Bacterial Spectrum and Antibiotic Resistance Pattern in Urinary Tract Infection Cases at a Tertiary Care Hospital

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Abstract: ***Urinary tract infections are among the more frequent bacterial illnesses observed in clinical settings worldwide. Any component of the urinary system can get infected with a urinary tract infection (UTI). Mostly infections affect the lower urinary system, especially the urethra and bladder. A UTI is more common in women than in males. If the infection is limited to the bladder, it may be uncomfortable and bothersome. Material and Methods: A total of 156 samples were obtained from patients exhibiting clinical indications of UTI at a tertiary care hospital in Gorakhpur. Standard microbiological procedures were used to isolate and identify microorganisms. Antibiotic susceptibility testing was carried out using the Kirby-Bauer disc diffusion technique in accordance with CLSI guidelines. Results: Out of the 156 samples tested, 66 (42.30%) showed bacterial growth, 11 (7.05%) showed fungal growth, and 79 (50.64%) were culture-negative. E. coli antibiotic susceptibility patterns revealed a troubling trend of multidrug resistance, particularly with commonly used antibiotics such as ampicillin, ciprofloxacin, and third-generation cephalosporin's. Conclusion: The findings of this study highlight the necessity of continual observation of uropathogens, as well as their resistance patterns, in guiding appropriate empirical therapy. Such data are critical for developing antibiotic stewardship strategies to tackle the growing issue of antimicrobial resistance in community and hospital settings.***

Keywords: Urinary tract infection, Bacterial spectrum, Antibiotic resistance, Uropathogens, E. coli, tertiary care hospital

1.Introduction

Urinary tract infections are among the more frequent bacterial illnesses observed in clinical settings worldwide (Mancuso et al., 2023). Majority of microbiology labs receive urine samples most common than any other type of specimen; however, most urine cultures create results that are medically inconsequential (Hansen et al., 2022). Bacteria growing in the urinary tract can cause an infection known as UTIs (Flores-Mireles et al., 2015). UTI-causing bacteria typically come from feces (Nielsen et al., 2014). There are two type of UTIs: lower UTIs, which affect the bladder and urethra, and upper UTIs, which affect the kidney, pelvis, and ureter (Fihn, 2003). UTIS can be acquired in the group or in a hospital. Community-acquired UTI is the second most common microbiological infection in the community (Odoki et al., 2019). Nosocomial UTIs are urinary tract infections that occur 48 hours after hospitalization (Iacovelli et al., 2014). UTIs can be asymptomatic or symptomatic, with sing ranging from mild burning micturition to bacteremia, sepsis, or even death (Najar et al., 2009). Female are most likely than males to get UTIs (8 women to 1 man), mostly because of anatomical and physiological variations (Czajkowski et al., 2021). Old age, poor metabolic control, diabetic nephropathy, vascular problems, and diabetes mellitus are extra risk factors (Al-Shahrani et al., 2025). Mostly the organisms that cause UTIs come from the regular vaginal, perineal, and fecal flora. E. coli, Klebsiella sp., Pseudomonas aeruginosa, and Proteus sp. are the more common gram-negative organisms (Zhou et al., 2023). Among gram-positive bacteria, Enterococcus faecalis and S. aureus are more common (Keogh et al., 2024). The primary problem with current antibiotic treatments is that antimicrobial resistance is rapidly spreading in hospitals and communities (Ventola, 2015). Keeping this mind, the objective of this research is to identify the bacterial spectrum and antibiotic resistance trend in urinary tract infections in a tertiary care hospital.

2.Material and Methods

Study Design and Period – This prospective study received ethical clearance from the Institutional Research Committee and Institutional Ethical Committee on 8 march 2025(MGUG/GGIMS$MDAC/IEC(HS)/2025/012). It was conducted at the Department of Microbiology, Shri Gorakshnath Medical College Hospital and Research Centre, Mahayogi

Gorakhnath University Gorakhpur, Uttar Pradesh, over a period of six month (January 2025 to June 2025).

Data Collection- We evaluated 156 urine sample for antibiotic sensitivity which were received from various clinical departments with suspicion of UTI.

Inclusion criteria:

(1) Clean catch midstream urine from male and female of all age group attended at medicine and Obstetrics and Gynecology OPD/IPD.

(2) Patient with symptomatic conditions like pelvic pain, increased to urine, pain with urination, blood in urine, back pain, nausea, vomiting and fever etc. will be included in the study.

Exclusion criteria: (1) Patients resulting polymicrobial growth, micrococcus, >3 types of colonies formed, contamination, insignificant growth will be excluded from the study.

