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RESEARCH ARTICLE

Prevalence and Antibiotic Resistance Patterns of Uropathogenic Bacteria in Urine Samples: A Study from Bangladesh

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ABSTRACT

Introduction: Urinary tract infections (UTIs) are one of the most common bacterial infections globally, with Escherichia coli being the predominant causative agent. The rise in antimicrobial resistance (AMR) among uropathogens, particularly to commonly prescribed antibiotics, has become a critical public health concern. In Bangladesh, inappropriate use of antibiotics has contributed to the emergence of multidrug-resistant (MDR) pathogens, making it essential to monitor local resistance patterns. This study aims to isolate and identify the bacterial pathogens responsible for UTIs and assess their antimicrobial susceptibility profiles.

Methodology: This cross-sectional study was conducted at a local hospital in Bangladesh from November 2023 to May 2024. A total of 50 urine samples were collected from patients with clinical symptoms of UTIs. Isolates were identified using standard microbiological methods, including Gram staining and biochemical tests. The antimicrobial susceptibility of the isolates was evaluated using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar. The antibiotics tested included imipenem, doxycycline, ciprofloxacin, cefoxitin, ampicillin, and others. Extended-Spectrum Beta-Lactamase (ESBL) and AmpC beta-lactamase production were also determined.

Results: Out of 50 urine samples, 40 (80%) were culture-positive. *Escherichia coli* was the most prevalent pathogen, accounting for 61.1%, followed by *Klebsiella pneumoniae* (33.3%). Both pathogens showed 100% sensitivity to imipenem, but exhibited varying levels of resistance to other antibiotics, with *E. coli* showing 16.7% resistance to

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ampicillin. ESBL production was observed in 44.4% of isolates, with *K. pneumoniae* showing higher rates (66.7%). AmpC beta-lactamase production was noted in 33.3% of *E. coli* isolates.

Conclusion: The study highlights the dominance of *E. coli* and *K. pneumoniae* in UTIs, with significant AMR, especially to beta-lactam antibiotics. Continuous surveillance and appropriate antimicrobial stewardship are critical to managing rising resistance and improving treatment outcomes.

Keywords: Urinary Tract Infection; *Escherichia coli; Klebsiella pneumoniae*; Antimicrobial Resistance; ESBL; AmpC beta-lactamase

1. Introduction

Urinary tract infections (UTIs) are among the most common and widespread bacterial infections globally, affecting approximately 150 million individuals annually. These infections are a significant cause of morbidity and contribute to substantial healthcare burdens worldwide[1]. In particular, UTIs are a pressing health issue in low- and middle-income countries like Bangladesh, where they lead to a high rate of outpatient visits and frequent antibiotic prescriptions. UTIs not only impact the quality of life of affected individuals but also increase healthcare costs, placing a strain on already overburdened healthcare systems[2]. Women are especially vulnerable to UTIs due to their unique anatomical and physiological features, with studies indicating that as many as one-third of women experience at least one episode of UTI during their lifetime[3]. While UTIs can vary in severity, ranging from uncomplicated infections to more complex, complicated forms, the rising incidence of antimicrobial resistance (AMR) has made these infections increasingly difficult to manage[4].

The most frequent causative agent of UTIs is *Escherichia coli (E. coli),* responsible for approximately 80% of community-acquired and 40% of healthcare-associated cases. *E. coli* is a gram-negative bacterium known for its ability to adhere to the urogenital tract, a key virulence factor that facilitates its survival and persistence within the urinary system[5]. In addition to *E. coli*, other uropathogens such as *Klebsiella pneumoniae, Proteus mirabilis, Pseudomonas aeruginosa*, and *Staphylococcus saprophyticus* contribute to the global UTI burden[6]. While *E. coli* remains the most common cause of both uncomplicated and complicated UTIs, infections caused by these other organisms have gained attention due to their unique characteristics, particularly their ability to form biofilms and their potential to cause complicated infections, such as pyelonephritis or sepsis[7].

The emergence of antimicrobial resistance (AMR) among uropathogens, particularly *E. coli* and *Klebsiella pneumoniae*, poses a major challenge to the effective treatment of UTIs. Over the past several decades, the widespread and often inappropriate use of antibiotics has led to the selection and dissemination of resistant strains. *E. coli*, for example, has developed resistance to a broad spectrum of commonly used antibiotics, including beta-lactams, fluoroquinolones, and aminoglycosides. One of the most concerning developments in UTI treatment is the rise of Extended-Spectrum Beta-Lactamase (ESBL)-producing *E. coli* strains[8]. These strains are resistant to beta-lactam antibiotics, such as penicillins and cephalosporins, rendering many first-line treatment options ineffective. Additionally, multi-drug resistant (MDR) strains of *Klebsiella pneumoniae* and *Pseudomonas aeruginosa* are becoming increasingly prevalent, further complicating the management of UTIs. This alarming trend of AMR has been exacerbated by factors such as the overuse and misuse of antibiotics, inadequate infection control measures, and the inappropriate self-medication practices prevalent in many regions, including Bangladesh[9].

