

PREVALENCE AND ANTIMICROBIAL RESISTANCE PATTERNS OF UROPATHOGENIC ESCHERICHIA COLI IN COMMUNITY-ACQUIRED URINARY TRACT INFECTIONS: A CROSS SECTIONAL STUDY

Ravi Kiran Koppolu¹, Ketha Venkateswarlu², Srinivas Karri³, V.M. Deepika Rebello⁴

Received : 05/06/2025
Received in revised form : 26/07/2025
Accepted : 14/08/2025

Keywords:

Urinary tract infection, *Escherichia coli*, antimicrobial resistance, multidrug resistance, community-acquired UTI.

Corresponding Author:

Dr. Ravi Kiran Koppolu,

Email: doctorkoppolu@gmail.com

DOI: 10.47009/jamp.2025.7.4.206

Source of Support: Nil,
Conflict of Interest: None declared

Int J Acad Med Pharm
2025; 7 (4); 1077-1081



¹Associate Professor, Department of Microbiology, Nimra Institute of Medical Sciences, Vijayawada, Andhra Pradesh, India.

²Assistant Professor, Department of Microbiology, Nimra Institute of Medical Sciences, Vijayawada, Andhra Pradesh, India.

³Assistant Professor, Department of Microbiology, Nimra Institute of Medical Sciences, Vijayawada, Andhra Pradesh, India.

⁴Postgraduate, Department of Social Preventive Medicine, Asrams Medical college, Eluru, Andhra Pradesh, India.

ABSTRACT

Background: Urinary tract infections (UTIs) are among the most frequent bacterial infections, with *Escherichia coli* being the predominant pathogen. The rise in antimicrobial resistance, particularly among community acquired strains, poses a significant public health concern and necessitates region specific surveillance. **Objectives:** To determine the prevalence of uropathogenic *Escherichia coli* in community acquired urinary tract infections and to analyze its antimicrobial resistance patterns in a tertiary care setting. **Materials and Methods:** This cross-sectional study was conducted in the Department of Microbiology, Nimra Institute of Medical Sciences, Jupudi, Vijayawada, from December 2024 to June 2025. A total of 100 midstream urine samples from clinically suspected community-acquired UTI cases were collected and processed. Culture and antimicrobial susceptibility testing were performed using standard CLSI 2024 guidelines. *E. coli* isolates were screened for multidrug resistance and ESBL production. **Result:** Out of 100 urine samples, 76 showed significant growth. *Escherichia coli* was the most prevalent organism (58/76; 76.3%). High resistance was noted to ampicillin (84.5%), co-trimoxazole (70.7%), and ciprofloxacin (63.8%), while low resistance was observed to imipenem (3.4%), fosfomycin (10.3%), and nitrofurantoin (15.5%). Multidrug resistance was identified in 67.2% of isolates, and 41.4% were ESBL producers. UTIs were more common in females (73%) and the 21–40 years age group (38%). **Conclusion:** The high prevalence of multidrug-resistant *E. coli* in community-acquired UTIs underscores the urgent need for judicious antibiotic use and continuous surveillance to guide empirical therapy effectively.

INTRODUCTION

Urinary tract infections (UTIs) represent one of the most frequently encountered bacterial infections in both community and primary healthcare settings, affecting individuals across all age groups and sexes. Globally, an estimated 150 million people are diagnosed with UTIs each year, with a substantial burden arising from community acquired cases.^[1] Women are disproportionately affected due to anatomical and hormonal factors, with nearly 50–60% expected to experience at least one UTI episode during their lifetime.^[1]

Among the causative agents, *Escherichia coli* (*E. coli*) remains the predominant uropathogen,

responsible for approximately 70–90% of community acquired UTIs.^[2] These uropathogenic *Escherichia coli* (UPEC) strains exhibit specialized virulence mechanisms like adhesins, siderophores, and toxins that facilitate colonization, invasion, and persistence in the urinary epithelium.^[2]

However, the growing challenge of antimicrobial resistance (AMR) among UPEC isolates has emerged as a critical public health threat, particularly in low and middle income countries, where empirical treatment often precedes microbiological confirmation.^[3] Studies from diverse community settings in South Asia and Africa have reported alarmingly high rates of resistance to commonly used antibiotics such as fluoroquinolones, co-trimoxazole,

and beta-lactams.^[3,4] The increasing detection of extended spectrum beta-lactamase (ESBL) producing and multidrug resistant (MDR) *Escherichia coli* strains further complicates treatment protocols, potentially leading to prolonged hospital stays, increased healthcare costs, and a higher risk of complications like pyelonephritis and urosepsis.^[4,5] In this context, periodic surveillance of local antimicrobial resistance patterns is essential to guide empirical therapy, strengthen antimicrobial stewardship, and curb the dissemination of resistant uropathogens. Despite the magnitude of the problem, data from community level studies in various regions of India remain limited, underscoring the need for targeted epidemiological investigations. Therefore, the present study was undertaken to determine the prevalence of uropathogenic *Escherichia coli* in community acquired urinary tract infections and to evaluate its antimicrobial resistance patterns in a defined population. The findings aim to guide rational antibiotic use and support targeted public health interventions.

