Section: Microbiology

Original Research Article

ETIOLOGICAL PROFILE & ANTIMICROBIAL SUSCEPTIBILITY PATTERNS OF BACTERIAL UROPATHOGENS: A ONE-YEAR RETROSPECTIVE STUDY

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ABSTRACT

Background: Urinary tract infections (UTIs) are common bacterial infections and are increasingly complicated by antimicrobial resistance. This study evaluated the etiological profile and antimicrobial susceptibility patterns of bacterial uropathogens among adults attending a tertiary-care hospital in Chennai, India. **Materials and Methods:** This retrospective observational study was conducted in the Department of Microbiology from January to December 2024. Adult urine specimens with significant bacterial growth were included. Bacterial identification was performed using standard microbiological methods. Antimicrobial susceptibility testing was performed using the modified Kirby–Bauer disc diffusion method and E-test, when required, according to Clinical and Laboratory Standards Institute (CLSI) 2023/2024 guidelines. **Results:** Of 16,866 urine specimens processed, 3,485 (20.66%) yielded significant bacterial growth. Gram-negative bacteria predominated (2,836; 81.37%). *Escherichia coli* was the most common isolate (1,395; 40.02%), followed by *Enterococcus faecalis* (571; 16.38%) and *Klebsiella pneumoniae* (521; 14.95%). Females accounted for 2,300 (66.0%) cases, and the 51–70-year age group was most represented (1,359; 39.0%). Diabetes mellitus was the most frequently documented risk factor (2,136; 61.29%). Gram-negative isolates showed substantial resistance to several commonly used antibiotics, whereas meropenem and nitrofurantoin retained comparatively higher activity. Linezolid and vancomycin showed high activity against Gram-positive isolates. **Interpretation and Conclusions:** Gram-negative bacteria, particularly Escherichia coli, predominated among culture-positive urine specimens and showed substantial antimicrobial resistance. Continuous local surveillance and antimicrobial stewardship are important for informing empirical therapy and limiting further resistance.

INTRODUCTION

Urinary tract infections (UTIs) may be asymptomatic (subclinical infection) or symptomatic (disease). Thus the term urinary tract infection encompasses a variety of clinical entities, including asymptomatic bacteriuria (ASB), cystitis, prostatitis, and pyelonephritis. The distinction between symptomatic UTI and ASB has major clinical implications. Uncomplicated urinary tract infection refers to an infection confined to the bladder or acute cystitis. Pyelonephritis occurs when the infection involves the renal parenchyma.

Complicated urinary tract infection is accompanied by symptoms that suggest the infection extends beyond the bladder, such as a fever or signs or symptoms of systemic illness. Catheter-associated bacteriuria can be either symptomatic (CAUTI) or asymptomatic. Among all affected populations, women experience the highest burden of disease due to several contributing factors such as anatomical structure, hormonal influences, and the short distance between the urethral opening and the anus, which facilitates bacterial colonization.[1] Individuals with

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diabetes mellitus are reported to have a three- to five-fold higher risk of developing UTIs compared with non-diabetic individuals. Common symptoms include painful urination (dysuria), which occurs in 80-90% of uncomplicated cases, urinary urgency in 60-70% of patients, and cloudy or foul-smelling urine in about 50-60% of affected individuals.[2]

Antimicrobial therapy remains the primary treatment strategy for UTIs. In many clinical settings, empirical broad-spectrum antibiotics are initiated before microbiological results become available. Although this practice may provide immediate symptom relief, it can contribute to treatment failure and the development of antimicrobial resistance. Inappropriate antimicrobial therapy may allow pathogens to persist within the urinary tract, increasing the likelihood of recurrent infections and poorer clinical outcomes.[3] Therefore, timely identification of the infecting organism and selection of appropriate targeted therapy are essential, particularly in the context of rising antimicrobial resistance.[4]

Antimicrobial resistance (AMR) has emerged as a significant public health challenge worldwide. A multicentre study conducted in India reported that 26.9% of Gram-negative urinary isolates were extended-spectrum β-lactamase (ESBL) producers and exhibited poor susceptibility to commonly prescribed antibiotics such as ciprofloxacin (35.8%), trimethoprim-sulfamethoxazole (30%), amoxicillin (17.7%), amoxicillin-clavulanate (41.6%), and nitrofurantoin (65.7%).[5,6] The growing prevalence of resistant organisms has made the treatment of community-acquired UTIs increasingly difficult and underscores the importance of continuous monitoring of local resistance patterns.