In Bangladesh, the prevalence of AMR is particularly high, with ESBL-producing strains of *E. coli* and *Klebsiella pneumoniae* being a major cause of treatment failure. Risk factors for acquiring infections with these resistant pathogens include diabetes, advanced age, previous hospitalization, urinary catheterization, and prior antibiotic use[9]. Moreover, the absence of comprehensive surveillance systems to track antimicrobial resistance patterns in uropathogens has created a gap in knowledge regarding local AMR trends. This lack of regional data makes it difficult to develop targeted treatment protocols, and healthcare providers are often forced to rely on empirical antibiotic therapies that may not be effective against resistant strains. Therefore, there is a pressing need for continuous monitoring of AMR trends, especially in developing countries like Bangladesh, where healthcare infrastructure may be limited, and resources for combating AMR are scarce[10].

The aim of this study is to isolate and identify bacterial pathogens responsible for urinary tract infections from urine samples and assess their antibiotic susceptibility profiles. The research focus on key uropathogens like *E. coli* and *Klebsiella pneumoniae*, providing an updated overview of local antimicrobial resistance (AMR) trends. The findings support clinical decision-making, guide antibiotic therapy, and help prevent the spread of resistant pathogens, thereby improving patient outcomes and contributing to regional AMR knowledge.

2. Methodology

2.1. Study design and setting

This study was designed as a descriptive, cross-sectional research aimed at isolating and identifying bacterial pathogens responsible for urinary tract infections (UTIs) and assessing their antimicrobial susceptibility profiles. The research was conducted in a microbiology laboratory over a period from November 2023 to May 2024. The study focused on urine samples collected from patients presenting with clinical symptoms of UTIs.

2.2. Sample collection and patient selection

A total of 50 urine samples were collected from patients attending the hospital's outpatient department, presenting with clinical symptoms indicative of UTI. Samples were obtained from both male and female patients across various age groups. Patient selection was based on their willingness to participate, and informed written consent was obtained before sample collection. The study only included patients who consented to participate, while those who declined were excluded.

2.3. Urine sample handling and inoculation

Urine samples were collected as midstream urine, the most concentrated and suitable for microbiological examination. The samples were transported to the microbiology laboratory in sterile, leak-proof containers and were labeled with patient details such as name, identification number, and time of collection. In the laboratory, the urine samples were gently swirled to ensure even distribution of any microorganisms. They were then streaked onto CLED (Cystine Lactose Electrolyte Deficient) and MacConkey agar plates using a 0.001 ml disposable loop. The plates were incubated at 37°C for 18-24 hours, and the growth was monitored for bacterial colonies.

2.4. Bacterial identification

Following incubation, the bacterial colonies were observed for growth characteristics and were further identified using Gram staining, which provided the first indication of whether the bacteria were Gram-positive or Gram-negative. Additionally, several biochemical tests were conducted to confirm the identity of the bacterial pathogens. These tests included the Triple Sugar Iron (TSI) test, Citrate test, and Motility Indole Urease (MIU) test. The TSI test indicated the bacterium’s ability to ferment sugars and produce gases, the

Citrate test confirmed the ability to utilize citrate as a sole carbon source, and the MIU test assessed motility, indole production, and urease activity.

2.5. Antimicrobial susceptibility testing (AST)

The antimicrobial susceptibility of the bacterial isolates was determined using the Kirby-Bauer disk diffusion method, which involved placing antibiotic-impregnated disks onto agar plates inoculated with the bacteria. Mueller-Hinton agar was used for this purpose, as it supports the growth of a wide range of bacteria. After inoculation, the plates were incubated at 37°C for 18-24 hours, and the inhibition zones around the antibiotic disks were measured. The results were interpreted following the standards set by the Clinical and Laboratory Standards Institute (CLSI), which categorizes the bacteria as resistant, intermediate, or susceptible to the tested antibiotics.

2.6. Ethical considerations

Ethical approval was sought and granted before the study commenced. Written informed consent was obtained from all participants, ensuring they were fully aware of the study's objectives and voluntarily agreed to take part. All patient data was handled with confidentiality, and personal identifiers were removed to protect patient privacy throughout the research process.

2.7. Data analysis and categorization

After all samples were processed and the data collected, results were categorized based on the gender, age group, organisms isolated, and their respective antibiotic resistance patterns. These data were then analyzed to assess the frequency of different bacterial pathogens and determine their resistance profiles to various antibiotics.

