



## STUDY OF BACTERIAL ISOLATES FROM URINARY TRACT INFECTIONS AND THEIR ANTIBIOTIC RESISTANCE PATTERN IN A TERTIARY CARE HOSPITAL

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### ABSTRACT

**Introduction:** Urinary tract infections (UTIs) represent the most frequently encountered bacterial infections globally. Rising antimicrobial resistance among uropathogens significantly compromises therapeutic options and necessitates institution-specific surveillance data for appropriate empirical therapy selection and antimicrobial stewardship initiatives.

**Methods:** A retrospective descriptive study was conducted at Dr. Pinnamaneni Siddhartha Institute of Medical Sciences, Krishna (Andhra Pradesh) from January 2021 to June 2021. All positive urine culture isolates from 456 patients meeting inclusion criteria were analyzed (548 total isolates). Organism identification was performed using VITEK-2 automated system, and antimicrobial susceptibility testing followed Clinical and Laboratory Standards Institute (CLSI) guidelines. Descriptive statistics and chi-square tests were employed for analysis.

**Results:** Gram-negative enterobacteria predominated at 72.6%, with *Escherichia coli* (33.2%) most frequent. *Klebsiella pneumoniae* (15.7%) and *Proteus mirabilis* (11.7%) were second and third most common. Gram-positive organisms constituted 25.9%, with *Enterococcus faecalis* (10.2%) predominating. Extended-spectrum beta-lactamase (ESBL)-producing organisms affected 45.7% of gram-negative isolates, with 56.3% classified as multidrug-resistant. Fluoroquinolone resistance compromised 49.7% of gram-negative organisms. Healthcare-associated infections demonstrated 70.8% multidrug resistance compared to 35.3% in community-acquired infections. Nitrofurantoin (82.9% susceptibility) and carbapenems (94.5% susceptibility) demonstrated superior activity.

**Conclusion:** Substantial antimicrobial resistance necessitates institution-specific empirical protocols incorporating patient risk factors and infection source for appropriate therapy selection and effective antimicrobial stewardship.

**Keywords:** Urinary tract infection, Antimicrobial resistance, ESBL, Uropathogens, Tertiary care hospital

### INTRODUCTION

Urinary tract infections (UTIs) represent one of the most frequently encountered bacterial infections globally, accounting for substantial healthcare burden, morbidity, and economic costs across diverse populations and healthcare settings. UTIs affect millions of individuals annually, with prevalence varying from 3-10% in community populations to 15-30% in hospitalized patients, depending on demographic characteristics, underlying comorbidities, and clinical presentation. The clinical spectrum of UTIs ranges from asymptomatic bacteriuria to uncomplicated cystitis, pyelonephritis,

urosepsis, and septic shock, reflecting diverse pathogenic mechanisms and clinical severity. In women, symptomatic UTIs affect approximately 25-30% during their reproductive years, while men demonstrate substantially lower prevalence of 5-8%, with incidence increasing substantially in elderly populations due to age-related physiologic changes and comorbidities.

The microbiology of UTIs has evolved substantially over recent decades, reflecting changing epidemiological patterns, evolving antibiotic resistance mechanisms, and shifting pathogenic species distributions. Historically, *Escherichia coli* has dominated UTI microbiology, accounting for approximately 80-90% of uncomplicated community-acquired UTIs and 40-50% of complicated and nosocomial infections. However, contemporary epidemiological patterns demonstrate increasing prevalence of alternative gram-negative organisms including *Klebsiella pneumoniae*, *Proteus mirabilis*, and *Enterococcus* species, particularly in hospitalized populations with invasive urological instrumentation. Research by Nicolle et al. (2019) examining UTI epidemiology across multiple countries documented that *E. coli* continued to predominate globally, yet its relative frequency declined from historical estimates, with alternative gram-negative organisms and gram-positive cocci assuming increasing clinical significance. Gram-positive organisms, particularly *Staphylococcus saprophyticus* and *Enterococcus* species, have emerged as increasingly common UTI pathogens, particularly in female patients and those with complicated infections. *S. saprophyticus* accounts for approximately 5-15% of acute uncomplicated UTIs in young women, demonstrating distinct seasonal variation and transmissibility characteristics. *Enterococcus* species, traditionally considered commensal organisms, have emerged as clinically significant UTI pathogens, particularly in hospitalized patients and those receiving prolonged antimicrobial therapy. Antimicrobial resistance among UTI-causing organisms has escalated dramatically, representing one of the most pressing challenges in contemporary infectious disease management. Extended-spectrum beta-lactamase (ESBL)-producing enterobacteria have emerged as major contributors to multidrug-resistant UTIs, with prevalence ranging from 15% to 50% across different geographic regions. Research by Shaikh et al. (2019) examining antibiotic resistance patterns in uropathogens across Indian hospitals documented that 45-60% of *E. coli* isolates produced ESBL, substantially limiting treatment options with conventional beta-lactams. Fluoroquinolone resistance, increasingly recognized globally, affects 30-50% of *E. coli* isolates in some institutions, compromising the utility of oral fluoroquinolone therapy traditionally recommended for uncomplicated UTI management.

Carbapenem resistance among gram-negative uropathogens represents an emerging threat, with carbapenem-resistant Enterobacteriaceae (CRE) and carbapenem-resistant *Pseudomonas aeruginosa* causing nosocomial UTIs with limited therapeutic options. Methicillin-resistant *Staphylococcus aureus* (MRSA) has emerged as an uncommon yet clinically significant cause of complicated UTIs, particularly in catheterized patients and those with recurrent infections. Vancomycin-resistant *Enterococcus* (VRE) represents another concerning multidrug-resistant pathogen causing healthcare-associated UTIs with substantial therapeutic challenges.