Laboratory Method

Specimen Processing:

1. To isolate the microbiological agents causing UTIs, urine specimens were semi-quantitatively cultured on blood agar and MacConkey agar media (HI media).

2. Conventional Biochemical tests were used to identify every bacterium that was isolated from urine in this investigation (Prasada Rao et al., 2022).

Antibiotic susceptibility testing (AST):

The test was performed by Kirby-Bauer disk diffusion method to find out which antibiotics are effective or not effective against the bacteria isolated from urine samples (Figure 1). It helps in identifying the appropriate antibiotic for treatment (Mohammad & Omer, 2018).

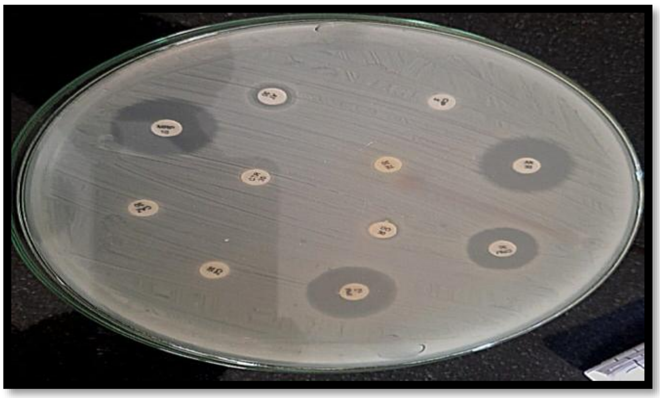

Figure 1: Antibiotic susceptibility testing

3.Results

Out of 156 samples were collected from clinically suspected patients of urinary tract infection, 66 samples showed bacterial growth, 11 samples showed fungus growth and the 79 samples were culture-negative Shown in (Table 1) and (Figure 2).

Table No. 1: According to Growth

Disease			
Total	Bacteria	Fungus	No growth
156	66 (42.30%)	11 (7.05%)	79 (50.64%)

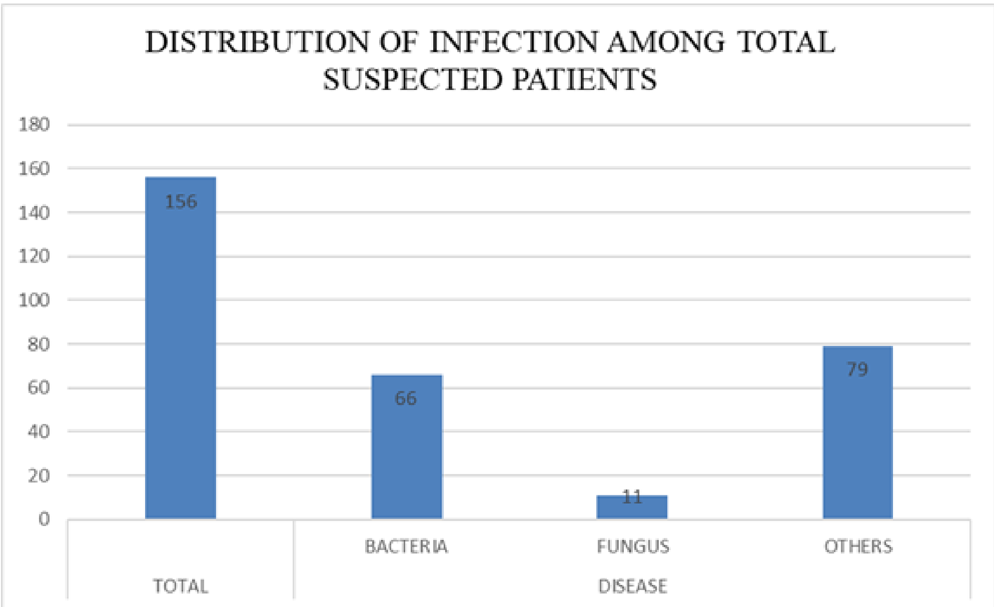

Figure 2: Column displaying the distribution among total suspected patient

Gender-wise distribution of urinary tract infection:

Female population: Similarly, among the female participants, (59.10%) were found to have a urinary tract infection.

Male population: Among the male participants include in the study, (40.90%) were found to be afflicted with urinary tract infection in shown (Table 2) and (Figure 3).

