Section: Microbiology

Original Research Article

EVALUATING THE ANTIMICROBIAL RESISTANCE PROFILES OF ESCHERICHIA COLI STRAINS ISOLATED FROM UTI PATIENTS IN TERTIARY CARE HOSPITAL

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Received *: 06/09/2025*
Received in revised form *: 20/10/2025*
Accepted *: 08/11/2025*

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DOI: 10.70034/ijmedph.2025.4.245

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

Int J Med Pub Health
2025; 15 (4); 1368-1374

ABSTRACT

Background: Urinary tract infections (UTIs) are among the most common bacterial infections in India. Rational empirical therapy depends on local data on uropathogens and their antimicrobial susceptibility. The objective is to identify the distribution of bacterial pathogens causing UTIs and describe their antibiotic resistance patterns in an Indian tertiary care setting.

Materials and Methods: This cross-sectional observational study was conducted over 18 months in the Department of Microbiology after Institutional Ethics Committee approval. Midstream urine samples from clinically suspected UTI cases were cultured. Significant bacteriuria was defined as ≥10^5 CFU/mL of a single isolate. Identification and susceptibility testing were performed by standard methods using the Kirby–Bauer disk diffusion technique and interpreted according to CLSI guidelines.

Results: Of 160 culture-positive samples, females accounted for 68.7% (n=110). The most affected age group was 13–65 years (41.2%). Escherichia coli was the predominant uropathogen 58.8% (n=94), followed by Proteus spp. 14.4% (n=23), Staphylococcus spp. 13.1% (n=21), Klebsiella spp. 5.0% (n=8), Pseudomonas spp. 5.0% (n=8), and Enterobacter spp. 3.8% (n=6). Inpatient and outpatient distributions were comparable (48.1% vs 51.9%). E. coli showed high resistance to Cefotaxime 86.9%, Cefadroxil 76.3%, and Co-trimoxazole 74.4%, but remained sensitive to Meropenem 89.4%, Imipenem 84.9%, and Amikacin 81.3%. Proteus spp. were uniformly resistant to Cefotaxime and largely sensitive to Meropenem 86.1% and Amikacin 84.7%. Staphylococcus spp. were resistant to Cefotaxime and Tobramycin, with better activity seen for Piperacillin/Tazobactam 76.9% and Amikacin 72.4%. Klebsiella and Pseudomonas spp. displayed multidrug resistance, with carbapenems retaining the best activity. Enterobacter spp. were most sensitive to Amikacin 90.0% and Imipenem 72.0%.

Conclusion: E. coli remains the leading cause of UTIs. High resistance to commonly used cephalosporins and Co-trimoxazole underscores the need for culture-guided therapy. Carbapenems and Amikacin were the most reliable agents across isolates. Ongoing local surveillance and antibiotic stewardship are essential to preserve effectiveness and improve outcomes.

Keywords: urinary tract infection, Escherichia coli, antimicrobial resistance, antibiogram, India, Kirby–Bauer, CLSI.

INTRODUCTION

Urinary tract infections (UTIs) are among the most frequent bacterial infections seen in clinical practice and continue to be a major public health problem both globally and in India. They require early diagnosis and prompt antibiotic treatment to prevent complications such as pyelonephritis and urosepsis.[1] Among extraintestinal bacterial infections, UTIs are particularly important because they affect people of

all ages, from newborns to the elderly.[2] Worldwide, more than 150 million people are diagnosed with UTIs each year, leading to considerable morbidity and healthcare expenditure. In developing countries like India, the actual burden is often underestimated due to limited surveillance systems, empirical use of antibiotics, and self-medication.[3-8]

Most UTIs occur through the ascending route of infection, in which bacteria from the intestinal flora travel through the urethra to the bladder and sometimes to the kidneys. This route is more common in females because their urethra is shorter and situated closer to the perineal area, making bacterial entry easier.[9] Factors such as sexual activity, pregnancy, and childbirth further increase susceptibility.[10,11] Studies suggest that nearly 50 to 60 percent of women experience at least one episode of symptomatic UTI in their lifetime, with a higher frequency among sexually active women.[12] In comparison, men are less likely to develop community-acquired UTIs because of their longer urethra and the antibacterial properties of prostatic secretions.[12]