The present study seeks to evaluate the distribution of urinary pathogens and their antimicrobial susceptibility profiles within the local population. The findings are expected to generate evidence that will support rational antibiotic prescribing, improve empirical treatment strategies, facilitate early identification of emerging resistance trends, contribute to antimicrobial stewardship efforts, reduce unnecessary antibiotic use and ultimately enhance patient outcomes while lowering healthcare expenditures.

MATERIALS AND METHODS

Study Setting

This is an observational, retrospective study, conducted in the Department of Microbiology at a Tertiary care hospital in Chennai, Tamil Nadu, India during the period of 1 year from January 2024 to December 2024. Ethical approval for the study was obtained from the Institutional Ethics Committee.

Study Population

All urine specimens received for culture and sensitivity test (CST) with positive bacterial growth, age>18years were included in the study. In case of more than one urine sample from a subject, only the first sample was considered for analysis. Samples with multiple isolates and fungal growths were excluded from the analysis. Inclusion and Exclusion criteria was showed in Table 1:

Table 1: Inclusion and Exclusion criteria

Inclusion Criteria	Exclusion Criteria
Age >/=18 years	Fungal growth
Urine specimen positive for bacterial growth on CST	Multiple bacterial isolates
Only the first sample considered when multiple samples were received from the same subject	-

The urine samples received during the study period were subjected to direct microscopy and culture identification by standard conventional microbiological techniques.

Determination of Antimicrobial Susceptibility

Modified Kirby-Bauer disc diffusion assay and E-tests (whenever required) on Muller Hinton agar was carried out to determine the antimicrobial susceptibility profiles as per CLSI 2023/2024 using standard antibiotic discs (HI media laboratories, Mumbai, India).

RESULTS

Of the total 16866 urine samples, 3485 samples showed growth (20.66%). Out of which, 2836 were Gram negative organisms (81.37%), 649 were Gram positive organisms (18.62%). The results are discussed below in Table 2:

Table 2: Distribution of Culture Positive Isolates (n=3485)

Isolates	Culture Positivity(n=3485)	%
Gram Negative	2836	81.37
Gram Positive	649	18.63
Total	3485	100

The demographic characteristics of the study population are presented in Table 3. Of the 3,485 patients included in the study, 1,185 (34.0%) were male and 2,300 (66.0%) were female. The largest

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proportion of patients belonged to the 51-70-year age group (1,359; 39.0%), followed by those aged 31-50 years (924; 26.5%), >71 years (627; 18.0%), and 18-30 years (575; 16.5%). The majority of patients were inpatients (3,347; 96.0%), while 138 (4.0%) were outpatients.

Table 3: Baseline Characteristics of the Study Population and Distribution of Urinary Isolates (n= 3485)

Variable	Category	Number of Patients (n)	Percentage (%)
Gender	Male	1185	34.0
	Female	2300	66.0
Age Group (years)	18–30	575	16.5
	31–50	924	26.5
	51–70	1359	39.0
	>71	627	18.0
Department	Inpatient	3347	96.0
	Outpatient	138	4.0

Among the 3,485 culture-positive urine samples, the highest proportion of isolates was obtained from the Urology Department (n=1,254; 35.98%), followed by General Medicine (n=493; 14.14%), Others (n=455; 13.05%), Nephrology (n=427; 12.25%), Obstetrics and Gynaecology (n=393; 11.27%), General Surgery (n=324; 9.29%), and the Intensive Medical Care Unit (n=139; 3.98%). The department-wise distribution of the isolates is shown in Figure 1.

