

Antimicrobial Susceptibility Pattern of Uropathogens Isolates from a Tertiary Hospital in Bangladesh

Khandaker M¹, Refat MNH², Ferdouse F³, Shormin M⁴, Ferdous S⁵, Hassan M⁶

Abstract :

Background: Urinary tract infection (UTI) causes considerable morbidity and mortality worldwide, predominantly in developing countries like Bangladesh. The empirical selection of antibiotics for the treatment of urinary tract infections frequently deviates from the drug susceptibility of the pathogens. **Objective:** This study aimed to explore the antimicrobial susceptibility pattern of uropathogens. **Materials and methods:** Mid stream urine samples from 1502 patients of suspected UTI were collected, cultured and subjected to appropriate biochemical tests. Samples were collected and tested at the microbiology laboratory of Shaheed Monsur Ali Medical College, Uttara, Dhaka from August 2022 to July 2023. The antimicrobial sensitivity test was carried out by disc diffusion technique using Muller- Hinton agar. Urine samples were cultured positive with a colony count equal or more than 105/ml. **Results:** Overall males to female ratio was 1:1.44. The predominant organisms isolated were *Escherichia coli* (78.5%) followed by *Pseudomonas Spp.* (6.2%), *Klebsiella spp.* (6.2%), *Staphylococcus aureus* (5.3%) and *Enterococcus* (4.7%). The majority of uropathogen is isolated were sensitive to imipenem (94%) followed by meropenem(85%), nitrofurantoin(86%) whereas, high level resistance was seen to azithromycin, ceftriaxone, cefixime followed by ciprofloxacin, cefuroxime in decreasing order of frequency. **Conclusion:** Various microorganisms are responsible for UTI explored in this study. Though antimicrobial resistance has already emerged against many antibiotics this study findings will guide clinicians to initiate the empiric antibiotic therapy for UTI.

Keywords: Antimicrobial Susceptibility, Uropathogens, Tertiary Hospital, Bangladesh

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Introduction:

Urinary tract infections (UTIs) are anticipated to affect 405 million people globally in both community and hospital settings. Approximately 0.23 million UTI-related deaths occurred in 2019, accounting for 5.2 million disability-adjusted life years (DALYs) ⁽¹⁾. The urinary tract infections that cause cystitis, pyelonephritis, and urosepsis are typically classified according to their location. Both Gram-positive and Gram-negative bacteria, as well as some fungi, can cause urinary tract infections. In all clinical settings, *Escherichia coli* is responsible for the majority of isolated pathogens; however, the local epidemiology of pathogens that cause infection might differ significantly ^(2,3). Urinary tract infection is applied to a variety of clinical condition ranging from asymptomatic presence of bacteria in the urine to severe infection of the kidney with resultant sepsis ⁽⁴⁾. It is one of the most common bacterial infections encountered by clinicians in developing countries ⁽⁵⁾. Most of urinary tract infections are caused by Gram-negative bacteria like, *E. Coli*, *Klebsiella* species, *Proteus mirabili*, *Pseudomonas aeruginosa*, *Acinetobacter*, and *Serratia*. 90% of UTI cases are caused by Gram-negative bacteria while only 10% of the cases are caused by Gram positive bacteria. Gram-positive bacteria include *Enterococcus*, *Staphylococcus*, and *Streptococcus agalactiae* ⁽⁶⁾.

UTIs are a major health problem in Bangladesh, causing recurrent infections, frequent treatment failure and considerable morbidity ^(7,8). UTI is also one of the main reasons for misuse of antibiotics leading to the escalating burden of antimicrobial resistance ⁽⁹⁾. A recent study carried out in Bangladesh in 2018 has shown that both *E. coli* and *Klebsiella* spp. were predominantly resistant to penicillin (85%, 95% respectively) followed by macrolide (70%, 76%), third-generation cephalosporins (69%, 58%), fluoroquinolones (69%, 53%) and carbapenem (5%, 9%) ⁽¹⁰⁾. The multi-drug resistant uropathogens are increasing over time.

Reducing the overuse and misuse of antibiotics requires constant monitoring of the patterns of antibiotic resistance and the etiology of infections in order to select appropriate antibiotics for empirical therapy. The study was undertaken to analyze the uropathogens and their antimicrobial susceptibility patterns, as it would be a useful guide for clinicians initiating the empiric antibiotic therapy.