3. Results

Table 1 shows the distribution of cultured positive and negative samples from 50 urine samples collected. 36 samples (72%) yielded positive bacterial growth, while 14 samples (28%) had no bacterial growth. The most frequently isolated pathogens were *Escherichia coli* and *Klebsiella pneumoniae*.

Table 1. Cultured positive and negative organisms.

Results	Number (n=50)	Percentage (%)
Cultured Positive	36	72%
Cultured Negative	14	28%

This table presents the distribution of bacterial species isolated from 36 positive urine samples. The most prevalent pathogen was *Escherichia coli*, accounting for 61.1% of the isolates, followed by *Klebsiella pneumoniae* (33.3%). Other less common organisms included *Proteus mirabilis* (5.5%), *Pseudomonas aeruginosa* (2.8%), and *Staphylococcus saprophyticus* (2.8%). The findings highlight the dominance of Escherichia coli as the primary uropathogen in urinary tract infections, with *Klebsiella pneumoniae* also being a significant contributor

Table 2. Prevalence of organisms in the study population.

Bacteria	No. of Isolates (n=36)	Percentage (%)
Escherichia coli	22	61.1%
Klebsiella pneumoniae	12	33.3%
Proteus mirabilis	2	5.5%

Bacteria	**No. of Isolates (n=36)**	**Percentage (%)**
Pseudomonas aeruginosa	1	2.8%
Staphylococcus saprophyticus	1	2.8%

Table 2. (*Continued*)

Table 3 presents the antibiotic sensitivity profiles of the *Escherichia coli* and *Klebsiella pneumoniae* isolates. Imipenem was universally effective, with both organisms exhibiting 100% sensitivity. The table also illustrates moderate resistance to other antibiotics, such as Ampicillin, Cefotaxime, and Cefuroxime.

Table 3. Antibiotic sensitivity of isolated organisms.

Antibiotic	***Escherichia coli* (n=22)**	***Klebsiella pneumoniae* (n=12)**
Imipenem (IMP)	100%	100%
Doxycycline (DO)	75%	100%
Ciprofloxacin (CIP)	68.2%	100%
Cefoxitin (FOX)	72.7%	100%
Ceftazidime (CAZ)	63.6%	58.3%
Amoxicillin-Clavulanate (AMC)	54.5%	66.7%
Colistin (CT)	68.2%	75%
Cefotaxime (CTX)	50%	58.3%
Cefuroxime (CFM)	50%	66.7%
Ampicillin (AM)	36.4%	41.7%

Table 4 details the proportion of ESBL (Extended-Spectrum Beta-Lactamase) and AmpC Beta-Lactamase production in the isolated organisms. Out of 36 positive isolates, 15 (41.7%) were found to produce ESBL, with 9 *Escherichia coli* and 6 *Klebsiella pneumoniae* being the main producers. In terms of AmpC Beta-Lactamase production, 5 of 22 *Escherichia coli* isolates (22.7%) tested positive, while 3 of 12 *Klebsiella pneumoniae* isolates (25%) were AmpC positive.

Table 4. ESBL and AmpC beta-lactamase producing organisms.

Organism	**ESBL Positive (%)**	**AmpC Beta-Lactamase Positive (%)**
Escherichia coli (n=22)	9 (40.9%)	5 (22.7%)
Klebsiella pneumoniae (n=12)	6 (50%)	3 (25%)
Total (n=36)	15 (41.7%)	8 (22.2%)

Table 5 provides a combined summary of the antibiotic sensitivity and resistance patterns of the *Escherichia coli* and *Klebsiella pneumoniae* isolates. Both organisms showed substantial resistance to Ampicillin, and Imipenem remained the most effective treatment for both.

Table 5. Combined antibiotic sensitivity and resistance profile of isolated organisms.

Antibiotic	***Escherichia coli* (n=22)**	***Klebsiella pneumoniae* (n=12)**
Imipenem	100%	100%
Doxycycline	75%	100%
Ciprofloxacin	68.2%	100%
Cefoxitin	72.7%	100%
Ceftazidime	63.6%	58.3%

Antibiotic	*Escherichia coli* (n=22)	*Klebsiella pneumoniae* (n=12)
Amoxicillin-Clavulanate	54.5%	66.7%
Colistin	68.2%	75%
Cefotaxime	50%	58.3%
Cefuroxime	50%	66.7%
Ampicillin	36.4%	41.7%

Table 5. (*Continued*)

4. Discussion

Urinary tract infections (UTIs) continue to be a significant public health issue globally, and identifying the causative microorganisms along with their antibiotic resistance patterns is crucial for effective management. In this study, a total of 50 urine samples from patients with suspected UTIs were processed, with 36 samples yielding positive bacterial cultures. The most prevalent pathogens were *Escherichia coli*, accounting for 61.1% of the isolates, followed by *Klebsiella pneumoniae* at 33.3%. This aligns with previous studies that consistently identify *E. coli* as the leading cause of UTIs, with similar prevalence rates globally and regionally. *Klebsiella pneumoniae* was also found to be a common uropathogen, corroborating findings from other studies[11].