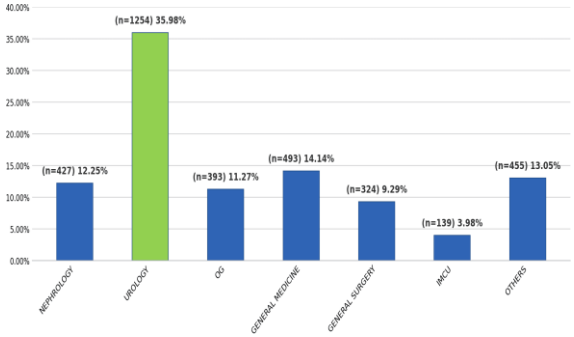


Figure 1: Department Wise Distribution of Positive Isolates(n=3485)

A total of 3,485 bacterial isolates were identified during the study period. *Escherichia coli* was the most frequently isolated organism, accounting for 1,395 isolates (40.02%), followed by *Enterococcus faecalis* (571, 16.38%) and *Klebsiella pneumoniae* (521, 14.95%). The distribution of the bacterial isolates and their respective proportions is presented in Table 4

Table 4: Organism Wise Distribution of Culture Positive Isolates (n=3485)

Organisms	No of Isolates(n=3485)	%
Escherichia Coli	1395	40.02
Enterococcus faecalis	571	16.38
Klebsiella Pneumoniae	521	14.95
Pseudomonas aeruginosa	373	10.70
Acinetobacter baumanii	264	7.57
Klebsiella Oxytoca	229	6.57
Staphylococcus aureus	78	2.23
Proteus mirabilis	22	0.63
Proteus vulgaris	13	0.37
Enterobacter Cloacae	17	0.48
Morganella Morganii	2	0.05
Total	3485	100

Among the 3,485 isolates included in the study, diabetes was the most frequently documented risk factor, occurring in 2,136 cases (61.29%). Other identified risk factors included urolithiasis (453, 13.0%), catheterization (156, 11.76%), hypertension (265, 7.6%), and urogenital surgery (227, 6.5%). The distribution of the identified risk factors is presented in Table 5.

Table 5: Risk Factors for UTI in Study Population(n=3485)

Risk Factors	Frequency (n=3485)	Percentage(%)
Diabetes	2136	61.29
Urolithiasis	453	13
Catheterization	156	11.76
Hypertension	265	7.6
Urogenital surgery	227	6.5

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The antimicrobial susceptibility profile of Enterobacterales shows variable resistance to Gentamicin (1276;58%) and Ciprofloxacin (1209;55%) and Ceftriaxone (902;41%), 1869 isolate showed susceptibility to Meropenem (85%) and Nitrofurantoin (1562;71%). The antimicrobial susceptibility distribution of Enterobacterales is presented in Figure 2.

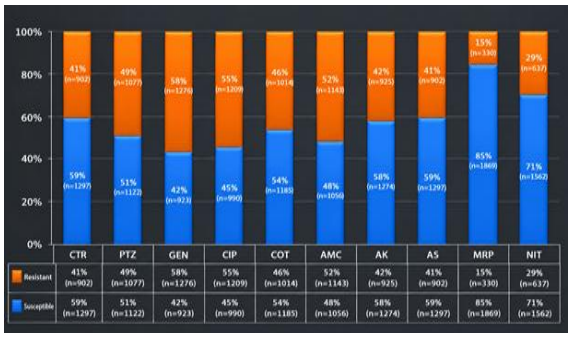


Figure 2: Antibiotic Susceptibility Pattern of Gram-Negative Isolates (Enterobacterales) (n=2199)