Materials and Methods :

This study was conducted on 1502 untreated patients with clinical symptoms of UTI referred to Microbiology Lab in Shaheed Monsur Ali medical College and Hospital during the period from August 2022 to July 2023. Clean catch midstream urine samples (MSU) were collected in sterile disposable containers (4-5 ml) and transported immediately to the laboratory. Urine specimens were subjected to general urine examinations using direct microscopy for white blood cell (WBC) counting. Urine samples were cultured on 5% blood agar, MacConkey, and Cystine-lactose-electrolyte deficient agar (CLED) using calibrated loops for semi-quantitative method and incubated in both aerobic and anaerobic conditions for 24 hours at 37°C. Cultures without any colony at the end of 24h incubation were further incubated for 48h. Samples with colony count equal or more than 10⁵CFU/ml were considered positive. The isolates were identified and confirmed using standard microbiological methods including Gram staining, colony morphology on media, growth on selective media, lactose and mannitol fermentation, H₂S production, catalase, oxidase, coagulase, indole, and citrate utilization, and urease test.

Results :

In this study, urine samples were taken from 1502 patients of suspected urinary tract infections. The mean age of the patients was 32 years (± 21.3 SD). Most of them were female (59%). 417 (27.8%) of them were belongs to ≤ 18 Years, 620 (41.3%) belongs to 19-40 years of age group, 306 (20.4%) belongs to the age

group of 41-60 years and rest 159 (10.6%) belongs to the age group of ≥ 60 years. Bacteria were isolated for 339 samples out of 1502 urine culture samples are distributed in the Table no 1. Of them Gram positive organisms isolates was Staph. Spp. (5.3%), the most Gram negative organisms isolates was E. coli (78.5%).

Table I: Type, number and percentage of blood culture isolates (n=339)

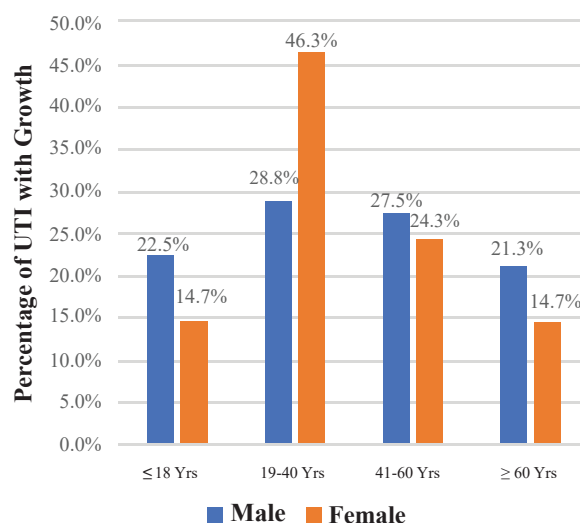
Organism	Number (%) of total no. of isolates
Gram Negative	
E. coli	266 (78.5%)
Pseudomonas	21 (6.2%)
Klebsiella	12 (3.5%)
Enterobacter	1 (0.3%)
Gram Positive	
Staph. Spp	18 (5.3%)
Enterococci	16 (4.7%)
Streptococci	5 (1.5%)
Total	339 (100%)

Bacterial isolates were found mostly in females but in both sexes significant growth (46.3% in female and 27.8% in male) was noticed between the age group of 19-40 years (Figure-1). The distribution of various bacterial isolates with antibiotic sensitivity are shown in Table 2. For E.coli was sensitive to imipenem (94%), amikacin (90%), nitrofurantoin (86%), gentamicin (85%), meropenem (85%), netilmicin (78%), ciprofloxacin (71%). Pseudomonas found sensitive to imipenem (90%), amikacin (81%), meropenem(71%), nitrofurantoin (67%), gentamicin (67%), ciprofloxacin(62%), ceftazidime(62%).Staphylococcus Spp found sensitive to vancomycin (78%), nitrofurantoin (78%), linezolid (72%), imipenem (67%). Enterococci was found sensitive to Vancomycin (94%), linezolid (88%), imipenem (81%), nitrofurantoin (75%), teicoplanin (75%).