Table 2: Gender-wise distribution of urinary tract infection

Gender	Frequency	Percentage
Female	39	59.10%
Male	27	40.90%
Total	66	100.00%

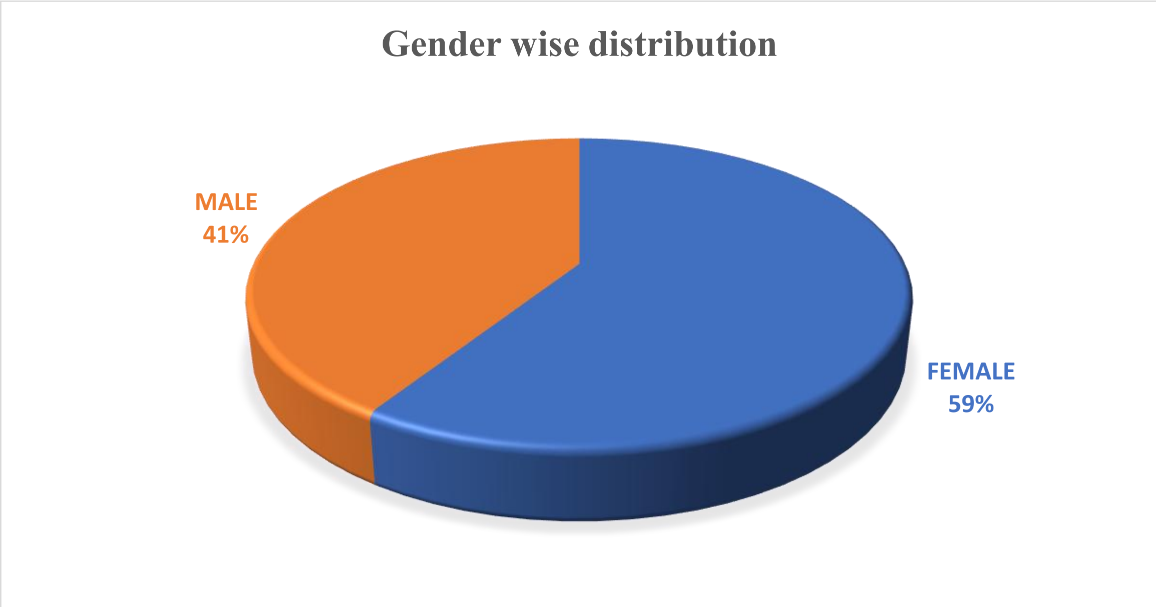

Figure 3: Pie gender-wise distribution of urinary tract infection

Isolated Species:

The most commonly isolated species were *Escherichia coli* (21 isolates), *Klebsiella species* (18), *Staphylococcus aureus* (11), *Proteus species* (6), *Enterobacter species* (4), *Pseudomonas aeruginosa* (2), *Coagulase-negative staphylococci* (*CoNS*) (2) and *Citrobacter koseri* (1) Were the most frequent number of bacterial species isolates.

Table 3: Bacterial species distribution in urinary tract infection

Bacteria spices	No. of isolates	Percentage
E. coli	21	31.82%
Klebsiella spp.	18	27.27%
Staphylococcus aureus	11	16.66%
Proteus spp.	6	9.09%
Enterobacter	4	6.06%
Pseudomonas aeruginosa	2	3.04%
CoNS	2	3.04%
Aeromonas	1	1.51%
Citerobacter koseri	1	1.51%
Total	66	100%