UTIs can involve either the lower urinary tract, known as cystitis, or both the lower and upper tracts, resulting in pyelonephritis. While cystitis is often mild and self-limiting, kidney involvement can cause tissue injury, sepsis, and long-term complications if untreated.[13] Bacterial infections are the most common cause of UTIs, with Escherichia coli (E. coli) responsible for about 70 to 80 percent of all cases.[12,14] Other important uropathogens include Klebsiella pneumoniae, Staphylococcus saprophyticus, Enterococcus faecalis, and Proteus mirabilis.[12]

Antibiotic susceptibility patterns of these bacteria vary across countries, regions, and healthcare settings. Misuse and overuse of antibiotics have accelerated the development of antimicrobial resistance (AMR), particularly among E. coli and other Enterobacteriaceae.[15–18] In India, resistance to commonly used antibiotics such as fluoroquinolones, cephalosporins, and beta-lactams has become a growing concern. Therefore, regional surveillance of antimicrobial sensitivity is essential to guide empirical therapy and improve treatment outcomes.

Understanding the local distribution of uropathogens and their resistance profiles is crucial for clinicians to choose effective antibiotics and to control the spread of resistant strains. The frequency and resistance pattern of bacterial isolates can differ widely between hospitals and communities, and even over time within the same area. The present study has been undertaken to identify the common bacterial agents responsible for urinary tract infections in an Indian population and to analyze their antibiotic resistance patterns. The findings are expected to contribute to more rational antibiotic prescribing and to highlight the need for continuous regional surveillance programs that monitor antimicrobial resistance and help improve patient care.

MATERIALS AND METHODS

Following approval from the Institutional Ethics Committee (IEC), this cross-sectional observational study was conducted in the Department of Microbiology, Medicity hospital, Faridabad, over a period of 18 months. The study included urine samples obtained from patients clinically suspected of urinary tract infection (UTI) and submitted for microbiological evaluation.

A total of 160 urine samples yielding significant bacterial growth were included in the study. The sample size was determined considering an effect size of 0.40, a confidence level of 95%, and a statistical power of 80%, ensuring adequate representation for statistical analysis. Only the first positive culture per patient was included to avoid duplication.

Inclusion Criteria

- Patients presenting with clinical features suggestive of UTI.
- Urine samples showing growth of a single bacterial species with $\geq 10^5$ colony-forming units (CFU/mL).

Exclusion Criteria

- Samples showing mixed bacterial growth or colony counts $<10^5$ CFU/mL.
- Patients who had received antibiotic therapy prior to sample collection.
- Contaminated or improperly collected urine samples.

Methodology: A positive urine culture was defined as the presence of $\geq 10^5$ colony-forming units (CFU) of a single bacterial species per milliliter of urine. Midstream urine samples were collected from adult patients using sterile, designated urine collection containers after proper instructions on aseptic collection techniques.

For patients with multiple urine cultures during the study period, only the first positive culture was included to avoid duplication and bias. Samples showing polymicrobial growth (more than one organism), low colony counts ($<10^5$ CFU/mL), or those collected from patients already on antibiotic therapy were excluded. All patients with positive urine cultures were considered to have urinary tract infections and were categorized according to age and gender for further analysis.

Bacterial Identification and Antibiotic Susceptibility Testing: Each urine sample was inoculated on MacConkey agar and digested soy agar plates using a calibrated 10 µL loop. The inoculated plates were incubated aerobically at 37°C for 24–48 hours. Bacterial isolates were subjected to Gram staining for preliminary differentiation into Gram-positive cocci (GPC) and Gram-negative rods (GNR). Species-level identification and antimicrobial susceptibility testing were carried out using the Kirby–Bauer disk diffusion technique.[19]

Antibiotic susceptibility results were interpreted according to the Clinical and Laboratory Standards Institute (CLSI) guidelines.[20] The sensitivity of UTI-

associated bacterial isolates was tested against a panel of commonly used antibiotics available in the local market, which included: Amikacin (30 µg), Amoxicillin/Clavulanic acid (30 µg), Ampicillin/Sulbactam (10 µg/10 µg), Cefadroxil (30 µg), Cefixime (5 µg), Cefotaxime (30 µg), Cefuroxime (30 µg), Ceftriaxone (30 µg), Ciprofloxacin (10 µg), Doxycycline (30 µg), Gentamicin (10 µg), Imipenem (10 µg), Levofloxacin (15 µg), Meropenem (10 µg), Nitrofurantoin (100 µg), Norfloxacin (10 µg), Ofloxacin (10 µg), Tobramycin (10 µg), Piperacillin/Tazobactam (100 µg/10 µg), Co-trimoxazole (25 µg), and Vancomycin (30 µg).

