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**Original Research Article**

# Bacteriological Profile and Antibacterial Drug Susceptibility Pattern of Microorganisms Causing Urinary Tract Infections (UTIs) in Adult Patients at a Tertiary Care Hospital

**Manashvi Lakhansinh Ravat[1], Mitsu Manharbhai Parsania[2], Anjaniba Sarvaiya[3]**

**[1]Senior Resident, BJ Medical College and Hospital, Ahmedabad, Gujarat, India**
**[2]Senior Resident, GMERS Medical College and Hospital, Morbi, Gujarat, India**
**[3]Senior Resident, GMERS Medical College and Hospital, Sola, Ahmedabad, Gujarat, India**

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**Corresponding author: Dr. Manashvi Lakhansinh Ravat**
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**Abstract**

**Introduction:** Urinary tract infections (UTIs) are among the most common bacterial infections encountered in clinical practice and are associated with significant morbidity and increasing antimicrobial resistance worldwide. The emergence of multidrug-resistant uropathogens has complicated empirical treatment strategies, making continuous surveillance of bacteriological profiles and antibiotic susceptibility patterns essential for effective management.

**Materials and Methods:** This prospective observational study was conducted in the Department of Microbiology at GMERS Medical College and Hospital, Sola, Ahmedabad, from July 2022 to January 2024 after institutional ethics approval. A total of 747 adult patients clinically suspected of UTI were included. Clean-catch midstream urine samples were processed using standard microbiological techniques. Semi-quantitative urine culture, organism identification, and antimicrobial susceptibility testing were performed according to standard biochemical methods and CLSI guidelines using the Kirby–Bauer disk diffusion method.

**Results:** Out of 747 urine samples, 348 (46.59%) were culture positive. Females constituted the majority of positive cases (67.53%), and the highest prevalence was observed in the 18–30 years age group (39.94%). Gram-negative bacilli accounted for 89.37% of isolates, while Candida species and Gram-positive cocci constituted 8.91% and 1.72%, respectively. Escherichia coli was the predominant pathogen isolated in 247 cases (70.98%), followed by Klebsiella pneumoniae in 40 cases (11.50%). Higher culture positivity was observed among inpatient samples (59.45%) compared to outpatient samples (38.38%). Antimicrobial susceptibility testing revealed high resistance to ampicillin, fluoroquinolones, and cephalosporins. E. coli demonstrated maximum resistance to ampicillin (82.5%) but retained good sensitivity to nitrofurantoin with only 8% resistance. ESBL production was observed in approximately 29–32% of isolates, while carbapenem resistance ranged from 25% to 44%. Gram-positive isolates remained sensitive to vancomycin and linezolid.

**Conclusion:** Urinary tract infections were predominantly caused by Gram-negative bacilli, especially Escherichia coli, with high resistance to commonly used antibiotics. Nitrofurantoin and aminoglycosides remained comparatively effective. Regular surveillance and antibiotic susceptibility testing are essential for appropriate management and control of antimicrobial resistance.

**Keywords:** Urinary Tract Infection; Uropathogens; Antimicrobial Resistance; Antibiotic Susceptibility; ESBL; Multidrug Resistance.

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## Introduction

Urinary tract infections (UTIs) remain one of the most frequently encountered bacterial infections in clinical practice, affecting individuals across all age groups and contributing substantially to global morbidity. [1] They involve microbial invasion of any part of the urinary system, ranging from the urethra to the kidneys, and may present with symptoms such as dysuria, frequency, urgency, and fever. UTIs are broadly categorized as community-acquired or healthcare-associated infections, each with distinct microbiological profiles and risk factors. [2] Epidemiological data indicate that UTIs are particularly common in females due to anatomical predisposition, though significant disease burden is also observed in males at extremes of age. [3] The condition not only affects patient quality of life but also imposes a considerable economic burden on healthcare systems. [4] The etiological spectrum of UTIs is dominated by bacterial pathogens, with Gram-negative bacilli accounting for the majority of cases. [5] Among these, Escherichia coli is consistently reported as the principal causative organism, followed by other Enterobacterales such as Klebsiella, Proteus, and Enterobacter species, along with non-fermenters like Pseudomonas aeruginosa. [6] Gram-positive organisms, including Enterococcus and Staphylococcus species, also contribute to a smaller yet clinically significant proportion of infections. [7] The pathogenesis typically involves ascending infection from the periurethral area, facilitated by virulence factors such as adhesins, biofilm formation, and toxin production. [8] Host factors including urinary stasis, catheterization, comorbidities, and immune status further influence susceptibility and disease progression. [9]