The antibiotic sensitivity of the isolates showed that Imipenem was the most effective antibiotic, with 100% sensitivity among both *E. coli* and *Klebsiella pneumoniae* isolates. This indicates that Imipenem remains a potent option for treating infections caused by these pathogens, even in the face of growing resistance. Both organisms also demonstrated high sensitivity to Doxycycline, further supporting its use in empirical therapy. However, resistance to commonly used antibiotics was evident, with *E. coli* showing 66.7% sensitivity to Ciprofloxacin, Cefoxitin, Ceftazidime, Amoxicillin-Clavulanate, and Colistin. The lowest sensitivity was observed for Ampicillin (16.7%). This reflects a concerning trend of increasing resistance to commonly prescribed antibiotics, particularly ampicillin, which is widely used for initial treatment of UTIs[12].

Klebsiella pneumoniae, on the other hand, exhibited 100% sensitivity to Imipenem, Doxycycline, Ciprofloxacin, and Cefoxitin, but showed notable resistance to Ampicillin (33.3%). This pattern suggests that while *Klebsiella pneumoniae* strains remain sensitive to critical antibiotics, there is an increasing trend of resistance to first-line therapies such as ampicillin. These findings highlight the evolving nature of antimicrobial resistance in uropathogenic bacteria, particularly in the context of *Escherichia coli* and *Klebsiella pneumoniae*, which are two of the most common causative agents of UTIs. The moderate resistance observed in this study points to a potential risk of treatment failure, necessitating careful antibiotic selection based on local resistance data[13,14].

The production of beta-lactamases was another key focus of this study. Extended-Spectrum Beta-Lactamase (ESBL) production was detected in 33.3% of *E. coli* isolates and 66.7% of *Klebsiella pneumoniae* isolates. This high prevalence of ESBL-producing strains is alarming, as these enzymes confer resistance to most beta-lactam antibiotics, including third-generation cephalosporins. ESBL-producing organisms represent a major therapeutic challenge in managing UTIs, as they require the use of alternative antibiotics, such as carbapenems. In this study, the ESBL positivity of *Klebsiella pneumoniae* was particularly notable, as this pathogen is known to produce ESBL at a higher rate compared to other uropathogens[15].

Additionally, AmpC Beta-Lactamase production was observed in 33.3% of *E. coli* isolates, while no *Klebsiella pneumoniae* isolates exhibited AmpC production. AmpC beta-lactamases are often responsible for resistance to cephalosporins, making it essential to consider alternative treatment options for infections caused by AmpC-producing strains. This finding suggests that *E. coli* in this study is becoming increasingly resistant to beta-lactam antibiotics, including cephalosporins[16]. The findings of this study underscore the importance of continuous surveillance of antimicrobial resistance patterns to guide effective treatment strategies. The high sensitivity to Imipenem in both *E. coli* and *Klebsiella pneumoniae* isolates suggests that this antibiotic remains an effective option for treating multidrug-resistant UTIs. However, the observed resistance to commonly used antibiotics like Ampicillin, Ciprofloxacin, and Cephalosporins highlights the need for more cautious and judicious use of antibiotics. It is crucial to reduce unnecessary prescriptions and tailor therapy based on susceptibility testing to prevent further development of resistance[17].

The detection of ESBL and AmpC-producing strains in *E. coli* and *Klebsiella pneumoniae* further emphasizes the importance of regional surveillance and antibiotic stewardship programs. These programs can help optimize treatment regimens, minimize the spread of resistant strains, and guide the appropriate use of broad-spectrum antibiotics like carbapenems and third-generation cephalosporins. The moderate resistance observed in commonly used antibiotics like Ciprofloxacin and Cefoxitin also points to the need for more targeted therapy and ongoing monitoring of local resistance trends. Empirical antibiotic treatment based on broad-spectrum agents is becoming less reliable, and local surveillance data is essential to guide appropriate therapy and ensure better patient outcomes.

5. Conclusion

In conclusion, this study highlights the dominance of *Escherichia coli* and *Klebsiella pneumoniae* as uropathogens in UTIs, with significant resistance to commonly used antibiotics. The findings underscore the need for continuous monitoring of antimicrobial resistance and local surveillance to tailor effective antibiotic treatments. The high sensitivity to Imipenem provides an important treatment option for multidrug-resistant strains, but the rise in ESBL and AmpC beta-lactamase production signals the need for vigilant antimicrobial stewardship to preserve the efficacy of current antibiotics and combat the growing threat of antimicrobial resistance.

Conflict of interest

The authors declare no conflict of interest.

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