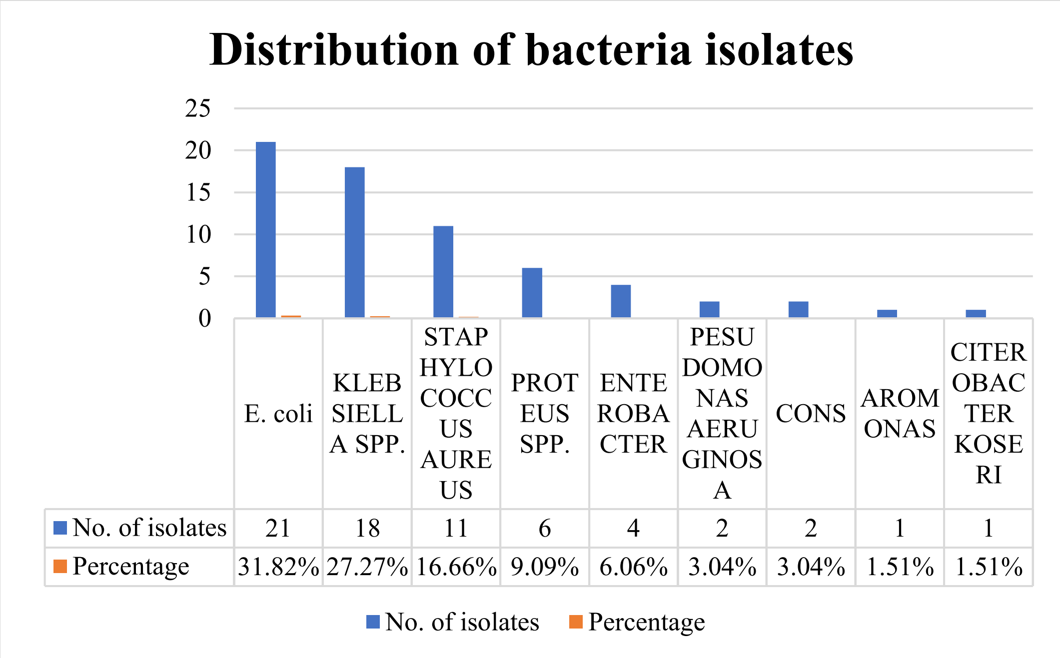

Figure 4: The distribution of bacterial species in the urinary tract infection instance is depicted by a bar graph

Isolates bacterial species and antibiotic resistance pattern: The most commonly isolated species were Escherichia coli (21 isolates), Klebsiella 49 species (18), Staphylococcus aureus (11), Proteus species (6), Enterobacter species (4), Pseudomonas aeruginosa (2), Coagulase-negative staphylococci (CoNS) (2) and Citrobacter koseri (1) Were the most frequent number of bacterial species isolates. The microbiological details of the bacteria that cause urinary tract infections and their resistance to antibiotics are displayed in Table 4 and 5.

Table no. 4: Antimicrobial resistance pattern of gram positive

	S. aureus (11)	CONS (2)
Levofloxacin (LE)	5 (45.45%)	1 (50.00%)
Vancomycin (VA)	3 (27.27%)	0 (00.00%)
Gentamicin (GEN)	2 (18.18%)	0 (00.00%)
Ciprofloxacin (CIP)	11 (63.63%)	1 (50.00%)
Clindamycin (CD)	6 (54.54%)	0 (00.00%)
Teicoplanin (TEI)	3 (27.27%)	1 (50.00%)
Doxycycline (DO)	6 (54.54%)	1 (50.00%)
Linezolid (LZ)	4 (36.36%)	0 (00.00%)
Tetracycline (TE)	4 (36.36%)	1 (50.00%)
Erythromycin (E)	6 (54.54%)	1 (50.00%)

Table no. 5: Antimicrobial resistance pattern of gram negative

	E. coli (21)	Klebsiella (18)	Proteus (6)	Enterobacter (4)	Pseudomonas (2)	Citrobacter (1)	*Aeromonas* (1)
Amikacin (AK)	3 (14.28%)	10(55.55%)	2(33.33%)	1 (25.00%)	1 (50.00%)	0 (00.00%)	0 (00.00%)
Gentamicin (GEN)	13(61.90%)	-	4(66.66%)	1 (25.00%)	-	0 (00.00%)	0 (00.00%)
Ofloxacin (OF)	13 (61.90)	-	-	-	1 (50.00%)	-	-
Ciprofloxacin (CIP)	17(80.95%)	10(55.55%)	2(33.33%)	2 (50.00%)	-	1 (100%)	1 (100%)
Levofloxacin (LE)	14(66.66%)	-	4(66.66%)	1 (25.00%)	-	-	-
Ceftriaxone (CTR)	13(61.90%)	11(61.11%)	4(66.66%)	2 (50.00%)	-	1 (100%)	-
Ceftazidime (CAZ)	14(66.66%)	14(77.77%)	4(66.66%)	2 (50.00%)	0 (00.00%)	1 (100%)	1 (100%)
Nitrofurantoin (NIT)	6 (28.57%)	-	-	-	-	-	-
Imipenem (IPM)	6 (28.57%)	11(61.11%)	1(16.66%)	1 (25.00%)	0 (00.00%)	0 (00.00%)	0 (00.00%)
Piperacillin-Tazobactam (PIT)	4 (19.04%)	-	-	-	-	-	1 (100%)
Cefepime (CPM)	16(76.19%)	6 (33.33%)	Not tested	2 (50.00%)	0 (00.00%)	-	1 (100%)
Meropenem (MRP)	4 (19.04%)	5 (27.77%)	1(16.66%)	0 (00.00%)	0 (00.00%)	0 (00.00%)	0 (00.00%)
Doxycycline (DO)	-	4 (22.22%)	-	-	-	-	-
Tigecycline (TGC)	-	-	-	-	-	0 (00.00%)	-

Data Analysis and Interpretation: Data analysis was performed using MS Excel, SPSS software and presented in number and percentage using graphs as well as tables. The sample size estimation was based on confidence level of 95% and a margin of error of 5%.

