus	40 (71.4%)	30 (46.9%)	0.007
Previous antibiotic use	38 (67.9%)	22 (34.4%)	<0.001
Urinary catheterization	28 (50.0%)	11 (17.2%)	<0.001
Recurrent UTI	24 (42.9%)	12 (18.8%)	0.004
Chronic kidney disease	15 (26.8%)	7 (10.9%)	0.022
Hospital stay >7 days	31 (55.4%)	18 (28.1%)	0.003

Multidrug-resistant organisms were isolated in **56 patients (46.7%)**. Diabetes mellitus was present in **71.4%** of patients with MDR infection compared with **46.9%** in the non-MDR group (**p=0.007**). Previous antibiotic exposure (**67.9% vs. 34.4%; p<0.001**) and urinary catheterization (**50.0% vs. 17.2%; p<0.001**) were strongly associated with MDR infection. Recurrent UTI, chronic kidney disease, and prolonged hospitalization also showed statistically significant associations, indicating that these clinical factors substantially increase the likelihood of resistant bacterial infections.

DISCUSSION

The present study evaluated the antimicrobial resistance pattern among patients with complicated urinary tract infection (cUTI) and demonstrated that Gram-negative bacilli were the predominant causative organisms, with *Escherichia coli* being the most frequently isolated pathogen, followed by *Klebsiella pneumoniae* and *Pseudomonas aeruginosa*. Nearly half of the isolates were multidrug-resistant (MDR), and high resistance rates were observed against ampicillin,

fluoroquinolones, and third-generation cephalosporins. In contrast, carbapenems, amikacin, and nitrofurantoin retained relatively good activity against most isolates. Diabetes mellitus, previous antibiotic exposure, urinary catheterization, recurrent UTI, and prolonged hospitalization were significantly associated with MDR infections, emphasizing the growing challenge of antimicrobial resistance in complicated UTIs.

The increasing burden of antimicrobial resistance highlighted in the present study is consistent with recent global evidence. Murray et al. reported that antimicrobial resistance has become one of the leading causes of infection-related mortality worldwide, contributing to millions of deaths annually. Their analysis emphasized that resistant Gram-negative organisms, particularly Enterobacterales, represent a major public health concern because of limited therapeutic options and increasing healthcare costs. The high prevalence of resistant isolates observed in the present study reflects this global trend and underscores the importance of continuous surveillance of antimicrobial susceptibility patterns (10).

Carbapenem resistance has emerged as another important therapeutic challenge. Pitout et al. described the worldwide dissemination of OXA-48-like carbapenemase-producing Enterobacterales and emphasized their increasing prevalence among healthcare-associated urinary tract infections. Although carbapenem susceptibility remained high in the present study, a small proportion of isolates demonstrated resistance, indicating the early emergence of highly resistant organisms that require close microbiological monitoring and strict infection-control practices (11).

The findings of the present study are also supported by the updated guidance from the Infectious Diseases Society of America (IDSA). Tamma et al. recommended that infections caused by extended-spectrum β -lactamase (ESBL)-producing Enterobacterales and carbapenem-resistant Enterobacterales should be managed using culture-directed therapy whenever possible. They further advised avoiding empirical use of antibiotics associated with high resistance rates and emphasized antimicrobial stewardship to preserve the efficacy of last-line agents. The marked resistance to third-generation cephalosporins and fluoroquinolones observed in our study reinforces these recommendations and highlights the importance of obtaining urine culture before initiating therapy (12).

The clinical impact of resistant urinary pathogens extends beyond individual patient outcomes. Cassini et al. demonstrated that infections caused by antibiotic-resistant bacteria account for a substantial burden of mortality and disability-adjusted life years across Europe. Their findings showed that resistant Gram-negative organisms contribute significantly to prolonged hospitalization and increased healthcare expenditure. Similarly, patients with multidrug-resistant infections in the present study experienced prolonged hospital stay, suggesting that antimicrobial resistance has important clinical and economic consequences (13).

A major strength of the present study was the assessment of multidrug-resistant organisms using standardized microbiological criteria. The definitions proposed by Magiorakos et al. have become the international reference for classifying multidrug-resistant, extensively drug-resistant, and pandrug-resistant bacteria. Applying these standardized definitions improves comparability across studies and facilitates surveillance of resistant pathogens. Nearly half of the bacterial isolates in the present study fulfilled MDR criteria, indicating a substantial burden of resistant organisms in patients with complicated UTI (14).