In recent years, the management of UTIs has become increasingly challenging due to the rapid emergence and spread of antimicrobial resistance among uropathogens. [10] Indiscriminate use of antibiotics, over-the-counter availability of antimicrobial agents, and incomplete treatment courses have accelerated the development of resistant strains, including extended-spectrum beta-lactamase (ESBL) and carbapenemase-producing organisms. This evolving resistance pattern has reduced the effectiveness of commonly used empirical therapies and necessitates reliance on culture and sensitivity testing for appropriate antibiotic selection. [11]

## Materials and Methods

This prospective observational study was conducted in the Department of Microbiology, Bacteriology Laboratory at GMERS Medical College and Hospital, Sola, Ahmedabad, after obtaining approval from the Institutional Ethics Committee.

The study was carried out over a period of one and a half years, from July 2022 to January 2024. Adult patients attending outpatient departments or admitted to various wards including Medicine, Surgery, Obstetrics and Gynecology, Orthopedics, and Dermatology with clinical features suggestive of urinary tract infection were considered for inclusion. A total of 747 patients aged above 18 years who presented with symptoms such as dysuria, frequency, urgency, fever, lower abdominal pain, or burning micturition and who provided informed consent were included in the study. Patients below 18 years of age, those with indwelling urinary catheters, and cases suspected of healthcare-associated UTIs were excluded. Detailed clinical history, demographic data, and presenting complaints were recorded for all participants prior to sample collection. Clean-catch midstream urine samples were collected in sterile, wide-mouthed, leak-proof containers following proper instructions to the patients. Approximately 5–10 mL of urine was collected and transported promptly to the microbiology laboratory, ensuring processing within two hours of collection. Samples not meeting quality criteria, such as improper labeling, contamination, leakage, or inadequate quantity, were rejected. Each sample was assigned a laboratory identification number for further processing and analysis.

All urine samples underwent macroscopic examination for appearance, turbidity, and color, followed by microscopic examination of centrifuged urine sediment to detect pus cells, red blood cells, epithelial cells, bacteria, and other elements. Gram staining was performed to identify the presence and type of microorganisms. Semi-quantitative culture was carried out using a calibrated loop on Nutrient agar, MacConkey agar, and CLED medium, followed by incubation at 37°C for 18–24 hours. Significant bacteriuria was defined as colony counts $\geq 10^5$ CFU/mL. Isolates were identified based on colony morphology, Gram staining, and standard biochemical tests. [12]

Antimicrobial susceptibility testing of the isolated organisms was performed using the Kirby–Bauer disk diffusion method on Mueller-Hinton agar, in accordance with Clinical and Laboratory Standards Institute (CLSI) guidelines. [13] Zones of inhibition were measured and interpreted as susceptible, intermediate, or resistant. The results were analyzed to determine the bacteriological profile and antimicrobial resistance patterns of uropathogens, which were then used to assess trends and guide appropriate therapeutic strategies.

## Results

In present study, out of 747 urine samples analyzed, 348 (46.59%) were culture positive while 399 (53.41%) showed no growth. Among the positive isolates, the majority were Gram-negative bacilli (89.37%), followed by Candida species (8.91%) and a small proportion of Gram-positive cocci (1.72%).

**Table 1: Culture Positivity and Distribution of Isolates**

| Category | Parameter | Number | Percentage (%) |
|---|---|---|---|
| **Total Samples** | Total urine samples | 747 | 100 |
| **Culture Results** | Culture positive | 348 | 46.59 |
| | Culture negative | 399 | 53.41 |
| **Type of Isolates (n=348)** | Gram-negative bacilli | 311 | 89.37 |
| | Gram-positive cocci | 6 | 1.72 |
| | Candida species | 31 | 8.91 |

A higher proportion of culture positivity was observed in females (67.53%) compared to males (32.47%). The highest number of positive cases was seen in the 18–30 years age group (39.94%), followed by 31–45 years (22.41%), indicating greater prevalence among young adults, particularly females.