CTR- Ceftriaxone, PTZ- Piperacillin tazobactam, GEN-Gentamicin, CIP- Ciprofloxacin, COT-Cotrimoxazole, AMC- Amoxycillin Clavulanate, AK- Amikacin, AS- Ampicillin Sulbactam, MRP-Meropenem, NIT- Nitrofurantoin

The antimicrobial susceptibility patterns of *Pseudomonas aeruginosa* and *Acinetobacter baumannii* varied across the antibiotics tested. Among P. aeruginosa isolates, susceptibility ranged from 43%(n=373) for amikacin to 100%(n=373) for colistin, while susceptibility among A. baumannii isolates showed 100%(n=264) for colistin. The comparative antimicrobial susceptibility profiles of P. aeruginosa and A. baumannii are presented in Figure 3.

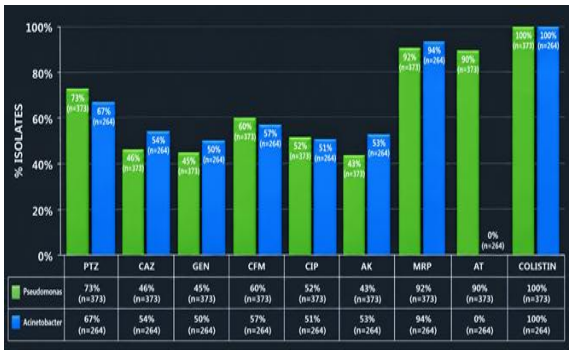


Figure 3: Antibiotic Susceptibility Pattern of Gram-Negative Bacilli (Non-Enterobacterales) (n=637)

PTZ-piperacillin tazobactam, CAZ- Ceftazidime, GEN- Gentamicin, CFM-Cefepime, CIP-Ciprofloxacin, AK-Amikacin, MRP- Meropenem, AT-Aztreonam

The antimicrobial susceptibility profile of *Staphylococcus aureus* isolates (n=78) demonstrated varying susceptibility to the tested antimicrobial agents. Susceptibility was 26% for penicillin(n=20) and cefoxitin(n=20), 47% for clindamycin(n=37), 58% for erythromycin (n=45), 45% for cotrimoxazole (n=35), and 65% for doxycycline(n=51). All S. aureus isolates were susceptible to vancomycin (n=78/78) and linezolid (n=78/78). The antimicrobial susceptibility pattern of S. aureus is presented in Figure 4.

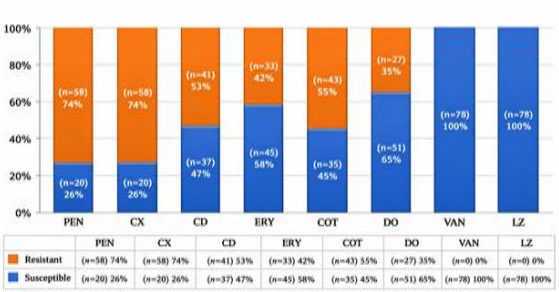


Figure 4: Antibiotic Susceptibility Pattern of Gram-Positive Cocci (Staphylococcus aureus) (n=78)

PEN-Penicillin, CX- Cefoxitin, CD-Clindamycin, ERY-Erythromycin, COT-Cotrimoxazole, DO-Doxycycline, VAN - Vancomycin, LZ-Linezolid

The antimicrobial susceptibility profile of *Enterococcus faecalis* demonstrated variable resistance patterns among the tested isolates. Resistance was observed to penicillin in 291 isolates (51%), gentamicin in 280 isolates (49%), vancomycin in 11 isolates (2%), and nitrofurantoin in 263 isolates (46%). All 571 isolates were susceptible to linezolid. The antimicrobial susceptibility distribution is presented in Figure 5.