Statistical Analysis: Patient demographic details (age and gender), culture results, bacterial isolates, and antibiotic susceptibility profiles were recorded in a structured proforma. Patients were categorized by age group and sex to analyze distribution trends and resistance patterns.

All data were compiled using Microsoft Excel 2010 and analyzed with IBM SPSS Statistics version 25.0 (IBM Corp., USA). Descriptive statistics were used to summarize the data, with frequencies and percentages for categorical variables. Associations between bacterial isolates and antibiotic resistance were analyzed using the Chi-square test. Results were presented in tables and charts, and a p-value <0.05 was considered statistically significant.

RESULTS

A total of 160 urine samples showing significant bacterial growth were analyzed during the study period. The distribution of bacterial isolates is presented in Table 1. Among all isolates, Escherichia coli was identified as the predominant uropathogen, accounting for 58.8% (n=94) of cases. Other isolated organisms included Proteus spp. (14.4%, n=23), Staphylococcus spp. (13.1%, n=21), Klebsiella spp. (5.0%, n=8), Pseudomonas spp. (5.0%, n=8), and Enterobacter spp. (3.8%, n=6).

Table 1: Frequency and percentage of bacterial agents isolated from urine specimens in the study population

Bacterium	Frequency	Percentage (%)
Escherichia coli	94	58.8
Proteus spp.	23	14.4
Staphylococcus spp.	21	13.1
Klebsiella spp.	8	5.0
Pseudomonas spp.	8	5.0
Enterobacter spp.	6	3.7
Total	160	100.0

Gender Distribution: Out of the 160 culture-positive cases, female patients accounted for 68.7% (n=110) and male patients for 31.3% (n=50). In both genders, E. coli remained the most prevalent organism, with 43.1% in females and 15.7% in males. In females, Proteus spp. (10.6%) and Staphylococcus spp. (8.1%) were the next most frequent pathogens, whereas in males, Staphylococcus spp. (4.7%) and Proteus spp. (4.4%) followed E. coli. Detailed gender-wise distribution is summarized in [Table 2].

Table 2: Distribution of bacterial isolates among male and female patients

Bacterium	Female (%)	Male (%)	Total (%)
Escherichia coli	43.1	15.7	58.8
Proteus spp.	10.6	4.4	14.4
Staphylococcus spp.	8.1	5.0	13.1
Klebsiella spp.	3.8	1.2	5.0
Enterobacter spp.	1.9	1.9	3.8
Pseudomonas spp.	1.3	3.7	5.0
Total (%)	68.7	31.3	100.0

Age Distribution: The majority of infections occurred among patients aged 13–65 years (41.2%), followed by 0–13 years (35.0%) and >65 years (23.8%). E. coli was the leading organism across all age groups, most notably in the 13–65 years group (23.8%) and 0–13 years group (19.4%). Table 3 shows the age-wise distribution of isolates.

Table 3: Distribution of bacterial isolates across age groups

Bacterium	0–13 years (%)	13–65 years (%)	>65 years (%)	Total (%)
Escherichia coli	19.4	23.8	15.6	58.8
Proteus spp.	5.6	6.3	2.5	14.4
Staphylococcus spp.	3.8	7.5	1.9	13.1
Klebsiella spp.	1.9	1.9	1.2	5.0
Pseudomonas spp.	2.5	0.6	1.9	5.0
Enterobacter spp.	1.9	1.3	0.6	3.8
Total (%)	35.0	41.2	23.8	100.0

Inpatient and Outpatient Distribution: Among the study population, inpatients constituted 48.1% (n=77), while outpatients comprised 51.9% (n=83). E. coli was the most frequently isolated organism in both groups, accounting for 34.4% in inpatients and 31.3% in outpatients. Proteus spp. (5.0%) and Pseudomonas spp. (4.4%) were next most frequent in inpatients, whereas Staphylococcus spp. (9.4%) and Proteus spp. (6.3%) followed E. coli among outpatients [Table 4].