MATERIALS AND METHODS

Study Design and Setting

This was a cross-sectional observational study conducted in the Department of Microbiology at Nimra Institute of Medical Sciences, Jupudi, Vijayawada, a tertiary care teaching hospital in Andhra Pradesh, India. The study was carried out over a period of seven months, from December 2024 to June 2025.

Study Population

Patients of all age groups and both sexes presenting to the outpatient and inpatient departments with clinically suspected community-acquired urinary tract infections (CA-UTIs) were included in the study. Community-acquired UTI was defined as symptomatic infection without recent hospitalization or urological intervention in the preceding 48 hours.

Inclusion Criteria

Patients presenting with symptoms of UTI (e.g., dysuria, frequency, urgency, suprapubic discomfort, or fever).

Midstream clean catch urine samples yielding significant bacteriuria ($\geq 10^5$ CFU/mL).

Patients not on prior antibiotic therapy for the past 72 hours.

Exclusion Criteria

Hospital acquired or catheter associated urinary tract infections.

Patients with known structural abnormalities of the urinary tract.

Individuals who had taken antibiotics in the previous 72 hours.

Contaminated or inadequately collected urine samples.

Sample Size and Sampling Technique

A total of 100 non duplicate urine samples were collected using consecutive sampling from patients meeting the inclusion criteria during the study period.

Sample Collection and Processing

Midstream urine samples were collected in sterile, wide-mouthed containers following proper patient instruction. Samples were transported to the microbiology laboratory within one hour of collection and processed immediately.

Urine culture was performed by semi-quantitative method using a calibrated loop (0.001 mL) on Cysteine Lactose Electrolyte Deficient (CLED) agar. The plates were incubated at 37°C for 18–24 hours. Colony counts of $\geq 10^5$ CFU/mL were considered significant.

Bacterial Identification and Antimicrobial Susceptibility Testing (AST)

Isolates were identified based on colony morphology, Gram staining, and standard biochemical tests. *Escherichia coli* isolates were further confirmed using conventional and automated identification systems when required.

Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar as per the guidelines of the Clinical and Laboratory Standards Institute (CLSI), 2024 edition. The antibiotics tested included ampicillin, co-trimoxazole, ciprofloxacin, nitrofurantoin, amoxicillin-clavulanate, ceftriaxone, gentamicin, imipenem, and fosfomycin.

Detection of Multidrug Resistance and ESBL Production

Multidrug resistance (MDR) was defined as resistance to three or more classes of antibiotics. ESBL production was screened using the phenotypic confirmatory disc diffusion test employing cefotaxime and cefotaxime-clavulanic acid discs.

Data Analysis

Data were entered and analyzed using Microsoft Excel 2021. Descriptive statistics were expressed as frequencies and percentages. Results were tabulated to show the distribution of isolates and resistance profiles.

Ethical Considerations

The study was approved by the Institutional Ethics Committee of Nimra Institute of Medical Sciences. Informed consent was obtained from all participants or their guardians prior to sample collection. All data were anonymized to ensure confidentiality.

RESULTS

Out of the 100 urine samples collected from patients with suspected community-acquired urinary tract infections (CA-UTIs), 76 samples (76%) yielded significant bacterial growth, whereas 24 samples (24%) showed no growth or were deemed insignificant (Table 1). Among the culture-positive cases, *Escherichia coli* (*E. coli*) was the most prevalent uropathogen, accounting for 58 of the 76 isolates (76.3%). The remaining 18 isolates (23.7%)

comprised other uropathogens, including *Klebsiella pneumoniae*, *Proteus mirabilis*, and *Enterococcus faecalis* (Table 1).

The detailed distribution of bacterial isolates revealed that *Klebsiella pneumoniae* was isolated in 8 cases (10.5%), followed by *Proteus mirabilis* and *Enterococcus faecalis*, each identified in 5 cases (6.6%) (Table 2). This underscores the dominance of *E. coli* as the primary pathogen in community-acquired UTIs.