**Table 2: Demographic Distribution of Culture Positive Cases (n = 348)**

| Variable | Category | Total Positive n (%) | Male n (%) | Female n (%) |
|---|---|---|---|---|
| **Gender** | Male | 113 (32.47%) | — | — |
| | Female | 235 (67.53%) | — | — |
| **Age Group (years)** | 18–30 | 139 (39.94%) | 28 (20.14%) | 111 (79.86%) |
| | 31–45 | 78 (22.41%) | 18 (23.08%) | 60 (76.92%) |
| | 46–60 | 64 (18.40%) | 34 (53.12%) | 30 (46.88%) |
| | >60 | 67 (19.25%) | 33 (49.25%) | 34 (50.75%) |

Culture positivity was higher in inpatient (ward) samples (59.45%) compared to outpatient samples (38.38%). Department-wise analysis revealed that the highest number of isolates were from Gynecology (39.36%), followed by Medicine (27.29%) and Surgery (26.72%), indicating a greater burden of UTIs in these clinical settings.

**Table 3: Clinical Setting and Department-wise Distribution of Culture Positive Cases**

| Category | Parameter | Total Samples | Positive Cases | Percentage (%) |
|---|---|---|---|---|
| **Clinical Setting** | Wards (IPD) | 291 | 173 | 59.45 |
| | OPD | 456 | 175 | 38.38 |
| **Department-wise Distribution (n=348)** | Medicine | — | 95 | 27.29 |
| | Gynecology | — | 137 | 39.36 |
| | Surgery | — | 93 | 26.72 |
| | TBCD | — | 17 | 4.88 |
| | Orthopedics | — | 6 | 1.72 |

**Table 4: Spectrum of Uropathogens Isolated (n = 348)**

| Category | Organism | Number | Percentage (%) |
|---|---|---|---|
| **Gram Negative Bacilli (n=311)** | E. coli | 247 | 70.98 |
| | Klebsiella pneumoniae | 40 | 11.50 |
| | Pseudomonas aeruginosa | 10 | 2.87 |
| | Klebsiella oxytoca | 7 | 2.03 |
| | Acinetobacter baumannii | 3 | 0.80 |
| | Enterobacter aerogenes | 2 | 0.57 |
| | Proteus spp. | 1 | 0.30 |
| | Enterobacter cloacae | 1 | 0.30 |
| **Other Isolates** | Enterococcus faecalis | 5 | 1.44 |
| | Staphylococcus saprophyticus | 1 | 0.30 |
| | Candida spp. | 31 | 8.91 |

High levels of antimicrobial resistance were observed among uropathogens, particularly against fluoroquinolones and cephalosporins.

E. coli showed maximum resistance to ampicillin (82.5%) but retained good sensitivity to nitrofurantoin (low resistance of 8%). ESBL production was noted in approximately 29–32% of isolates, while carbapenem resistance ranged from 25% to 44%. Non-fermenters demonstrated moderate resistance but remained fully sensitive to colistin.

Gram-positive isolates showed high resistance to penicillin and fluoroquinolones but remained sensitive to vancomycin and linezolid.

**Table 5: Antimicrobial Resistance Pattern and Resistance Mechanisms of Uropathogens**

| Category | Parameter | E. coli (%) | Klebsiella (%) | Enterobacter (%) | Proteus (%) | Pseudomonas (%) | Acinetobacter (%) | Enterococcus (%) |
|---|---|---|---|---|---|---|---|---|
| Antibiotic Resistance | Ampicillin | 82.5 | Intrinsic | Intrinsic | Intrinsic | — | — | — |
| | Ceftriaxone | 66.8 | 70.2 | 66.6 | 100 | — | — | — |
| | Cefepime | 57.8 | 63.8 | 66.6 | 100 | — | — | — |
| | Ciprofloxacin | 72.4 | 80.8 | 66.6 | 0 | 50 | 100 | 100 |
| | Levofloxacin | 65.1 | 63.8 | 66.6 | 0 | — | — | — |
| | Nitrofurantoin | 8 | 65.9 | 66.6 | Intrinsic | — | — | — |
| | Amikacin | 44 | 59.5 | 66.6 | 100 | — | — | — |
| | Gentamicin | 32.3 | 44.6 | 66.6 | 0 | 60 | 33.3 | — |
| | Cotrimoxazole | 57.4 | 53.1 | 66.6 | 100 | — | — | — |
| | Colistin | — | — | — | — | 0 | 0 | — |
| | Penicillin | — | — | — | — | — | — | 80 |
| | Ampicillin (GP) | — | — | — | — | — | — | 20 |
| | Vancomycin | — | — | — | — | — | — | 0 |
| | Linezolid | — | — | — | — | — | — | 0 |

