

Bacterial Profile and Antibiotic Resistance Patterns in Urinary Tract Infections at a Tertiary Care Hospital

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Abstract:

Introduction: One of the most prevalent illnesses in people is a urinary tract infection (UTI). Despite the availability and widespread usage of antimicrobial medications, bacterial UTIs have been on the rise. Antibiotic resistance is a serious global issue that has emerged in recent years as a direct result of the widespread and improper use of antimicrobial drugs.

Materials and Methods: The study was carried out over a 12-month period at Bhagwan Mahavir Institute of Medical Sciences among various age groups of both males and girls. Urine samples from 270 patients in the intensive care unit and various hospital and medical college units were collected. After being collected, all pee samples were processed for aerobic bacterial culture within an hour.

Results: Out of a total of 270 patients, 180 (66.66%) samples isolates were detected positive. The most common organism found positive was Escherichia Coli. Gram-negative isolates shown better sensitivity to nitrofurantoin and gentamicin whereas, Gram-positive isolates demonstrated good susceptibility to vancomycin and linezolid, and showed resistance to penicillin.

Conclusion: The pattern of resistance to commonly used antibiotics for treating UTI alerts us against indiscriminate usage of antibiotics.

Keywords: urinary tract infection, antibiotic resistance, bacteriological profile, gram negative, uropathogens.

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Introduction

Among the most frequent bacterial infections seen in clinical practice, urinary tract infections (UTIs) are a major cause of morbidity in all age groups [1]. They are responsible for a significant percentage of hospital admissions and outpatient visits. The treatment of UTIs has become more difficult due to the rising incidence of antibiotic resistance in uropathogens, which also presents a significant public health concern [2]. Current understanding of local bacterial profiles and resistance trends is necessary for empirical therapy, which is frequently started before culture findings are available [3]. This investigation was carried out in a tertiary care hospital to determine the prevalent bacterial infections that cause UTIs and to examine their patterns of antibiotic resistance.

Methods

Study Duration: The study was conducted over a period of 12 months from January 2025-December 2025 in Bhagwan mahavir institute of medical sciences.

Participants: A total of 270 patients were selected for this study.

This was a one-year retrospective laboratory-based study carried out in a tertiary care hospital's microbiology department. Included were all urine samples obtained from patients who had UTIs that were clinically suspected. Analyses were performed on samples exhibiting substantial bacteriuria ($\geq 10^5$ CFU/mL). Contaminated specimens and duplicate samples from the same patient were not included.

Standard microbiological methods were used to cultivate urine samples on MacConkey agar and CLED. Gramme staining, biochemical testing, and colony morphology were used to identify the bacterial isolates. The Kirby-Bauer disc diffusion method was used to test for antimicrobial susceptibility on Mueller-Hinton agar, and the Clinical and Laboratory Standards Institute (CLSI) criteria were followed in the interpretation of the results. Descriptive statistics were used to analyse the data, and the results were presented as percentages and frequencies.

Results

During the course of the study, 180 (36%) of the 270 urine samples that were processed revealed significant bacterial growth. UTIs were more prevalent in women, and the reproductive age group had the highest frequency. Total of 270 urine samples were processed from the patients out of which 180 was culture-positive as presented in table 1.

Table 1: Distribution of Urine Samples and Culture Positivity (n = 270)

Parameter	Number (n)	Percentage (%)
Total urine samples processed	270	100
Culture-positive samples	180	66
Culture-negative samples	90	34

Most of the isolates were gram-negative microbes. *Pseudomonas aeruginosa*, *Proteus* species, *Klebsiella* species, and *Escherichia coli* were the next most prevalent pathogens. *Staphylococcus saprophyticus* and *Enterococcus* species were

frequently isolated among Gram-positive organisms. Mostly samples were positive for *E. coli* followed by *Klebsiella* spp. The bacterial profile of all 180 positive samples was processed for the uropathogen isolates as shown in table 2.

Table 2: Bacterial Profile of Uropathogens Isolated

Organism	Number (n)	Percentage (%)
<i>E. coli</i>	90	50
<i>Klebsiella</i> spp.	36	20
<i>P. aeruginosa</i>	14	7.7
<i>Proteus</i> spp.	12	6.6
<i>Enterococcus</i> spp.	16	8.8
<i>Staphylococcus saprophyticus</i>	10	5.5
Total	180	100

Antibiotics that are often prescribed, such as ampicillin, cotrimoxazole, and fluoroquinolones, have high rates of resistance. Gram-negative isolates shown better sensitivity to nitrofurantoin and

gentamicin whereas, Gram-positive isolates demonstrated good susceptibility to vancomycin and linezolid, and showed resistance to penicillin.

Table 3: Antibiotic Resistance Pattern of Gram-Negative Isolates (n = 148)

Antibiotic	Resistant n (%)
Ampicillin	130 (82.5)
amoxicillin	94 (59.4)
Ciprofloxacin	108 (67.9)
Gentamicin	60 (38.6)
Nitrofurantoin	26 (16.7)
Cotrimoxazole	110 (68.9)

Table 4: Antibiotic Resistance Pattern of Gram-Positive Isolates (n = 32)

Antibiotic	Resistant n (%)
Penicillin	20 (83.5)
Erythromycin	14 (49.5)
Linezolid	2 (6.3)
Vancomycin	4 (18.3)
High-level gentamicin	10 (32.5)

Discussion

E. coli's dominance as the main uropathogen in this investigation is in line with results from other

national and worldwide investigations [4]. Anatomical and physiological reasons may be responsible for the increased incidence of UTIs in females [5]. The concerning degree of first-line

antibiotic resistance draws attention to the expanding issue of antibiotic abuse and the necessity of prudent antibiotic prescription practices [6].

Nitrofurantoin's continued usage as an efficacious empirical treatment for simple UTIs is supported by the preservation of sensitivity to the drug. Because it restricts treatment options, raises healthcare expenditures, and lengthens hospital stays, the high incidence of ESBL-producing pathogens is concerning. To direct empirical treatment and create antibiotic stewardship guidelines, regular tracking of antimicrobial resistance patterns is crucial [7].

Conclusion

This study shows that the most common cause of UTIs is gram-negative bacteria, especially *E. coli*. The significance of culture-based diagnosis and antimicrobial susceptibility testing was highlighted by the significant degree of resistance to widely used antibiotics that was found. Combating the growing issue of antimicrobial resistance requires the adoption of antibiotic stewardship programs and regular monitoring of local resistance patterns.

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