

Pattern of Organisms and Their Sensitivity in Patients Suffering from UTI Attending in a Private Chamber-A Perspective Study from 2021-2023

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DOI: <https://doi.org/10.36348/sjimps.2024.v10i12.008>

Received: 08.11.2024 | Accepted: 03.12.2024 | Published: 16.12.2024

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Abstract

Background: Urinary tract infections (UTIs) are prevalent bacterial infections with a considerable impact on healthcare systems. Given the increasing antibiotic resistance globally, particularly in high-frequency regions such as Bangladesh, identifying prevalent pathogens and understanding their resistance patterns is essential for effective treatment. **Objective:** This study aims to analyze the common pathogens causing UTIs in a private outpatient setting in Bangladesh and evaluate their antibiotic susceptibility profiles to guide empirical therapy and enhance local treatment protocols. **Methodology:** This three-year prospective observational study (2021-2023) involved 58 UTI patients from a private chamber in Bangladesh. Urine samples were cultured, and bacterial isolates were identified and tested for antibiotic susceptibility to commonly used drugs, including cephalosporins, carbapenems, and fluoroquinolones. Data on organism frequency, resistance, and sensitivity were analyzed. **Results:** Escherichia coli was the most common pathogen (58.6%), followed by Klebsiella spp. (20.7%) and Methicillin-sensitive Staphylococcus aureus (MSSA) (13.8%). High sensitivity was observed for E. coli to Imipenem (100%) and Meropenem (96%), while significant resistance was noted to Ciprofloxacin (48.5%) and Cefixime (48%). MSSA and Klebsiella spp. similarly showed high susceptibility to carbapenems, with notable resistance to fluoroquinolones in MSSA. **Conclusion:** The high prevalence of E. coli as the primary UTI pathogen and its resistance patterns in this private setting underscore the necessity of targeted antibiotic selection. The study advocates for carbapenems in cases with suspected resistance and highlights the importance of regular sensitivity testing and antibiotic stewardship in outpatient settings to improve patient outcomes and mitigate resistance.

Keywords: Urinary Tract Infections, Escherichia Coli, Antibiotic Resistance.

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INTRODUCTION

Urinary tract infections (UTIs) are one of the most frequently encountered bacterial infections, impacting a wide range of individuals and placing a considerable burden on healthcare systems globally. These infections are predominantly caused by bacterial organisms, although the specific causative agents and their resistance patterns can vary based on regional and environmental factors [1-4]. Effective management of UTIs requires not only prompt diagnosis but also an understanding of the organisms involved and their antibiotic sensitivity profiles to prescribe the most effective treatment. However, the global rise of

antibiotic resistance has complicated UTI treatment, emphasizing the need for localized studies to monitor and respond to resistance trends [5-7].

In Bangladesh, where self-medication and overuse of antibiotics are common, antibiotic resistance among UTI pathogens is a growing concern. Private healthcare settings, such as clinics and chambers, often see a high volume of UTI cases, where treatment is frequently tailored for quick relief and patient convenience [8-11]. This study focuses on patients with UTIs attending a private chamber from 2021 to 2023, aiming to identify the predominant organisms causing

these infections and assess their susceptibility to commonly used antibiotics. This setting allows for a closer look at the patterns in outpatient care, which may differ from those observed in larger hospitals due to differences in patient demographics and treatment practices.

The prospective nature of this study enables the collection of up-to-date data on UTI pathogens and their resistance profiles over a recent three-year period, reflecting current trends and challenges in UTI management. By analyzing organisms from UTI patients and evaluating their sensitivity to various antibiotics, the study seeks to offer clinicians essential information to inform their treatment decisions. A focus on private clinic data is particularly valuable, as it represents a segment of healthcare where empirical antibiotic prescriptions are common, often without prior sensitivity testing.

Understanding the specific pathogens and their resistance patterns in a private outpatient setting is critical, as it helps in devising tailored treatment approaches that align with the actual resistance profile observed in this healthcare segment. The study will also provide insights into any shifts in resistance patterns, such as the emergence of multi-drug-resistant organisms, which have significant implications for patient outcomes and treatment costs. These insights can guide practitioners in selecting appropriate first-line therapies, reducing treatment failures, and preventing the unnecessary escalation of antibiotics.