The distribution of uropathogens showed that Escherichia coli was the predominant isolate (70.98%), followed by Klebsiella pneumoniae (11.5%) and Candida species (8.91%). Other organisms such as Pseudomonas, Acinetobacter, and Enterobacter were isolated in smaller proportions. This indicates that Gram-negative bacilli, particularly E. coli, are the major causative agents of urinary tract infections in the study population.

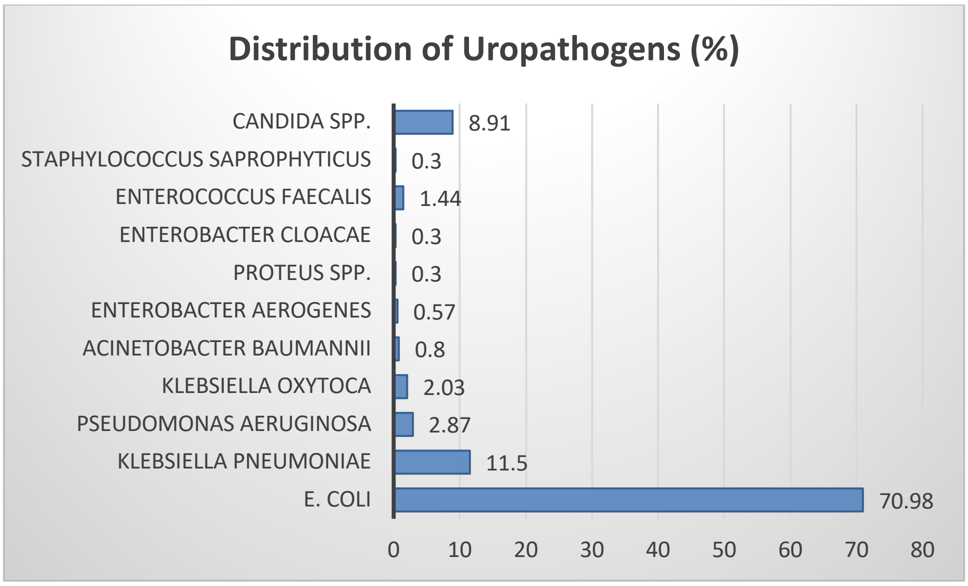


**Figure 1: Distribution of Uropathogens (%)**

**Table 6: Resistance Mechanisms (GNB)**

| Organism | ESBL (%) | AmpC (%) | Imipenem (%) | Meropenem (%) | Ertapenem (%) | CRE (%) |
|---|---|---|---|---|---|---|
| E. coli | 29.15 | 0.81 | 36.8 | 25.5 | 36 | 25.1 |
| Klebsiella spp. | 31.91 | 0.40 | 51 | 46.8 | 57.4 | 44.68 |
| Enterobacter | — | — | 66.6 | 66.6 | 66.6 | 66.66 |

## Discussion

The present study demonstrated a culture positivity rate of 46.59%, indicating a substantial burden of urinary tract infections (UTIs) in our tertiary care setting. This finding is comparable to the prevalence reported by Alebachew et al. [14] (2025) among geriatric patients (44.4%) and by Meena et al. [15] (2021) (55.34%), suggesting a consistently high prevalence of UTIs across different populations and regions. However, lower rates have been documented in certain populations, such as 10.3% in HIV-infected individuals by

Tessema et al. [16] (2020) and 23.7% by Adugna et al. [17] (2021), which may reflect differences in study populations, healthcare access, and diagnostic criteria. Such variability highlights the influence of demographic and clinical factors on UTI prevalence and emphasizes the importance of context-specific epidemiological data.

In our study, females constituted the majority of culture-positive cases (67.53%), which aligns with findings from multiple studies. Bhargava et al. [18] (2022) reported a female predominance of 60.7%, while Abedin et al. [19] observed 78.9% of cases among females. Similarly, Tessema et al. [16] (2020) demonstrated that females were significantly more likely to develop UTIs.