Table 2: The distribution of bacterial isolates with antibiotic sensitivity

Name of the Antibiotic	Organism Specific Sensitivity (%)						
	E. coli	Enterobacter	Enterococci	Klebsiella	Pseudomonas	Staph. Spp	Streptococci
Amikacin	90	0	56	67	81	28	0
Amoxicilin	0	0	25	0	14	11	0
Amoxyclav	0	0	0	0	0	6	0
Ampicillin	10	100	44	17	24	44	80
Azithromycin	3	0	0	0	10	11	0
Aztreonam	58	0	0	0	10	11	0
Cefixime	36	100	0	58	19	6	0
Ceftazidime	64	0	0	42	62	6	0
Ceftriaxone	64	100	0	67	48	6	40
Cefuroxime	49	100	0	67	19	28	60

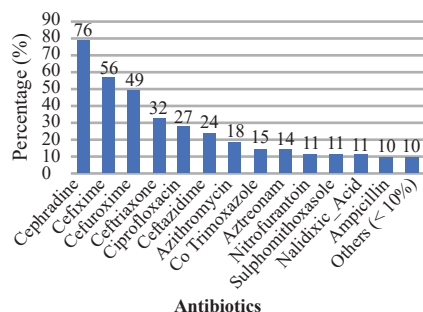
Figure-1: Sex Distribution of Bacterial Isolates



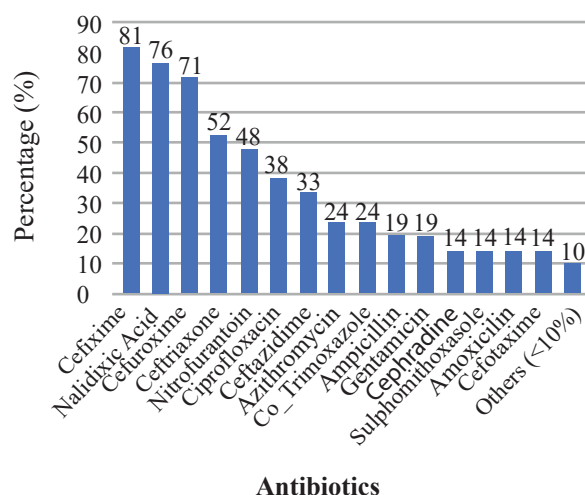
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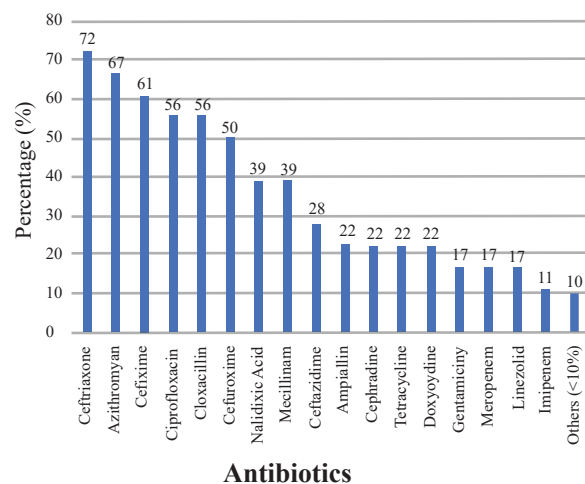
Co_Trimoxazole	24	0	19	8	24	11	0
Cephadrine	7	100	0	0	0	17	0
Chloramphenicol	0	0	44	0	0	22	0
Ciprofloxacin	71	0	0	75	62	17	40
Cefipime	5	0	0	25	0	0	0
Cefaclor	3	0	0	0	0	6	0
Cloxacillin	1	0	44	0	5	17	0
Doxycycline	4	0	6	8	0	11	20
Erythromycin	0	0	44	0	0	11	0
Gentamicin	85	100	81	92	67	28	0
Imipenem	94	100	19	92	90	67	80
Levofloxacin	29	0	88	8	29	0	0
Linezolid	1	0	6	0	0	72	80
Mecillinam	18	100	69	67	14	11	0
Meropenem	85	0	0	75	71	44	100
Mupirocin	0	0	0	0	0	0	20
Nalidixic_Acid	6	100	0	25	5	11	0
Netilmicin	78	0	75	58	67	0	0
Nitrofurantoin	86	100	6	58	48	78	60
Pipe_Tazobactam	69	0	0	8	57	6	0
Polymyxin_B	0	0	31	0	5	0	0
Sulphomithoxasol	27	0	0	25	24	0	20
Tetracycline	6	100	50	8	0	28	0
Tigecycline	0	0	94	0	0	11	0
Vancomycin	0	0	6	0	0	78	80
Colistin	67	0	56	8	62	0	0
Fosfomycin	0	0	75	0	0	0	0
Teicoplanin	0	0	38	0	0	22	80
Penicillin	0	0	0	0	0	0	60
Tobramycin	8	0	0	42	5	0	0
Rifampicin	0	0	0	0	0	17	0