Antimicrobial susceptibility testing of the 58 *E. coli* isolates demonstrated high resistance to Ampicillin (84.5%), Co-trimoxazole (70.7%), and Ciprofloxacin (63.8%). Moderate resistance was observed to Amoxicillin-clavulanate (55.2%) and Ceftriaxone (50%), while low resistance rates were noted for Nitrofurantoin (15.5%), Fosfomycin (10.3%), and

Imipenem (3.4%) (Table 3). These findings indicate significant resistance to commonly prescribed oral antibiotics.

Further analysis revealed that 67.2% of *E. coli* isolates ($n = 39$) were multidrug-resistant (MDR), defined as resistance to at least three different antimicrobial classes. Additionally, 24 isolates (41.4%) exhibited extended-spectrum beta-lactamase (ESBL) production, further complicating treatment options (Table 4).

In terms of demographic distribution, females constituted the majority (73%) of UTI cases, compared to 27% in males. The highest burden of infection was observed in the 21–40 years age group (38%), highlighting the increased susceptibility in sexually active young adults (Table 4).

Table 1: Culture Positivity and Organism Distribution (N = 100)

Parameter	Number of Cases	Percentage (%)
Total urine samples collected	100	100
Culture-positive cases	76	76.0
No growth / Insignificant growth	24	24.0
<i>E. coli</i> among positive cultures	58	76.3
Non- <i>E. coli</i> isolates (total)	18	23.7

Table 2: Distribution of Uropathogens (n = 76 Positive Cultures)

Isolated Organism	Number of Isolates	Percentage (%)
<i>Escherichia coli</i>	58	76.3
<i>Klebsiella pneumoniae</i>	8	10.5
<i>Proteus mirabilis</i>	5	6.6
<i>Enterococcus faecalis</i>	5	6.6

Table 3: Antimicrobial Resistance Pattern of *E. coli* Isolates (n = 58)

Antibiotic	Resistant Isolates (n)	Resistance Rate (%)
Ampicillin	49	84.5
Co-trimoxazole	41	70.7
Ciprofloxacin	37	63.8
Nitrofurantoin	9	15.5
Amoxicillin-clavulanate	32	55.2
Ceftriaxone	29	50.0
Gentamicin	13	22.4
Imipenem	2	3.4
Fosfomycin	6	10.3

Table 4: Multidrug Resistance and Demographic Profile

Parameter	Number (n)	Percentage (%)
Multidrug-resistant <i>E. coli</i>	39	67.2
ESBL-producing <i>E. coli</i>	24	41.4
Female patients with UTI	73	73.0
Male patients with UTI	27	27.0
Patients aged 21–40 years	38	38.0