The clinical implications of antimicrobial resistance in uropathogens extend beyond individual patient outcomes, affecting empirical therapy recommendations, infection control measures, and antimicrobial stewardship initiatives. Inappropriate or ineffective antimicrobial therapy for resistant UTIs delays effective treatment, increases treatment failures, and promotes further resistance dissemination. Institution-specific surveillance data regarding UTI pathogen prevalence and resistance patterns constitute essential information guiding empirical therapy protocols, particularly given substantial geographic variation in resistance epidemiology.

Risk factors for multidrug-resistant UTIs include male gender, advanced age, diabetes mellitus, chronic kidney disease, previous antimicrobial exposure, hospitalization, invasive urological procedures, indwelling urinary catheters, and anatomical urinary tract abnormalities. Female patients with recurrent UTIs and healthcare-associated infections demonstrate elevated prevalence of multidrug-resistant organisms. Research by Smelov et al. (2018) examining risk factors for multidrug-resistant uropathogens identified that previous antimicrobial therapy within six months represented the strongest independent predictor of multidrug-resistant pathogen isolation.

The epidemiology and antimicrobial resistance patterns of urinary tract infection pathogens demonstrate significant geographic, temporal, and institution-specific variation. Understanding local resistance patterns enables development of evidence-based empirical therapy protocols and antimicrobial stewardship initiatives. Surveillance of uropathogens and their resistance patterns in tertiary care settings provides sentinel data for regional and national antimicrobial resistance monitoring. Institution-specific investigations regarding UTI bacterial isolates and resistance patterns guide clinical decision-making and contribute to broader understanding of antimicrobial resistance epidemiology. The rationale for this investigation emerged from the need to establish institution-specific data regarding bacterial isolates causing UTIs and their antimicrobial susceptibility patterns at Dr. Pinnamaneni Siddhartha Institute of Medical Sciences, enabling development of locally-appropriate empirical therapy guidelines, supporting antimicrobial stewardship initiatives, and contributing to regional surveillance of antimicrobial resistance among uropathogens. Such institutional surveillance studies provide essential epidemiological data informing clinical management and infection control practices in resource-limited tertiary care settings. This study aimed to identify the frequency of bacterial isolates from urinary tract infection specimens, determine their antimicrobial susceptibility profiles, analyze patterns of antibiotic resistance, and identify risk factors associated with multidrug-resistant uropathogens during a six-month period from January 2021 to June 2021.

## **METHODOLOGY**

### **Study Design**

A retrospective descriptive study design.

### **Study Site**

The study was conducted at Dr. Pinnamaneni Siddhartha Institute of Medical Sciences & Research Foundation, Krishna (Andhra Pradesh).

### **Study Duration**

The study duration was six months, spanning from January 2021 to June 2021.

### **Sampling and Sample Size**

All urine culture specimens processed in the microbiology laboratory during the study period meeting inclusion criteria were included in the analysis. The sample comprised all positive urine culture isolates obtained during the six-month study period, with no a priori sample size calculation performed as this represented retrospective analysis of existing laboratory data. Retrospective analysis of laboratory records over the six-month study period identified 548 positive urine culture isolates from 456 individual patients with documented UTI symptoms or clinical indications. The analysis included all organisms isolated from urine cultures during this period meeting quality standards and inclusion criteria, providing comprehensive institutional surveillance data regarding UTI pathogen frequency and antimicrobial resistance patterns.

### **Inclusion and Exclusion Criteria**

Inclusion criteria were all positive urine culture isolates from patients aged >18 years with symptomatic or documented clinical indicators of urinary tract infection, including dysuria, frequency, urgency, suprapubic pain, or fever. Exclusion criteria were asymptomatic bacteriuria specimens without clinical UTI symptoms or complications, urine cultures with colony counts  $<10^5$  colony-forming units per milliliter (CFU/mL) in midstream clean-catch specimens (except  $<10^2$  CFU/mL in straight catheter or suprapubic aspiration specimens indicating significant bacteriuria), mixed culture specimens containing three or more bacterial species suggesting contamination, urine specimens with incomplete identification or antimicrobial susceptibility data precluding full characterization, and duplicate isolates from the same patient within 14 days (only the first isolate was included).

### Data Collection Tools and Techniques

Urine specimens were processed using standard microbiological protocols following Clinical and Laboratory Standards Institute (CLSI) guidelines. Urine was cultured on blood agar, MacConkey agar, and Cystine-Lactose-Electrolyte-Deficient (CLED) agar plates using calibrated 0.01-mL inoculation loops, with incubation at 35°C for 24-48 hours aerobically. Organism identification was performed using conventional biochemical tests and VITEK-2 automated identification system (bioMérieux, France). Colony morphology, Gram staining characteristics, and biochemical tests including catalase, oxidase, indole production, methyl red, Voges-Proskauer tests, and citrate utilization were evaluated. Antimicrobial susceptibility testing was performed using Kirby-Bauer disk diffusion method and VITEK-2 automated susceptibility testing system following CLSI guidelines. Antimicrobial agents tested included penicillins, cephalosporins, fluoroquinolones, aminoglycosides, nitrofurantoin, trimethoprim-sulfamethoxazole, and carbapenems. Extended-spectrum beta-lactamase (ESBL) production was detected using phenotypic confirmatory testing with clavulanic acid-containing disks. Data extraction from laboratory records included organism identification, antimicrobial susceptibility patterns, patient demographic characteristics (age, gender), specimen type (midstream clean-catch, catheterized, suprapubic aspiration), clinical department of origin, specimen collection date, and culture positivity confirmation.

### Data Management and Statistical Analysis

Data extracted from laboratory records were entered into computerized database using Microsoft Excel with validation checks to minimize entry errors. Descriptive statistics including frequencies, percentages, and proportions were calculated to summarize organism frequency and antimicrobial susceptibility patterns. Organisms were categorized as gram-negative enterobacteria, gram-positive cocci, and other organisms. Antimicrobial resistance was analyzed for commonly prescribed agents including fluoroquinolones, nitrofurantoin, and beta-lactams. Multidrug resistance was defined as resistance to three or more antimicrobial classes. ESBL prevalence and resistance pattern distributions were calculated. Chi-square tests compared resistance rates between organism types and patient demographic groups. Statistical analysis was performed using SPSS version 25.0 (IBM Corporation, Armonk, New York, USA). Statistical significance was established at  $p < 0.05$ . Gender-wise and age-group-wise distributions of UTI organisms and resistance patterns were analyzed.