Figure 2: Antibiotic Resistance for E. coli

Out of 266 E.coli (Figure-2) isolates, resistance was found for cephradine (79%), cefixime (56%), cefuroxime (49%), ceftriaxone (32%), ciprofloxacin (27%), ceftazidime (24%) and azithromycin (18%). Out of 12 Klebsiella isolates, resistance was found for azithromycin (100%), ampicillin (58%), ceftriaxone (33%), nitrofurantoin (33%), cefixime (33%), cefuroxime (25%) and cotrimoxazole (25%).

Figure 3: Antibiotic Resistance for pseudomonas

Out of 21 *Pseudomonas* (Figure-3) isolates, resistance was found for cefixime (81%), nalidixic acid (76%), cefuroxime (71%), ceftriaxone (52%), nitrofurantoin (48%), ciprofloxacin (38%), ceftazidime (33%), azithromycin (24%), co-trimoxazole (24%) and ampicillin (19%).

Figure 4: Antibiotic Resistance for Staph spp

Out of 21 *Staph.Spp* (Figure-4) isolates, resistance was found for ceftriaxone (72%), azithromycin (67%), cefixime (61%), ciprofloxacin (56%), cloxacillin (56%), nalidixic Acid (56%), mecillinam (39%) and ceftazidime (28%). Out of 5 *Streptococci Spp.* isolates resistance was found for azithromycin (100%),

ceftriaxone (60%), ciprofloxacin (60%), doxycycline (60%), erythromycin (60%), cefuroxime (40%) and sulphomithoxazole (40%).

Discussion :

The majority (88.5%) of uropathogens in this study were Gram negative and mostly caused by the *E. coli* (78.5%). In another study conducted in Bangladesh *E. coli* (51.6%) was also found as the predominant causative pathogen⁽¹⁰⁾. In this study, bacterial isolates were found mostly in female but in both sex significant growth (46.3% in female and 27.8% in male) was noticed between the age group of 19-40 years that indicates that individuals in the reproductive age group, irrespective of sex, are more likely to develop UTI. Woman is at great risk for UTI primarily because of the significantly shorter urethra and closer proximity to the rectum. The female genitalia may become colonized with pathogenic bacteria that can more easily enter the urethra. In addition, woman lack the bacteriostatic protection that prostatic secretions offer the male⁽¹¹⁾. *E. coli* found sensitive to imipenem (94%), amikacin (90%), nitrofurantoin (86%), gentamicin (85%), meropenem (85%), and ciprofloxacin (71%). *Pseudomonas* found sensitive to imipenem (90%), amikacin (81%), meropenem (71%), nitrofurantoin (67%), gentamicin (67%), ciprofloxacin (62%) and ceftazidime (62%). *Staphylococcus spp.* found sensitive to vancomycin (78%), nitrofurantoin (78%), linezolid (72%) and imipenem (67%). *Enterococci* was found sensitive to vancomycin (94%), linezolid (88%), imipenem (81%) and nitrofurantoin (75%). Uropathogens isolates in this study were found to be susceptible to imipenem, nitrofurantoin and amikacin as reported in other studies, whereas Gram negative organisms were found sensitive to amikacin^(12,13). *E. coli* isolates was predominantly resistant to cephradine (79%) and cefixime (56%),

Klebsiellatoazithromycin (100%) andampicillin (58%), Pseudomonas tocefexime (81%) and nalidixic acid (76%). On the other hand Staphylococci and Streptococci Spp.was predominantly resistant to ceftriaxone andazithromycin which were also noted in other studies ^(10,12,14).

Conclusion :

The rise in drug-resistant bacteria poses a severe threat to public health and presents a significant therapeutic challenge to medical professionals globally, but especially in our nation. Only by developing and strictly enforcing local therapeutic standards based on the susceptibility patterns of infections found in our own community will the problem be adequately addressed. Furthermore, ongoing surveillance and monitoring of antimicrobial resistance could facilitate the development of our protocol of care.

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