4.Discussion

In the present investigation of 156 urine samples obtained from clinically suspected UTI patients, 66 (42.40%) indicate substantial bacterial growth. 11 (7.10%) showed fungal growth, 79 (50.74%) were culture negative. These findings demonstrate that UTIs are a common clinical condition not all presumed cases are caused by bacteria emphasizing the need of receiving a proper laboratory diagnosis before beginning therapy (Bitew et al., 2022). Escherichia coli was the most commonly isolated bacteria (32%), follow by Klebsiella spp. (27.50%), Staphylococcus aureus (16.70%), Proteus spp. (9.11%), Enterobacter (6.10%), Pseudomonas aeruginosa (3.50%), Coagulase-negative Staphylococcus (CoNS) (3.40%), Aeromonas (1.61%) and Citrobacter koseri (1.61%). This distribution is consistent with previous study found that identified E. coli as the leading cause of UTIs (Guentzel, 1996). An examination of antibiotic susceptibility patterns revealed that E. coli was highly resistant to Cefepime (76.19%) and Ciprofloxacin (80.95%). In contrast, Meropenem (19.04%), and Piperacillin-Tazobactam (19.04%) showed lower resistance rates (Tsai et al., 2023). This shows that carbapenems and some combinations of beta-lactam/beta-lactamase inhibitors are still effective against E. coli. Additionally, Klebsiella species have demonstrated strong resistance to Ciprofloxacin (55.55%) and Ceftazidime (77.77%). The increased efficacy of Doxycycline, Meropenem, and Cefepime suggests that these drugs may still be useful in treating infections caused by this bacterium. [Mathi et al., 2008]. Staphylococcus aureus demonstrated significant resistance to Ciprofloxacin (63%), Clindamycin (54%), and Doxycycline (54%), whereas Vancomycin, Teicoplanin, and Linezolid remained effective, indicating that glycopeptides and oxazolidinones are reliable choices for treating infections caused by this pathogen (Ejaz et al., 2024; Wi et al., 2025). 50% of Coagulase-Negative Staphylococci (CoNS) were resistant to erythromycin, teicoplanin, ciprofloxacin, levofloxacin, and doxycycline (Ma et al., 2011). The importance of carbapenems in treating multidrug-resistant strains was highlighted by the fact that Proteus species exhibited good sensitivity to Imipenem, Meropenem, and Piperacillin-Tazobactam (each with 16% resistance), but high resistance to cephalosporins such as Ceftazidime and Ceftriaxone (66% each) (Elshamy & Aboshanab, n.d.). The Enterobacter spp. were completely resistant to tetracycline and 50% resistant to numerous other medicines including ceftriaxone and ciprofloxacin. Positive reactivity to doripenem, imipenem and total sensitivity to tobramycin, indicated the utility of aminoglycosides and carbapenems in treating severe infections (Davin-Regli et al., 2019). Pseudomonas spp. were totally killed by the majority tested antibiotics, including carbapenems and third-generation cephalosporins, although resistance to Aztreonam and Ofloxacin was detected outlining the significance of careful antibiotic selection based on sensitivity testing (AlBahrani et al., 2023). Finally, gentamicin, amikacin, meropenem and tigecycline proved to have been completely efficient against Citrobacter koseri. It exhibited 50% resistance to multiple commonly used antibiotics, including ceftriaxone, ceftazidime, and ciprofloxacin. This shows the growing issue of resistance, especially in diseases that are rarely isolated (Huang et al., 2023). In the end, the study shows that common uropathogens are extremely resistant to conventional antibiotics like third-generation cephalosporins and fluoroquinolones. Carbapenems and certain aminoglycosides continue to be viable treatment options, although regular supervision and judicious prescription are essential (Kot et al., 2021).

5.Conclusion

This study indicates the high prevalence of the urinary tract infections (UTIs) in healthcare Settings, with bacterial growth detected in 42.30 % of suspected cases. Females were more commonly affected than males, which is consistent with realized anatomical risk factors. The most commonly isolated bacteria were Escherichia coli, followed by Klebsiella, Staphylococcus aureus, and Proteus species. Antibiotic susceptibility patterns confirmed a concerning trend of multidrug resistance, especially with routinely used antibiotics such as ampicillin, ciprofloxacin, and third-generation cephalosporins. However, carbapenems (such as imipenem and meropenem) and aminoglycosides (such as amikacin and gentamicin) continued to be most effective against a large number of bacterial isolates.

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