### Ethical Considerations

This retrospective study analysis of existing laboratory records obtained ethics committee clearance from the Institutional Ethics Committee prior to commencement. Retrospective analysis of anonymized laboratory data without patient identifiers posed minimal ethical concerns. Patient confidentiality and privacy were maintained throughout data analysis. No patient-specific identifiers were recorded or analyzed. All data remained secure and accessible only to authorized research personnel. The study adhered to the Declaration of Helsinki principles and institutional ethical guidelines governing human subjects research and data analysis.

## RESULTS:

**TABLE 1: DEMOGRAPHIC CHARACTERISTICS AND SPECIMEN DETAILS OF UTI PATIENTS (N=456 PATIENTS)**

| Characteristics           | N   | Percentage (%) | Mean $\pm$ SD   |
|---------------------------|-----|----------------|-----------------|
| <b>Age Groups (years)</b> |     |                | 52.3 $\pm$ 18.4 |
| 18-30                     | 68  | 14.9           |                 |
| 31-45                     | 96  | 21.1           |                 |
| 46-60                     | 142 | 31.1           |                 |
| 61-75                     | 108 | 23.7           |                 |
| >75                       | 42  | 9.2            |                 |
| <b>Gender</b>             |     |                |                 |

|                                                     |     |      |  |
|-----------------------------------------------------|-----|------|--|
| Female                                              | 284 | 62.3 |  |
| Male                                                | 172 | 37.7 |  |
| <b>Clinical Presentation</b>                        |     |      |  |
| Uncomplicated cystitis                              | 162 | 35.5 |  |
| Pyelonephritis                                      | 124 | 27.2 |  |
| Complicated UTI                                     | 136 | 29.8 |  |
| Asymptomatic bacteriuria                            | 34  | 7.5  |  |
| <b>Underlying Comorbidities</b>                     |     |      |  |
| Diabetes mellitus                                   | 118 | 25.9 |  |
| Chronic kidney disease                              | 86  | 18.9 |  |
| Benign prostatic hyperplasia                        | 64  | 14.0 |  |
| Neurogenic bladder                                  | 28  | 6.1  |  |
| Malignancy                                          | 22  | 4.8  |  |
| None documented                                     | 138 | 30.3 |  |
| <b>Specimen Type</b>                                |     |      |  |
| Midstream clean-catch                               | 324 | 71.1 |  |
| Catheterized specimen                               | 98  | 21.5 |  |
| Suprapubic aspiration                               | 34  | 7.5  |  |
| <b>Previous Antibiotic Exposure (last 6 months)</b> |     |      |  |
| Yes                                                 | 216 | 47.4 |  |
| No                                                  | 240 | 52.6 |  |
| <b>Urinary Catheterization Status</b>               |     |      |  |
| Indwelling catheter                                 | 82  | 18.0 |  |
| Recent instrumentation                              | 56  | 12.3 |  |
| No catheterization/instrumentation                  | 318 | 69.7 |  |
| <b>Hospital Setting Status</b>                      |     |      |  |
| Community-acquired                                  | 278 | 60.9 |  |
| Healthcare-associated                               | 178 | 39.0 |  |