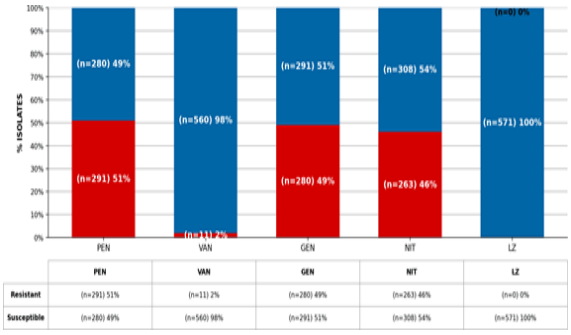


Figure 5: Antibiotic Susceptibility Pattern of Gram-Positive Cocci (*Enterococcus faecalis*) (n=571)

PEN-Penicillin, VAN-Vancomycin, GEN-Gentamycin, NIT-Nitrofurantoin, LZ-Linezolid.

DISCUSSION

Through the one-year retrospective study for the period (January 2024 to December 2024) a total number of 16866 non-duplicative urinary samples were tested, with a culture positivity of 3823 (22.66%).

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Women are known to have a higher risk of developing urinary tract infections (UTIs) owing to anatomical characteristics such as a shorter urethra and its close proximity to the rectum. In agreement with these observations, our study found a higher prevalence of UTIs among females (n=2300;66%) compared to males (n=1185;34%). Comparable findings have been documented by Kasew et al. and Sood et al., both of whom reported a greater occurrence of UTIs in females.[7,8]

Advancing age is recognized as an important risk factor for urinary tract infections (UTIs). In the present study, the participants ranged in age from 18 to 90 years, with the highest proportion of cases observed in the 51-70 years age group (n = 1359, 39%). These findings are in concordance with those of Raval et al,[9] from Vadodara, India, who similarly reported a greater prevalence of UTIs among older age groups. However, Mohapatra et al and Mechel T et al,[10,11] reported the highest prevalence of UTI among age groups 19-35 years and 21-30 years respectively.

In the present study, Gram-negative bacteria were the predominant causative agents of urinary tract infections, accounting for 81.38% (n=2836) of all isolates, whereas Gram-positive bacteria constituted 18.62% (n=649). Among the Gram-negative isolates, *Escherichia coli* was the most frequently identified pathogen (n=1395, 40.02%), followed by *Klebsiella pneumoniae* (n=521, 14.95%), *Pseudomonas aeruginosa* (n=373, 10.70%), and other Gram-negative organisms (n=547, 15.70%). Among the Gram-positive isolates, *Enterococcus faecalis* were the most common (n=537, 15.40%), followed by *Staphylococcus aureus* (n=78, 2.24%).

These findings are consistent with those of several recent studies like Kumar et al and Smitha et al,[12,13] that have similarly reported a predominance of Gram-negative Uro pathogens in UTIs. The persistent dominance of *Escherichia coli* may be attributed to its diverse virulence determinants and its ability to effectively colonize and infect the urinary tract in both community-acquired and healthcare-associated settings. Furthermore, the high prevalence of Gram-negative bacteria, particularly members of the Enterobacteriaceae family, can be explained by their efficient adherence to the uroepithelium through virulence factors such as adhesins, pili, fimbriae and P-fimbriae receptors, which facilitate colonization of the urogenital mucosa and subsequent infection,[14]

Diabetics are at higher risk of urinary tract infection due to the unfavorable metabolic changes such as elevated blood sugar levels, which suppress the immune system. In our study 61%(n=2136) UTI patients were diabetics, similar findings were found in study by Jagadeesan et al.[15]

The antibiogram analysis revealed that *Escherichia coli*, the predominant Uro pathogen, exhibited high levels of resistance to several commonly prescribed antibiotics. Most Gram-negative isolates demonstrated considerable resistance to first-line therapeutic agents such as ampicillin, ceftriaxone, norfloxacin, and cotrimoxazole, which are frequently used in the management of UTIs. Among the tested antibiotics, carbapenems showed the highest activity against *Escherichia coli* isolates, with a susceptibility rate of approximately (n=1869;85%), followed by nitrofurantoin (n=1562;71%). Other Gram-negative pathogens also displayed relatively good susceptibility to carbapenems, piperacillin-tazobactam, and ceftazidime.