Objective

The findings of this study are expected to contribute to more effective UTI management in private settings by informing evidence-based antibiotic selection and reducing reliance on empirical treatments. Additionally, the study could prompt further efforts to promote responsible antibiotic use and patient education on the risks of resistance. Public health initiatives that align treatment practices in private and public sectors will be crucial in combating the spread of resistant UTI pathogens across communities.

METHODOLOGY

Study Type

This study is a prospective observational analysis conducted to identify patterns of organisms causing UTIs and assess their antibiotic sensitivity profiles in a private healthcare setting over a three-year period (2021-2023). By examining UTI pathogens among outpatients, the study provides current data on

antibiotic resistance trends relevant to local healthcare practices.

Study Design

The study employed a descriptive cross-sectional design to document organism types and antibiotic susceptibility profiles from UTI patients attending a private chamber. Data were collected on an ongoing basis, allowing for continuous monitoring of resistance patterns across the study period.

Study Population

The study included 58 patients diagnosed with UTIs who visited a private outpatient chamber from 2021 to 2023. Inclusion criteria were patients of all ages and sexes diagnosed with UTI based on clinical presentation and laboratory findings. Exclusion criteria involved patients who were undergoing antibiotic treatment before sample collection or who had incomplete clinical or microbiological data.

Data Collection

Urine samples were collected aseptically from patients with confirmed UTI diagnoses. The specimens were processed in a microbiology laboratory following standard protocols for culture and sensitivity testing.

Bacterial isolates from the urine samples were identified using standard biochemical tests and/or automated methods. The study documented five primary organisms: *Escherichia coli*, *Klebsiella spp.*, MSSA (Methicillin-sensitive *Staphylococcus aureus*), *Acinetobacter spp.*, and *Enterococcus spp.*

Antibiotic susceptibility was determined for commonly prescribed antibiotics, including cephalosporins, carbapenems, aminoglycosides, fluoroquinolones, and other classes. Susceptibility results were interpreted based on established clinical breakpoints.

Data Analysis

The frequency and percentage of each organism type and age demographics of the study population were calculated. This provided insight into the prevalence of various pathogens and the distribution of UTI cases across different age groups. Sensitivity and resistance rates were calculated for each antibiotic across different organisms. These patterns were summarized to identify the most and least effective antibiotics for each pathogen. Sensitivity patterns were tracked to observe any changes in antibiotic resistance among common UTI pathogens over the study period. This involved comparing resistance rates across the three years and assessing the emergence of multi-drug-resistant organisms.

RESULTS

Table 1: Type of organism (N=58)

Type of organism	Frequency (n)	Percentage (%)
Escherichia Coli	34	58.6
Klebsiella spp	12	20.7
MSSA	8	13.8
Acinetobacter spp	2	3.4
Enterococcus spp	2	3.4

Most of the organism found in this study was Escherichia Coli (58.6%) followed by Klebsiella spp (20.7%), MSSA (13.8%), Acinetobacter spp (3.4%) and Enterococcus spp (3.4%).

Table 2: Demographic profile of the study subjects (N=58)

Age (years)	Frequency (n)	Percentage (%)
≤20	15	25.9
21 - 30	28	48.3
31 - 40	10	17.2
41 - 50	2	3.4
>50	3	5.2

Most of the study subjects were in age group 21 – 30 years (48.3%) followed by ≤20 years (25.9%), 31 – 40 years (17.2%), and >50 years (5.2%) and 41 – 50 years (3.4%).