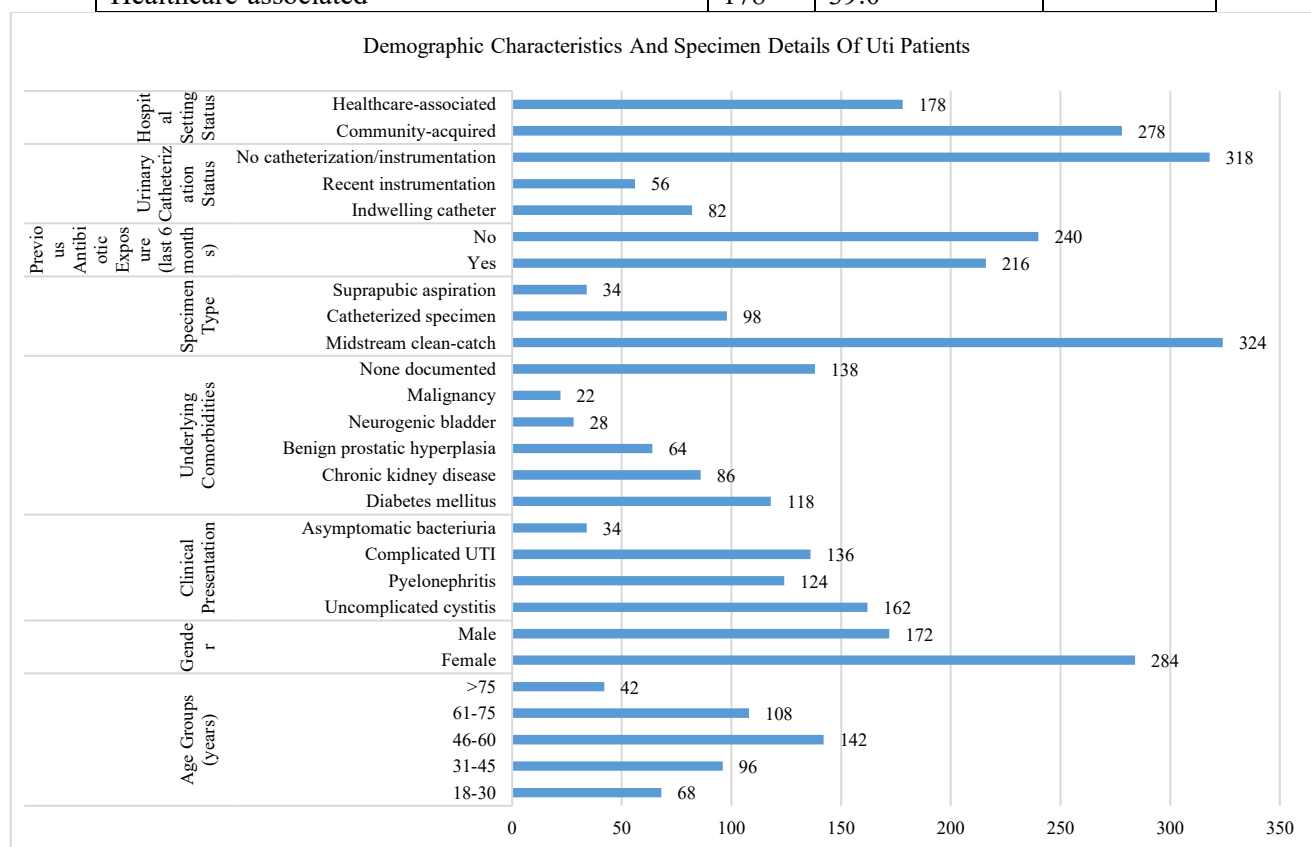
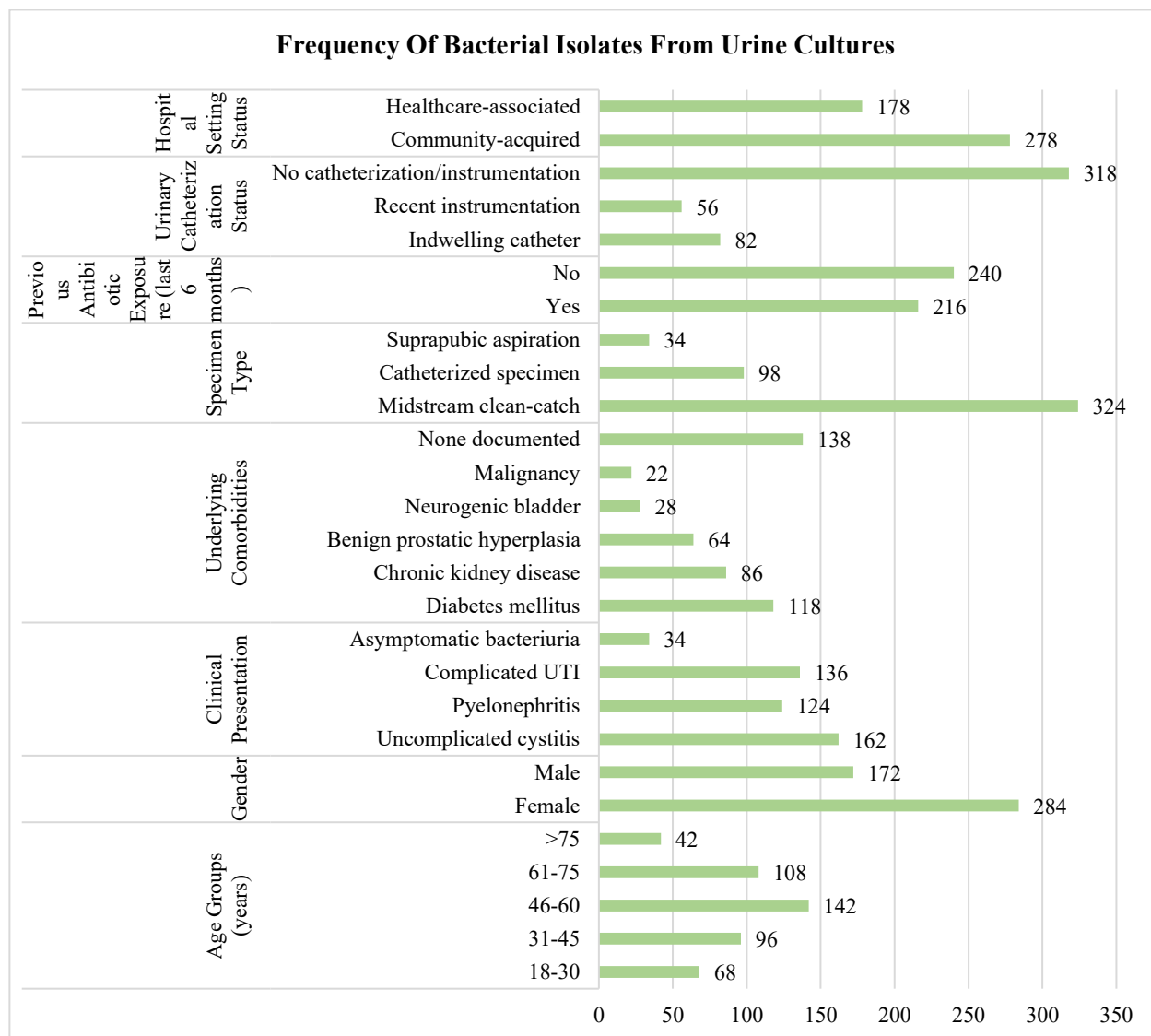