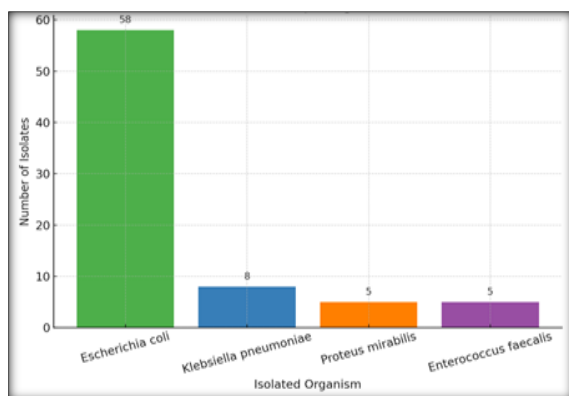


Figure 1: Distribution of Uropathogens

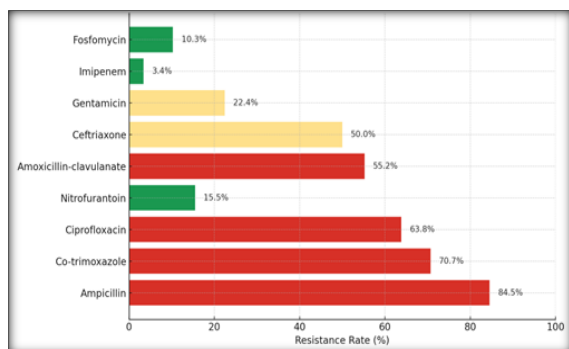


Figure 2: Antimicrobial Resistance Pattern of *E. coli* Isolates

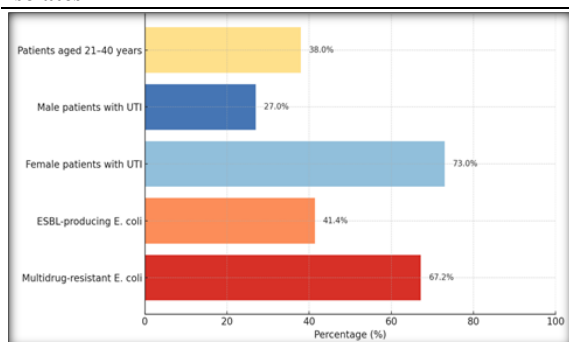


Figure 3: Multidrug Resistance and Demographic Profile

DISCUSSION

This study reaffirms the dominance of *Escherichia coli* as the principal pathogen in community-acquired urinary tract infections (CA-UTIs), with a prevalence of 76.3% among culture-positive isolates. Similar findings have been consistently reported in various global settings, underscoring the conserved virulence and ecological adaptability of uropathogenic *E. coli* (UPEC).^[6,7] UPEC strains possess key virulence determinants, including fimbriae, hemolysins, and iron acquisition systems, enabling efficient colonization of the urinary tract and evasion of host defences.^[7]

Our results highlight a troubling pattern of antimicrobial resistance among *E. coli* isolates, particularly to first-line oral antibiotics such as ampicillin (84.5%), co-trimoxazole (70.7%), and ciprofloxacin (63.8%). These resistance rates are

consistent with those reported in tertiary care centers across Saudi Arabia, East Africa, and Southeast Asia, where similar resistance patterns have emerged due to widespread empirical antibiotic use, self-medication, and unregulated access to antimicrobials.^[8,9] In contrast, resistance to nitrofurantoin (15.5%), fosfomycin (10.3%), and imipenem (3.4%) remains relatively low, suggesting these agents still retain therapeutic value in uncomplicated lower UTIs, as corroborated by findings from The Gambia, Ethiopia, and Korea.^[10,11,12]

The detection of multidrug resistance (MDR) in 67.2% and ESBL production in 41.4% of *E. coli* isolates is alarming. These figures reflect the global emergence of MDR clones and horizontal gene transfer of resistance elements such as beta-lactamases and fluoroquinolone resistance plasmids.^[8,12] Studies from Ethiopia and Bangladesh have similarly shown a high burden of ESBL-producing *E. coli* among outpatients, indicating widespread community dissemination of resistant strains.^[12,13]

The demographic distribution in our study, with a higher proportion of female patients (73%) and peak incidence among the 21–40 years age group, parallels established epidemiological trends. This is attributable to shorter female urethral anatomy and increased sexual activity during reproductive age, as highlighted in previous reports from sub-Saharan Africa and Asia.^[9,11]

These findings underscore the urgent need for localized surveillance programs, adherence to antibiotic stewardship guidelines, and reinforcement of culture-based diagnostic approaches, even in outpatient settings. Empirical therapies must be regularly reviewed and aligned with regional resistance data to prevent treatment failures and reduce the public health burden of AMR.

Limitations of the study include the single center design and limited sample size, which may not fully represent broader community patterns. Moreover, molecular characterization of resistance genes was not performed, which would have strengthened the understanding of underlying mechanisms.

CONCLUSION

This study reaffirms *Escherichia coli* as the predominant pathogen in community-acquired urinary tract infections, accounting for over three-fourths of culture positive cases. The high prevalence of multidrug resistance and ESBL production among isolates highlights a growing challenge in managing these infections using standard empirical therapies. Alarming high resistance to commonly prescribed oral antibiotics such as ampicillin, co-trimoxazole, and ciprofloxacin underscores the urgent need for continuous regional surveillance and evidence based antibiotic stewardship. Retention of sensitivity to agents like nitrofurantoin, fosfomycin, and imipenem

offers hope for effective treatment. Rational prescribing practices and routine culture based diagnosis are essential to mitigate the spread of resistant uropathogens.