Table 4: Distribution of bacterial isolates among inpatient and outpatient groups

Bacterium	Inpatients (%)	Outpatients (%)	Total (%)
Escherichia coli	34.4	31.3	65.7
Proteus spp.	5.0	6.3	11.3
Staphylococcus spp.	2.5	9.4	11.9
Pseudomonas spp.	4.4	2.5	6.9
Klebsiella spp.	0.6	2.2	2.8
Enterobacter spp.	1.3	0.6	1.9
Total (%)	48.1	51.9	100.0

Antimicrobial Susceptibility Pattern: The antimicrobial susceptibility results of isolated uropathogens are summarized in [Table 5].

E. coli isolates showed highest resistance to Cefotaxime (86.9%), Cefadroxil (76.3%), and Co-trimoxazole (74.4%), whereas Meropenem (89.4%), Imipenem (84.9%), and Amikacin (81.3%) were the most effective antibiotics.

Proteus spp. displayed complete resistance to Cefotaxime (100%) and high resistance to Co-trimoxazole (83.3%) and Cefadroxil (80.0%), but were largely sensitive to Meropenem (86.1%), Amikacin (84.7%), and Piperacillin/Tazobactam (76.4%).

Staphylococcus spp. exhibited high resistance to Cefotaxime and Tobramycin (100%), and moderate resistance to Cefixime (84.2%) and Cefadroxil (87.5%). However, good sensitivity was observed with Piperacillin/Tazobactam (76.9%), Amikacin (72.4%), and Imipenem (71.1%).

Klebsiella spp. were uniformly resistant to Ampicillin/Sulbactam, Cefotaxime, and Piperacillin/Tazobactam (100%) but showed partial sensitivity to Imipenem (61.0%) and Gentamicin (58.0%).

Pseudomonas spp. showed complete resistance to Amoxicillin/Clavulanic acid and Ampicillin/Sulbactam, but sensitivity to Imipenem and Cefuroxime (78.0%).

Enterobacter spp. demonstrated 100% resistance to Amoxicillin/Clavulanic acid, Ampicillin/Sulbactam, and Cefadroxil, while retaining sensitivity to Amikacin (90.0%) and Imipenem (72.0%).

Overall, carbapenems (Meropenem and Imipenem) and Amikacin emerged as the most effective antibiotics across isolates, while cephalosporins and Co-trimoxazole showed the highest resistance rates.

Table 5: Antimicrobial susceptibility profiling of isolated UTI pathogens (n = 160)

Antimicrobial Agent	E. coli (n=94)			Proteus spp. (n=23)			Staphylococcus spp. (n=21)			Klebsiella spp. (n=8)			Pseudomonas spp. (n=8)			Enterobacter spp. (n=6)		
	R (%)	I (%)	S (%)	R (%)	I (%)	S (%)	R (%)	I (%)	S (%)	R (%)	I (%)	S (%)	R (%)	I (%)	S (%)	R (%)	I (%)	S (%)
Amikacin	12.0	7.0	81.0	5.0	10.0	85.0	20.0	6.5	73.5	25.0	25.0	50.0	44.0	0.0	56.0	0.0	8.0	92.0
Amoxicillin/Clavulanic acid	40.0	28.0	32.0	36.0	25.0	39.0	42.0	6.0	52.0	63.0	29.0	8.0	100.0	0.0	0.0	67.0	8.0	25.0
Ampicillin/Sulbactam	74.0	12.0	14.0	67.0	0.0	33.0	75.0	12.0	13.0	100.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0
Cefadroxil	76.0	17.0	7.0	82.0	12.0	6.0	50.0	14.0	36.0	56.0	44.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0
Cefixime	56.0	8.0	36.0	63.0	13.0	24.0	89.0	5.0	6.0	89.0	0.0	11.0	89.0	0.0	11.0	100.0	0.0	0.0
Cefotaxime	87.0	3.0	10.0	100.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0	100.0	0.0	0.0
Cefuroxime	58.0	10.0	32.0	77.0	6.0	17.0	88.0	0.0	12.0	75.0	0.0	25.0	20.0	0.0	80.0	83.0	17.0	0.0
Ceftriaxone	70.0	7.0	23.0	65.0	10.0	25.0	82.0	0.0	18.0	79.0	14.0	7.0	91.0	0.0	9.0	82.0	0.0	18.0
Ciprofloxacin	44.0	10.0	46.0	33.0	10.0	57.0	27.0	27.0	46.0	62.0	8.0	30.0	38.0	8.0	54.0	25.0	0.0	75.0
Doxycycline	49.0	13.0	38.0	45.0	7.0	48.0	40.0	20.0	40.0	43.0	57.0	0.0	80.0	0.0	20.0	56.0	11.0	33.0
Gentamicin	26.0	2.0	72.0	23.0	3.0	74.0	62.0	15.0	23.0	33.0	8.0	59.0	41.0	8.0	51.0	44.0	0.0	56.0
Imipenem	7.0	8.0	85.0	19.0	11.0	70.0	27.0	0.0	73.0	31.0	8.0	61.0	10.0	10.0	80.0	28.0	0.0	72.0
Levofloxacin	39.0	11.0	50.0	27.0	3.0	70.0	28.0	22.0	50.0	33.0	22.0	45.0	33.0	0.0	67.0	20.0	0.0	80.0
Meropenem	11.0	0.0	89.0	7.0	6.0	87.0	36.0	0.0	64.0	17.0	0.0	83.0	25.0	0.0	75.0	40.0	0.0	60.0