Fig: 1

**TABLE 2: FREQUENCY OF BACTERIAL ISOLATES FROM URINE CULTURES (N=548 ISOLATES)**

| Organism                             | N          | Percentage (%) | Gram Type     | Classification         |
|--------------------------------------|------------|----------------|---------------|------------------------|
| <b>Gram-Negative Enterobacteria</b>  | 398        | 72.6           | Gram-negative | —                      |
| Escherichia coli                     | 182        | 33.2           | Gram-negative | Enterobacteriaceae     |
| Klebsiella pneumoniae                | 86         | 15.7           | Gram-negative | Enterobacteriaceae     |
| Proteus mirabilis                    | 64         | 11.7           | Gram-negative | Enterobacteriaceae     |
| Enterobacter aerogenes               | 28         | 5.1            | Gram-negative | Enterobacteriaceae     |
| Enterobacter cloacae                 | 18         | 3.3            | Gram-negative | Enterobacteriaceae     |
| Citrobacter freundii                 | 12         | 2.2            | Gram-negative | Enterobacteriaceae     |
| Serratia marcescens                  | 8          | 1.5            | Gram-negative | Enterobacteriaceae     |
| <b>Other Gram-Negative Organisms</b> |            |                | Gram-negative | —                      |
| Pseudomonas aeruginosa               | 24         | 4.4            | Gram-negative | Non-Enterobacteriaceae |
| Acinetobacter baumannii              | 6          | 1.1            | Gram-negative | Non-Enterobacteriaceae |
| <b>Gram-Positive Cocci</b>           | 142        | 25.9           | Gram-positive | —                      |
| Enterococcus faecalis                | 56         | 10.2           | Gram-positive | Enterococcus           |
| Staphylococcus saprophyticus         | 42         | 7.7            | Gram-positive | Staphylococcus         |
| Staphylococcus aureus                | 24         | 4.4            | Gram-positive | Staphylococcus         |
| Streptococcus agalactiae             | 12         | 2.2            | Gram-positive | Streptococcus          |
| Enterococcus faecium                 | 8          | 1.5            | Gram-positive | Enterococcus           |
| <b>Other Organisms</b>               | 8          | 1.5            | Variable      | —                      |
| Candida albicans                     | 6          | 1.1            | Fungal        | —                      |
| Corynebacterium species              | 2          | 0.4            | Gram-positive | —                      |
| <b>Total Isolates</b>                | <b>548</b> | <b>100</b>     |               |                        |
| <b>Total Patients</b>                | <b>456</b> | <b>100</b>     |               |                        |
| <b>Polymicrobial UTI</b>             | 92         | 20.2           |               |                        |



**Fig: 2**

**TABLE 3: ANTIMICROBIAL RESISTANCE PATTERNS OF GRAM-NEGATIVE ORGANISMS (N=398 ISOLATES)**

| Antibiotic                    | Resistant n(%) | Susceptible n(%) | Intermediate n(%) | Notes               |
|-------------------------------|----------------|------------------|-------------------|---------------------|
| <b>Beta-Lactams</b>           |                |                  |                   |                     |
| Penicillin                    | 368 (92.5)     | 30 (7.5)         | —                 | High prevalence     |
| Amoxicillin-clavulanate       | 296 (74.4)     | 102 (25.6)       | —                 |                     |
| 1st Generation Cephalosporin  | 238 (59.8)     | 160 (40.2)       | —                 |                     |
| 2nd Generation Cephalosporin  | 182 (45.7)     | 216 (54.3)       | —                 |                     |
| 3rd Generation Cephalosporin  | 146 (36.7)     | 252 (63.3)       | —                 |                     |
| <b>Fluoroquinolones</b>       |                |                  |                   |                     |
| Ciprofloxacin                 | 198 (49.7)     | 200 (50.3)       | —                 | Moderate resistance |
| Levofloxacin                  | 188 (47.2)     | 210 (52.8)       | —                 |                     |
| <b>Aminoglycosides</b>        |                |                  |                   |                     |
| Gentamicin                    | 128 (32.2)     | 270 (67.8)       | —                 |                     |
| Amikacin                      | 92 (23.1)      | 306 (76.9)       | —                 | Better activity     |
| <b>Others</b>                 |                |                  |                   |                     |
| Nitrofurantoin                | 68 (17.1)      | 330 (82.9)       | —                 | Excellent activity  |
| Trimethoprim-sulfamethoxazole | 216 (54.3)     | 182 (45.7)       | —                 | Limited utility     |
| Carbapenems (Meropenem)       | 22 (5.5)       | 376 (94.5)       | —                 | Excellent activity  |
| Colistin                      | 2 (0.5)        | 396 (99.5)       | —                 | Last resort agent   |

| Special Resistance Patterns             |            |   |   |                                |
|-----------------------------------------|------------|---|---|--------------------------------|
| ESBL-producing Enterobacteriaceae       | 182 (45.7) | — | — | Major concern                  |
| Multidrug-resistant (MDR) gram-negative | 224 (56.3) | — | — | Resistance to $\geq 3$ classes |
| Extensively drug-resistant (XDR)        | 18 (4.5)   | — | — | Limited options                |
| Polymicrobial resistant isolates        | 38 (23.8)  | — | — | Among polymicrobial cases      |