This consistent trend can be attributed to anatomical and physiological predispositions such as shorter urethral length and proximity to the perianal region. Additionally, the highest positivity rate in our study was observed in the 18–30 years age group, which is in agreement with Bhargava et al. [18] (2022), where younger adult females were more affected. In contrast, Alebachew et al. [14] (2025) reported higher prevalence among geriatric populations, indicating that susceptibility varies with age and associated comorbidities.

The bacteriological profile in our study revealed a predominance of Gram-negative bacilli (89.37%), with Escherichia coli accounting for 70.98% of isolates. This observation is consistent with several studies across different geographical regions. Tessema et al. [16] (2020) reported E. coli in 69.6% of cases, Sharmin et al. [20] (2020) in 74.1%, and Abedin et al. [19] in 63.1%. Similarly, Meena et al. [15] (2021) and Bhargava et al. [18] (2022) also identified E. coli as the leading uropathogen, although with slightly lower proportions. Other organisms such as Klebsiella pneumoniae, Pseudomonas aeruginosa, and Proteus species were isolated in smaller proportions, which is in agreement with studies by Said et al. [21] (2021), Adugna et al. [17] (2021), and Girma et al. [22] (2022). The consistent predominance of E. coli across studies reinforces its primary role in the pathogenesis of UTIs globally. The antimicrobial susceptibility pattern observed in our study revealed high resistance to commonly used antibiotics, particularly ampicillin, fluoroquinolones, and cephalosporins.

Similar resistance patterns have been reported in several studies. Tessema et al. [16] (2020) documented high resistance to ampicillin (93.8%) and cotrimoxazole (62.5%), while Fenta et al. [23] (2020) observed complete resistance to ampicillin and high resistance to tetracycline. Meena et al. [15] (2021) also reported significant resistance of E. coli to cotrimoxazole and ciprofloxacin. Additionally, Bashir et al. [24] (2021) and Said et al. [21] (2021) highlighted widespread resistance to multiple commonly prescribed antibiotics.

In contrast, our study demonstrated better susceptibility to nitrofurantoin, aminoglycosides, and carbapenems, which is consistent with findings from Pandey et al. [25] (Nepal), Sharmin et al.20, and Ait-Mimoune et al. [26]. These observations underscore the importance of selecting empirical therapy based on local antibiograms and reinforce the continued effectiveness of certain antibiotics such as nitrofurantoin. The emergence of multidrug resistance (MDR) and advanced resistance mechanisms represents a major concern in the management of UTIs. In our study, the presence of ESBL-producing organisms and carbapenem resistance reflects a growing trend of antimicrobial resistance.

Comparable findings have been reported by Tessema et al. [16] (2020), where MDR was observed in 78.3% of isolates, and by Fenta et al. [23] (2020), who reported MDR in 66% of cases. Bhargava et al. [18] (2022) also documented a high prevalence of MDR organisms (96%), indicating a widespread issue across different regions.

Furthermore, studies by Alebachew et al. [14] (2025) and Adugna et al. [17] (2021) have highlighted the emergence of carbapenem resistance, which poses a significant threat to treatment options. These findings emphasize the urgent need for continuous surveillance, rational antibiotic use, and implementation of antimicrobial stewardship programs.

This study has certain limitations. It was conducted at a single tertiary care center, which may limit the generalizability of the findings. The exclusion of catheter-associated and healthcare-associated UTIs may have led to underrepresentation of certain resistant pathogens.

Additionally, molecular characterization of resistance mechanisms was not performed, which could have provided deeper insights into antimicrobial resistance patterns.

## Conclusion

The present study highlights a high burden of urinary tract infections in a tertiary care setting, with a predominance of Gram-negative bacilli, particularly Escherichia coli. Females and young adults were more commonly affected, consistent with global trends.

The study also reveals a concerning increase in antimicrobial resistance, especially against commonly used antibiotics such as fluoroquinolones and cephalosporins. However, antibiotics like nitrofurantoin, aminoglycosides, and carbapenems remain effective treatment options. These findings underscore the importance of routine culture and sensitivity testing, periodic surveillance of antimicrobial resistance patterns, and rational antibiotic prescribing to improve clinical outcomes and limit the spread of resistant organisms.

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