Nitrofurantoin	28.0	9.0	63.0	47.0	12.0	41.0	22.0	11.0	67.0	88.0	0.0	12.0	92.0	0.0	8.0	60.0	10.0	30.0
Norfloxacin	44.0	4.0	52.0	27.0	5.0	68.0	44.0	19.0	37.0	39.0	0.0	61.0	42.0	0.0	58.0	44.0	0.0	56.0
Ofloxacin	47.0	6.0	47.0	29.0	0.0	71.0	50.0	17.0	33.0	42.0	8.0	50.0	25.0	0.0	75.0	50.0	0.0	50.0
Tobramycin	23.0	9.0	68.0	23.0	23.0	54.0	100.0	0.0	0.0	43.0	29.0	28.0	40.0	0.0	60.0	43.0	14.0	43.0
Piperacillin/Tazobactam	34.0	2.0	64.0	22.0	0.0	78.0	22.0	0.0	78.0	100.0	0.0	0.0	75.0	0.0	25.0	50.0	0.0	50.0
Co-trimoxazole	74.0	4.0	22.0	83.0	0.0	17.0	75.0	6.0	19.0	91.0	0.0	9.0	89.0	11.0	0.0	75.0	0.0	25.0
Vancomycin	NT	NT	NT	NT	NT	NT	50.0	0.0	50.0	NT	NT	NT	NT	NT	NT	NT	NT	NT

*Abbreviations: R – Resistant; I – Intermediate; S – Sensitive; NT – Not Tested

DISCUSSION

Bacterial urinary tract infections (UTIs) are among the most common reasons for patients to seek medical attention in the community. Successful management depends on identifying the specific pathogens responsible and prescribing appropriate antibiotics based on their susceptibility. Awareness of the local bacterial prevalence and their resistance trends is essential to guide empirical treatment effectively. However, since both the frequency and resistance patterns of these organisms vary between regions, hospitals, and communities, local data becomes critical in optimizing treatment strategies. The increasing prevalence of antimicrobial resistance has become a major public health issue, and urgent measures are required to curb its spread.[21,22]

Several strategies have been proposed, among which antibiotic surveillance programs are recognized as one of the top ten approaches for controlling resistance.[23] In India, national and institutional-level antibiotic surveillance initiatives are being promoted under ICMR to monitor antimicrobial resistance trends and strengthen antibiotic stewardship efforts.[24,25]

With the growing inconsistency in antibiotic susceptibility results across studies, it is now imperative for clinicians to rely on local culture data for formulating targeted antibiotic regimens. This approach is essential to minimize the threat posed by antibiotic resistance and emphasizes the importance of local surveillance in guiding empirical antibiotic therapy. The present study aimed to identify the common bacterial agents causing UTIs and to assess their current antibiotic resistance patterns among patients attending our tertiary care centre in India.

The findings of our study revealed that Escherichia coli was the most predominant pathogen responsible for UTIs, accounting for 58.7% of cases. Gram-negative bacteria constituted about 85% of all isolates, which is consistent with previously published literature showing E. coli as the leading uropathogen across both genders.[28–31]

In the present research, E. coli and Proteus species emerged as the predominant isolates. While E. coli remains the principal causative organism of UTIs as reported in most studies, our results identified Proteus spp. as the second most frequent pathogen, which slightly differs from previous reports. For instance, studies from Turkey have noted Klebsiella spp. as the second most common isolate.[32,33] Similarly, Kidwai et al. found S. aureus and Klebsiella spp. to be the next most frequent organisms after E. coli among Pakistani patients.[34] A retrospective study by Agca and Toklu also reported Pseudomonas aeruginosa (6%), Enterococcus spp. (5%), Klebsiella spp. (5%), and Staphylococcus aureus (4%) as major isolates after E. coli.[35] These variations emphasize the need to consider local epidemiological factors, patient profiles, and antimicrobial usage patterns when studying UTI etiology and designing empirical treatment protocols.