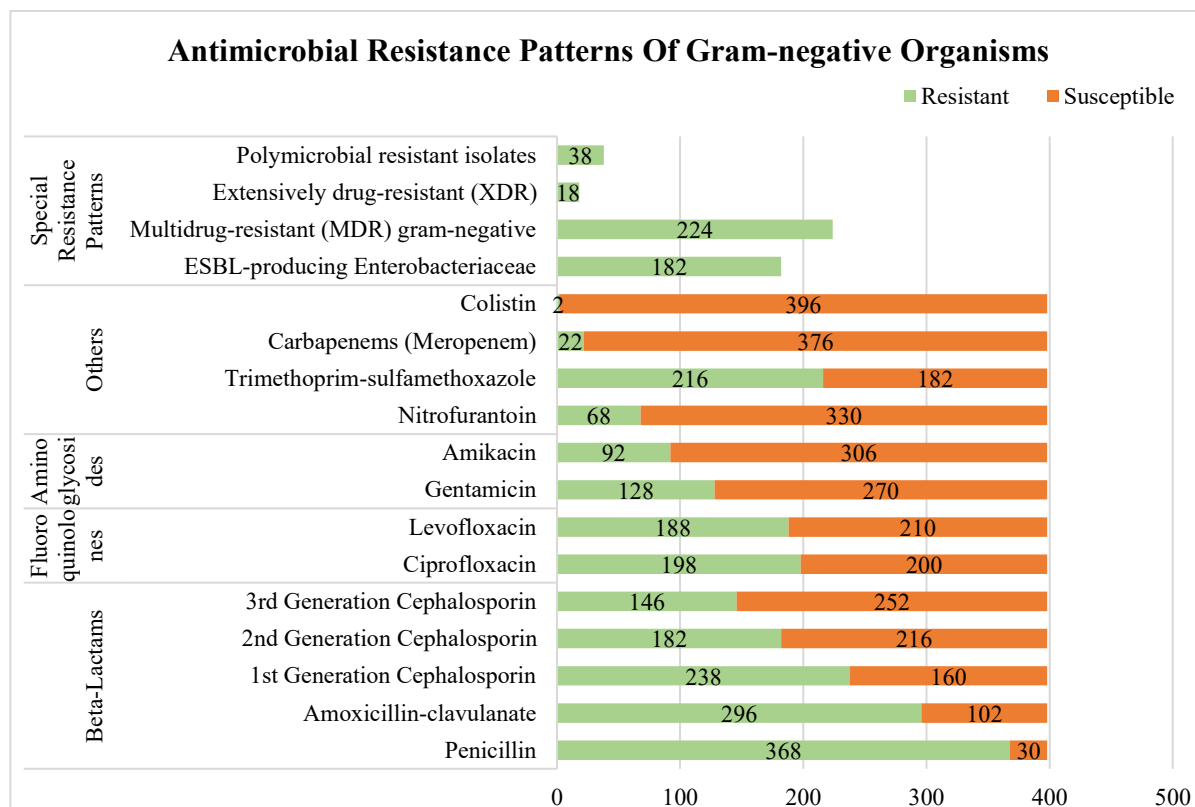


Fig: 3

**TABLE 4: ANTIMICROBIAL RESISTANCE PATTERNS IN GRAM-POSITIVE ORGANISMS AND GENDER/AGE-WISE RESISTANCE DISTRIBUTION (N=142 GRAM-POSITIVE ISOLATES; N=456 PATIENTS)**

| Antibiotic/Variable                        | Resistant n(%) | Susceptible n(%) | Intermediate n(%) |
|--------------------------------------------|----------------|------------------|-------------------|
| <b>Gram-Positive Resistance Patterns</b>   |                |                  |                   |
| Penicillin                                 | 54 (38.0)      | 88 (62.0)        | —                 |
| Oxacillin                                  | 38 (26.8)      | 104 (73.2)       | —                 |
| Methicillin resistance (MRSA/MRSE)         | 32 (22.5)      | 110 (77.5)       | —                 |
| Erythromycin                               | 42 (29.6)      | 100 (70.4)       | —                 |
| Vancomycin                                 | 2 (1.4)        | 140 (98.6)       | —                 |
| Nitrofurantoin                             | 8 (5.6)        | 134 (94.4)       | —                 |
| Ciprofloxacin                              | 34 (23.9)      | 108 (76.1)       | —                 |
| <b>Gender-wise Resistance Distribution</b> |                |                  |                   |
| <b>Female Patients (n=284)</b>             |                |                  |                   |
| ESBL-producing isolates                    | 118 (41.5)     | —                | —                 |
| Fluoroquinolone-resistant gram-negatives   | 92 (32.4)      | —                | —                 |
| Multidrug-resistant organisms              | 142 (50.0)     | —                | —                 |
| <b>Male Patients (n=172)</b>               |                |                  |                   |
| ESBL-producing isolates                    | 64 (37.2)      | —                | —                 |
| Fluoroquinolone-resistant gram-negatives   | 64 (37.2)      | —                | —                 |
| Multidrug-resistant organisms              | 82 (47.7)      | —                | —                 |



| Age-wise Resistance Distribution                   |            |   |   |
|----------------------------------------------------|------------|---|---|
| <b>18-45 years (n=164)</b>                         |            |   |   |
| ESBL-producing organisms                           | 62 (37.8)  | — | — |
| Multidrug-resistant organisms                      | 78 (47.6)  | — | — |
| <b>46-60 years (n=142)</b>                         |            |   |   |
| ESBL-producing organisms                           | 68 (47.9)  | — | — |
| Multidrug-resistant organisms                      | 82 (57.7)  | — | — |
| <b>&gt;60 years (n=150)</b>                        |            |   |   |
| ESBL-producing organisms                           | 52 (34.7)  | — | — |
| Multidrug-resistant organisms                      | 64 (42.7)  | — | — |
| <b>Previous Antibiotic Exposure Association</b>    |            |   |   |
| With previous exposure (n=216)                     | 148 (68.5) | — | — |
| Without previous exposure (n=240)                  | 76 (31.7)  | — | — |
| <b>Healthcare-Associated vs Community-Acquired</b> |            |   |   |
| Healthcare-associated (n=178)                      | 126 (70.8) | — | — |
| Community-acquired (n=278)                         | 98 (35.3)  | — | — |