Among the Gram-positive isolates, all *Staphylococcus aureus* strains were susceptible to linezolid and vancomycin (n=78;100% each). Similarly, *Enterococcus faecalis* demonstrated excellent susceptibility to linezolid (n=571;100%) and vancomycin (n=560;98%), while showing moderate susceptibility to nitrofurantoin (n=308;54%). These findings are in agreement with those reported by Sweih et al,[16] Chooramani et al,[17] and other contemporary studies.

The high level of antimicrobial resistance observed in this study reflects the growing challenge of antibiotic resistance in India, which has been reported to be substantially higher than that in several developed countries, including the United Kingdom, the United States, Australia, and South Africa.[18] Evaluation of susceptibility patterns using the WHO AWaRe (Access, Watch, and Reserve) classification revealed higher resistance rates among commonly used Access-group antibiotics, including penicillins, amoxicillin, gentamicin, and cotrimoxazole. In contrast, Reserve-group agents such as linezolid, vancomycin,
colistin and aztreonam retained comparatively better activity against the isolates. This trend mirrors global observations, where increasing resistance to frequently prescribed first-line antibiotics has led to greater dependence on broader-spectrum and reserve antimicrobials.

These findings emphasize the critical need for robust antimicrobial stewardship programs to optimize antibiotic use and preserve the effectiveness of existing therapeutic options. The declining efficacy of empirical antibiotics, particularly cotrimoxazole and norfloxacin, highlights the importance of continuous surveillance of local resistance patterns. Multiple factors contribute to the emergence and spread of antimicrobial resistance in India, including self-medication, over-the-counter availability of antibiotics without prescriptions, poor adherence to treatment regimens, inadequate patient awareness, financial constraints, irrational prescribing practices, insufficient monitoring of susceptibility trends and the initiation of antibiotic therapy before obtaining appropriate culture specimens.[19] Collectively, these factors promote inappropriate antibiotic use and accelerate the development of resistance.

Proper insertion and maintenance bundles are to be strictly followed to prevent Catheter associated Urinary Tract Infections (CA-UTI) since MDR organisms are being commonly reported in CA-UTI. The surveillance of CA-UTI in India has to be

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strengthened to monitor the trends in antimicrobial resistance.[20]

In line with the recommendations of the Infectious Diseases Society of America, empirical treatment of UTIs should be guided by local antimicrobial susceptibility data, antibiotic availability and individual patient characteristics to ensure optimal clinical outcomes while minimizing the risk of further resistance development.

The study has limitations that should be considered when interpreting the findings. First, the investigation was carried out at a single tertiary-care center and involved a relatively limited number of participants. Second, molecular analysis of antimicrobial resistance determinants was not undertaken. Incorporating molecular characterization in future studies could provide additional information regarding the genetic basis and mechanisms contributing to the resistance patterns identified in the present study.

CONCLUSION

Antimicrobial resistance among urinary pathogens represents a growing public health problem in India. The lack of adequate microbiology laboratory facilities in many parts of the country often limits routine culture-based diagnosis, leading to widespread empirical use of antibiotics. Incomplete or inappropriate antibiotic therapy for UTI may result in persistent or recurrent infection and may contribute to the selection of antimicrobial-resistant organisms. Therefore, culture-guided antimicrobial therapy and appropriate treatment duration are important to achieve clinical and microbiological eradication while minimizing antimicrobial resistance. Since antimicrobial susceptibility patterns vary over time and across healthcare settings, periodic assessment of the local antibiogram is essential for the selection of appropriate empirical therapy. The findings of the present study provide valuable information on the prevalent Uropathogens and their antimicrobial susceptibility profiles in our hospital. Such data can support evidence-based antibiotic prescribing, improve patient outcomes and help mitigate the increasing threat of antimicrobial resistance.

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