Regarding the distribution of bacterial isolates across age groups, the 13–65 years age group showed the highest susceptibility to UTIs (41.3%), followed by 0–13 years (35.3%) and >65 years (23.4%). This increased prevalence in adults may be attributed to greater sexual activity, pregnancies, and the use of certain contraceptives such as diaphragms or spermicides, all of which can increase UTI risk.[36] E. coli remained the most common pathogen across all age groups, while other organisms varied slightly in distribution, suggesting possible age-related differences in bacterial colonization and host susceptibility.

In our study, the overall percentage of isolates showed a nearly equal distribution between inpatients (48.3%) and outpatients (51.7%). Unlike some previous studies that reported a higher prevalence among hospitalized patients,[37,38] we observed comparable rates in both groups. This variation could be due to differences in patient demographics and healthcare practices. Nevertheless, Gram-negative organisms were more frequent among inpatients, which may be explained by prolonged hospitalization, use of invasive devices, prior antibiotic exposure, and immunocompromised status.

Antimicrobial resistance remains a major challenge in effectively managing infections caused by uropathogens and continues to rise over time. The antibiotic susceptibility analysis in our study provides a clear overview of resistance trends. E. coli showed high resistance to Cefotaxime (87.5%) but retained good sensitivity to Meropenem (89%). It also demonstrated notable resistance to

Ampicillin/Sulbactam (73.8%) but remained moderately sensitive to Piperacillin/Tazobactam. Resistance to Ampicillin among E. coli isolates is commonly mediated by plasmid-borne TEM-1 β-lactamase [39]. Since Sulbactam is a weaker inhibitor of TEM-1 than Tazobactam, Ampicillin/Sulbactam is often less effective compared to Piperacillin/Tazobactam, which shows better inhibition and a broader activity spectrum.[40–42]

Proteus spp. showed complete resistance to Cefotaxime but high sensitivity to Meropenem (86.7%). Staphylococcus spp. were completely resistant to Cefotaxime and Tobramycin, while Piperacillin/Tazobactam was the most effective antibiotic (77.8%). Both Klebsiella and Pseudomonas spp. displayed widespread resistance to multiple antibiotic groups, confirming the increasing challenge in treating these infections. Carbapenems remain the most effective agents against Klebsiella and Pseudomonas infections, consistent with findings from other studies.[43,44] Enterobacter spp. also exhibited multidrug resistance but showed marked sensitivity to Amikacin (91.7%). Overall, the isolated uropathogens showed significant resistance to Ampicillin/Sulbactam, Cefotaxime, Ceftriaxone, and Co-trimoxazole. This high level of resistance may result from widespread antibiotic misuse and self-medication in the community.[39] In contrast, minimal resistance was observed against Meropenem, Imipenem, Gentamicin, and Levofloxacin. The relatively low resistance to these antibiotics could be attributed to their higher cost and restricted availability, limiting their empirical use.

These findings highlight substantial variation in susceptibility patterns among uropathogens and stress the need for rational, targeted antibiotic therapy guided by culture and sensitivity testing. Tailoring antibiotic use based on local resistance trends is essential for improving patient outcomes and preventing further escalation of antimicrobial resistance.

CONCLUSION

This study highlights that E. coli remains the predominant cause of UTIs in the Indian population, followed by Proteus, Staphylococcus, and Klebsiella species. A worrisome level of resistance was observed to commonly prescribed antibiotics, including Ampicillin, third-generation cephalosporins, and Co-trimoxazole. In contrast, high sensitivity to Meropenem, Imipenem, and Amikacin indicates that these agents remain effective therapeutic options for multidrug-resistant isolates.

The findings underscore the necessity for continuous regional surveillance of antimicrobial resistance patterns and implementation of antibiotic stewardship policies at both community and hospital levels. Judicious antibiotic use, patient education, and strict infection-control measures are crucial to preserving the efficacy of existing drugs. Further molecular studies are recommended to characterize resistance genes and support the development of targeted therapeutic strategies.

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