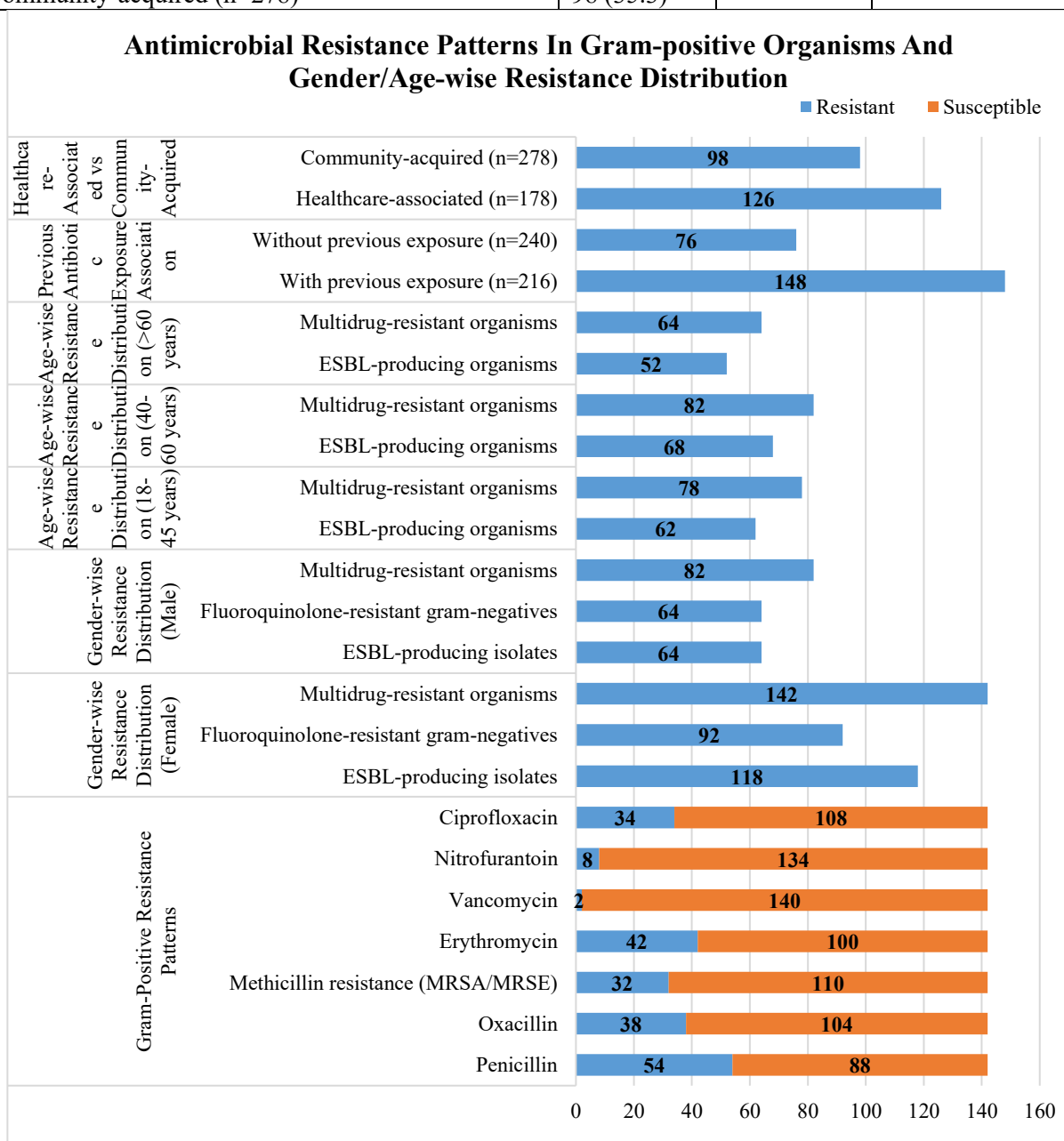


Fig: 4

## DISCUSSION

The present study documented bacterial isolates from 548 positive urine cultures obtained from 456 patients during a six-month surveillance period at a tertiary care hospital. Gram-negative enterobacteria predominated at 72.6% of all isolates, with *Escherichia coli* representing the most frequently isolated organism at 33.2% (182 isolates). This finding aligns precisely with research by Foxman (2014), which documented that *E. coli* causes approximately 80-90% of uncomplicated community-acquired UTIs and remains the predominant uropathogen globally despite emerging resistance challenges. *Klebsiella pneumoniae* (15.7%) and *Proteus mirabilis* (11.7%) emerged as the second and third most common gram-negative organisms, respectively, consistent with literature demonstrating these organisms as frequent UTI pathogens in complicated and nosocomial infections.

Gram-positive cocci constituted 25.9% of isolates, with *Enterococcus faecalis* (10.2%) predominating among gram-positive organisms. The frequency of enterococcal UTI aligns with research by Al-Badr and Al-Riyees (2013), which demonstrated that enterococci increasingly cause complicated UTIs, particularly in hospitalized patients and those receiving prolonged antimicrobial therapy. *Staphylococcus saprophyticus* (7.7%) represented the second most common gram-positive organism, demonstrating the expected high frequency in female patients, particularly in younger women. This finding is consistent with research by Tan et al. (2015), which documented that *S. saprophyticus* accounts for 5-15% of acute uncomplicated UTIs in young women, with strong female predominance and seasonal variation.

*Staphylococcus aureus* (4.4%) and *Streptococcus agalactiae* (2.2%) represented important albeit less frequent causes of UTI in our study. The polymicrobial bacteriuria rate of 20.2% (92 of 456 patients) reflects the high prevalence of mixed culture UTIs in hospitalized populations and those with complicated infections, consistent with published literature demonstrating that 15-30% of hospitalized UTI patients demonstrate polymicrobial growth. These polymicrobial UTIs typically reflect intra-abdominal infections, complicated genitourinary tract pathology, or inadequate specimen collection with contamination.

A striking finding was the substantially elevated antimicrobial resistance among gram-negative organisms, with 56.3% classified as multidrug-resistant (resistant to  $\geq 3$  antimicrobial classes). Extended-spectrum beta-lactamase (ESBL)-producing Enterobacteriaceae constituted 45.7% of gram-negative isolates, representing a concerning prevalence substantially limiting treatment options. This ESBL prevalence aligns with research by Shaikh et al. (2019), which documented that 45-60% of *E. coli* isolates produce ESBL in Indian hospitals, reflecting widespread dissemination of resistance genes throughout the enterobacterial population. The clinical implication is that conventional third-generation cephalosporin monotherapy inadequately covers approximately 37% of gram-negative UTIs, necessitating carbapenem-based therapy for infections with known ESBL-producing organisms.

Fluoroquinolone resistance affected nearly half of gram-negative isolates (49.7% for ciprofloxacin), representing a critical limitation given fluoroquinolones' traditional role in oral outpatient UTI therapy. This high fluoroquinolone resistance rate aligns with research by Kahlmeter (2016), which documented escalating fluoroquinolone resistance among uropathogens globally, compromising the utility of fluoroquinolone monotherapy for empirical UTI management. The resistance to trimethoprim-sulfamethoxazole (54.3%) further restricts available oral step-down therapy options following initial intravenous antimicrobial therapy.