The predominance of Gram-negative multidrug-resistant pathogens observed in this study agrees with the review by Mazzariol et al., who reported that *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* remain the leading MDR uropathogens worldwide. Their review also highlighted increasing resistance to fluoroquinolones, cephalosporins, and β -lactam antibiotics while demonstrating preserved susceptibility to carbapenems and aminoglycosides in many settings. These observations closely resemble the antimicrobial susceptibility profile identified in the present study (15).

Recent therapeutic trials have demonstrated the importance of newer antimicrobial agents for resistant urinary pathogens. Kaye et al., in the EPIC trial, reported that plazomicin was an effective treatment option for complicated urinary tract infections caused by multidrug-resistant Enterobacterales and was associated with lower relapse rates compared with conventional therapy. Although plazomicin was not evaluated in the present study, the increasing frequency of MDR isolates identified highlights the potential need for newer antibiotics in selected patients with resistant infections (16).

Similarly, Wagenlehner et al. demonstrated that once-daily plazomicin was non-inferior to meropenem in the treatment of complicated urinary tract infections and acute pyelonephritis caused by resistant Gram-negative bacteria. Their findings support the role of newer aminoglycosides as valuable alternatives in carefully selected patients while emphasizing the importance of culture-guided therapy. The high susceptibility of isolates to amikacin observed in the present study further suggests that aminoglycosides continue to retain significant activity against many resistant uropathogens (17).

The growing threat of antimicrobial resistance has also been recognized by the World Health Organization. The 2024 WHO Bacterial Priority Pathogens List identified resistant Enterobacterales, *Pseudomonas aeruginosa*, and *Acinetobacter*

baumannii as pathogens requiring urgent research and development of new antimicrobial agents. The predominance of these organisms in complicated urinary tract infections, as observed in the present study, reinforces the need for robust antimicrobial stewardship, improved infection prevention measures, and continued surveillance at institutional and national levels (18).

The continued emergence of ESBL-producing organisms further complicates empirical antibiotic selection. Paterson and Bonomo emphasized that ESBL-producing Enterobacterales have become one of the most important causes of healthcare-associated infections because they exhibit resistance to multiple β -lactam antibiotics while frequently carrying resistance determinants to several other antimicrobial classes. The high resistance to cephalosporins observed in the present study likely reflects the increasing prevalence of ESBL-producing organisms among hospitalized patients (19).

Current international treatment recommendations also advocate rational antibiotic prescribing based on microbiological evidence. Gupta et al. emphasized that empirical antibiotic therapy should always consider local antimicrobial susceptibility patterns and should be modified promptly once urine culture and susceptibility results become available. Although their guideline primarily addresses acute cystitis and pyelonephritis, its principles of culture-directed therapy and judicious antimicrobial use are equally applicable to complicated urinary tract infections. The findings of the present study strongly support routine urine culture and susceptibility testing before initiation of definitive antimicrobial therapy (20). The present study has certain limitations. It was conducted at a single tertiary care center with a relatively limited sample size of 120 patients, which may affect generalizability. Molecular characterization of resistance mechanisms such as ESBL and carbapenemase genes was not performed. Nevertheless, standardized microbiological methods and CLSI-guided susceptibility testing provide reliable data regarding the prevailing antimicrobial resistance pattern in complicated urinary tract infections.

CONCLUSION

Complicated urinary tract infections are increasingly caused by multidrug-resistant Gram-negative bacteria, with *Escherichia coli* remaining the predominant pathogen. High resistance to fluoroquinolones and third-generation cephalosporins, together with the emergence of carbapenem resistance, presents a significant therapeutic challenge. Diabetes mellitus, previous antibiotic exposure, urinary catheterization, recurrent infections, and prolonged hospitalization were important predictors of multidrug-resistant infection. Continuous surveillance of local resistance patterns, routine urine culture with susceptibility testing, strict antimicrobial stewardship, and evidence-based empirical antibiotic selection are essential to improve clinical outcomes and curb the spread of antimicrobial resistance.

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