REFERENCES

1. Mohapatra S, Panigrahy R, Tak V, J V S, K C S, Chaudhuri S, et al. Prevalence and resistance pattern of uropathogens from community settings of different regions: an experience from India. *Access Microbiol.* 2022 Feb 9;4(2):000321. doi: 10.1099/acmi.0.000321. PMID: 35355869; PMCID: PMC8941965.
2. Niranjana V, Malini A. Antimicrobial resistance pattern in *Escherichia coli* causing urinary tract infection among inpatients. *Indian J Med Res.* 2014 Jun;139(6):945-8. PMID: 25109731; PMCID: PMC4165009.
3. Islam MA, Islam MR, Khan R, Amin MB, Rahman M, Hossain MI, et al. Prevalence, etiology and antibiotic resistance patterns of community-acquired urinary tract infections in Dhaka, Bangladesh. *PLoS One.* 2022 Sep 15;17(9):e0274423. doi: 10.1371/journal.pone.0274423. PMID: 36107878; PMCID: PMC9477272.
4. Carmona-Cartaya Y, Hidalgo-Benito M, Borges-Mateus LM, Pereda-Navales N, González-Molina MK, Quiñones-Pérez D. Community-Acquired Uropathogenic *Escherichia coli*, Antimicrobial Susceptibility, and Extended-Spectrum Beta-Lactamase Detection. *MEDICC Rev.* 2022 May 16;24(2):20-25. doi: 10.37757/mr2022.v24.n2.2. PMID: 35648059.
5. Hamadalneel YB, Ahmed HO, Alamin MF, Almahy WM, Almustafa ZM, Yousif YM, et al. Prevalence and Antimicrobial Sensitivity Patterns of Uropathogens in Wad Medani, Sudan: A Three Years, Cross-Sectional Study. *Infect Drug Resist.* 2024 May 28; 17:2131-2140. doi: 10.2147/IDR.S464501. PMID: 38828377; PMCID: PMC11143980.
6. Ahmed SS, Shariq A, Alsallloom AA, Babikir IH, Alhomoud BN. Uropathogens and their antimicrobial resistance patterns: Relationship with urinary tract infections. *Int J Health Sci (Qassim).* 2019 Mar-Apr;13(2):48-55. PMID: 30983946; PMCID: PMC6436442.
7. Kot B. Antibiotic Resistance Among Uropathogenic *Escherichia coli*. *Pol J Microbiol.* 2019 Dec;68(4):403-415. doi: 10.33073/pjm-2019-048. Epub 2019 Dec 5. PMID: 31880885; PMCID: PMC7260639.
8. Alameer KM, Abuageelah BM, Alharbi RH, Alfaifi MH, Hurissi E, Haddad M, et al. Retrospective Analysis of Antibiotic Resistance Patterns of Uropathogenic *Escherichia coli* with Focus on Extended-Spectrum β -Lactamase at a Tertiary Central Hospital in Saudi Arabia. *Health Sci Rep.* 2025 Jan 23;8(1):e70378. doi: 10.1002/hsr.2.70378. PMID: 39867706; PMCID: PMC11757819.
9. Mlugu EM, Mohamedi JA, Sangeda RZ, Mwambete KD. Prevalence of urinary tract infection and antimicrobial resistance patterns of uropathogens with biofilm forming capacity among outpatients in Morogoro, Tanzania: a cross-sectional study. *BMC Infect Dis.* 2023 Oct 5;23(1):660. doi: 10.1186/s12879-023-08641-x. PMID: 37798713; PMCID: PMC10557311.
10. Kebbeh A, Dsane-Aidoo P, Sanyang K, Darboe SMK, Fofana N, Ameme D, et al. Antibiotics susceptibility patterns of uropathogenic bacteria: a cross-sectional analytic study at Kanifing General Hospital, The Gambia. *BMC Infect Dis.* 2023 Oct 25;23(1):723. doi: 10.1186/s12879-023-08373-y. PMID: 37880663; PMCID: PMC10599079.
11. Lee DS, Lee SJ, Choe HS. Community-Acquired Urinary Tract Infection by *Escherichia coli* in the Era of Antibiotic Resistance. *Biomed Res Int.* 2018 Sep 26; 2018:7656752. doi: 10.1155/2018/7656752. PMID: 30356438; PMCID: PMC6178185.
12. Diriba A, Gizaw S, Alemu F, Tesfaye K, Tesfaye E, Chali M, et al. Prevalence, antimicrobial sensitivity patterns and associated factors of urinary tract infection among patients attending Nekemte Comprehensive Specialized Hospital, Western Ethiopia, 2024: a cross-sectional study. *BMC Infect Dis.* 2025 Apr 7;25(1):474. doi: 10.1186/s12879-025-10788-8. PMID: 40197208; PMCID: PMC11977877.
13. Muhammad A, Khan SN, Ali N, Rehman MU, Ali I. Prevalence and antibiotic susceptibility pattern of uropathogens in outpatients at a tertiary care hospital. *New Microbes New Infect.* 2020 Jun 13; 36:100716. doi: 10.1016/j.nmni.2020.100716. PMID: 32637123; PMCID: PMC7330609.