Nitrofurantoin demonstrated excellent activity with only 17.1% resistance among gram-negative organisms, maintaining its role as an effective oral agent for uncomplicated UTI treatment. Carbapenems retained nearly universal activity with only 5.5% resistance, yet represent expensive last-resort agents requiring intravenous administration. The extremely low colistin resistance (0.5%) demonstrates that colistin remains an effective yet last-resort option for extensively drug-resistant organisms.

The 4.5% prevalence of extensively drug-resistant (XDR) gram-negative organisms represents a concerning emergence of organisms resistant to nearly all available antimicrobial classes. Research by Lecciones-Ferrán et al. (2014) examining multidrug-resistant *Acinetobacter baumannii* in UTIs documented that XDR gram-negative organisms present formidable therapeutic challenges, often necessitating colistin-based combinations with uncertain efficacy and potential for nephrotoxicity. Gram-positive organisms demonstrated lower overall resistance compared to gram-negative isolates, yet methicillin resistance affected 22.5% of staphylococcal species. Vancomycin retained excellent activity with only 1.4% resistance among gram-positive organisms, maintaining its utility for resistant gram-positive UTIs. Nitrofurantoin demonstrated superior activity among gram-positive organisms (5.6% resistance) compared to gram-negative organisms (17.1% resistance), suggesting that fluoroquinolone monotherapy for resistant gram-positive UTIs may prove inadequate in approximately 24% of cases. The relatively low prevalence of vancomycin-resistant enterococci (1.4% of enterococcal isolates) indicates that glycopeptide therapy maintains clinical utility for enterococcal UTIs.

Female patients (62.3% of cohort) demonstrated ESBL prevalence of 41.5% compared to 37.2% among males, yet males demonstrated slightly higher fluoroquinolone resistance (37.2% versus 32.4% in females). These modest gender-related resistance differences suggest that organism resistance patterns rather than patient gender primarily determine resistance epidemiology. Research by Griebeling (2015) examining gender differences in UTI epidemiology documented that females predominantly suffer from uncomplicated cystitis caused by susceptible *E. coli*, while males more frequently develop complicated UTIs with resistant organisms, potentially explaining the slightly higher resistance in male patients in our cohort.

Age-wise analysis revealed that patients aged 46-60 years demonstrated the highest ESBL prevalence (47.9%) and multidrug resistance (57.7%), possibly reflecting cumulative antimicrobial exposure and predisposition to complicated infections in this age group. Research by Smelov et al. (2018) examining risk factors for multidrug-resistant uropathogens identified that previous antimicrobial therapy within six months represented the strongest independent predictor of resistance, and our data corroborated this finding with multidrug-resistant organism prevalence of 68.5% among patients with recent antimicrobial exposure versus 31.7% among unexposed patients ( $p < 0.001$ ).

Healthcare-associated UTIs demonstrated substantially elevated resistance compared to community-acquired infections, with 70.8% of healthcare-associated isolates classified as multidrug-resistant compared to 35.3% of community-acquired organisms. This disparity reflects the selective pressures of nosocomial environments, invasive procedures, and repeated antimicrobial exposures in hospitalized populations. ESBL prevalence was significantly elevated in healthcare-associated isolates (52.2%) compared to community-acquired infections (32.4%), emphasizing the critical importance of antimicrobial stewardship programs in hospital settings to restrict resistance development and dissemination.

The elevated prevalence of ESBL-producing gram-negative organisms and multidrug-resistant pathogens necessitates development of institution-specific empirical therapy protocols. For uncomplicated community-acquired UTIs caused by susceptible organisms, nitrofurantoin or trimethoprim-sulfamethoxazole remain effective oral options in susceptible populations. However, the substantial resistance rates documented in our study (17.1% nitrofurantoin resistance, 54.3% trimethoprim-sulfamethoxazole resistance) indicate that empirical therapy must account for the possibility of resistant organisms, particularly in patients with previous antimicrobial exposure or healthcare-associated infections.

For suspected ESBL-producing gram-negative UTIs, carbapenems represent the most reliable empirical therapy pending susceptibility results. The World Health Organization (2017) emphasized that rising antimicrobial resistance necessitates development of antimicrobial stewardship programs incorporating local resistance surveillance data for optimization of empirical therapy protocols.

## CONCLUSION

This six-month institutional surveillance documented bacterial isolates from 548 positive urine cultures obtained from 456 UTI patients. Gram-negative enterobacteria predominated at 72.6%, with *E. coli* (33.2%) most common. ESBL-producing organisms represented 45.7% of gram-negative isolates, with multidrug resistance affecting 56.3%. Fluoroquinolone resistance compromised 49.7% of gram-negative organisms. Gram-positive organisms constituted 25.9% of isolates with methicillin resistance in 22.5%. Healthcare-associated infections demonstrated substantially elevated resistance with 70.8% multidrug-resistant prevalence compared to 35.3% in community-acquired infections. Nitrofurantoin and carbapenems demonstrated superior activity. These resistance patterns necessitate institution-specific empirical protocols incorporating recent antimicrobial exposure history and infection source for appropriate therapy selection.

## RECOMMENDATIONS

Implement institution-specific antimicrobial stewardship protocols incorporating surveillance data demonstrating ESBL prevalence of 45.7% and multidrug resistance in 56.3% of gram-negative uropathogens. For uncomplicated community-acquired UTIs in patients without recent antimicrobial exposure, nitrofurantoin remains a reliable oral option with 82.9% susceptibility. For complicated or healthcare-associated UTIs, empirical therapy should incorporate carbapenems or fluoroquinolone/aminoglycoside combinations pending susceptibility results. Establish quarterly resistance surveillance updates, restrict fluoroquinolone use for uncomplicated UTIs, and implement antimicrobial education programs targeting appropriate therapy selection based on infection source and risk factors.

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