Table 3: Sensitivity and resistant pattern of different organism (N=58)

	Cephadrine	Ceftriaxone	Cefixime	Ceftazidime	Cefepime	Imipenem	Meropenem	Co-trimoxazole	Gentamicine Gentabac	Netilmycine	Ciprofloxacin Civox	Levofloxacin Levobac	Doxycycline	Nitrofurantoin	Amikacin Amibac	Aztreonam
Escherichia Coli																
Sensitive	11 (61.1)	16 (69.6)	13 (52.0)	15 (65.2)	16 (66.7)	16 (100.0)	24 (96.0)	10 (52.6)	19 (79.2)	15 (88.2)	14 (42.4)	16 (69.6)	15 (48.4)	12 (92.3)	22 (81.5)	16 (72.7)
Resistant	6 (33.3)	7 (30.4)	12 (48.0)	8 (34.8)	8 (33.3)		1 (4.0)	8 (42.1)	3 (12.5)	1 (5.9)	16 (48.5)	6 (26.1)	13 (41.9)	1 (7.7)	1 (3.7)	6 (27.3)
Intermediate	1 (5.6)								2 (8.3)	1 (5.9)	3 (9.1)	1 (4.3)	3 (9.7)		4 (14.8)	
MSSA																
Sensitive	5 (83.3)	1 (50.0)	2 (100.0)	1 (50.0)	4 (80.0)	5 (100.0)	6 (100.0)	3 (37.5)	5 (71.4)	5 (83.3)			3 (50.0)	2 (50.0)	5 (71.4)	1 (50.0)
Resistant	1 (6.7)	1 (50.0)		1 (50.0)	1 (20.0)			5 (62.5)	2 (28.6)	1 (6.7)	2 (100.0)	2 (100.0)	3 (50.0)	2 (25.0)	2 (28.6)	1 (50.0)
Intermediate														2 (25.0)		

Klebsiella spp																
Sensitive	4 (33.3)	8 (80.0)	9 (75.0)	8 (72.7)	10 (83.3)	9 (100.0)	11 (100.0)	8 (80.1)	9 (81.8)	6 (85.7)	9 (90.0)	5 (83.3)	6 (60.0)	4 (66.7)	10 (90.9)	9 (75.0)
Resistant	8 (66.7)	2 (20.0)	3 (25.0)	2 (27.3)	2 (16.7)			1 (10.0)	1 (9.1)	1 (14.3)	1 (10.0)	1 (16.7)	2 (20.0)	1 (16.7)	1 (9.1)	2 (16.7)
Intermediate								1 (10.0)	1 (9.1)				2 (20.0)	1 (16.7)		1 (8.3)
Acinetobacter																
Sensitive		2 (100.0)	2 (100.0)	2 (100.0)	1 (50.0)	2 (100.0)	2 (100.0)	2 (100.0)	2 (100.0)	1 (100.0)	2 (100.0)	1 (100.0)	2 (100.0)		2 (100.0)	
Resistant		0 (0.0)	0 (0.0)	0 (0.0)		0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)		0 (0.0)	
Intermediate					1 (50.0)											
Enterococcus spp																
Sensitive						1 (100.0)	1 (100.0)				2 (100.0)		2 (100.0)	1 (100.0)	1 (100.0)	1 (100.0)
Resistant											0 (0.0)	1 (100.0)				

Most sensitive antibiotics for *Escherichia Coli* were Imipenem (100.0%), Meropenem (96.0%), Nitrofurantoin (92.3%), Netilmicine (88.2%), Amikacin Amibac (81.5%), Gentamicine gentabac (79.2%), Aztreonam (72.7%) and Levofloxacin (69.9%). Most resistant antibiotics for *Escherichia Coli* were Ciprofloxacin Civox (48.5%), Cefixime (48.0%), Co-trimoxazole (42.1%), Doxycycline (41.9%), Ceftazidime (34.8%), Cephadrine (33.3%) and Ceftriaxone (30.4%).

Most sensitive antibiotics for MSSA were Cephixime (100.0%), Imipenem (100.0%), Meropenem (100.0%), Cephadrine (83.3%), Netilmicine (83.3%), Cefepime (80.0%), Gentamicine gentabac (71.4%), Amikacin Amibac (71.4%) and Gentamicine gentabac (68.7%). Most resistant antibiotics for MSSA were Ciprofloxacin Civox (100.0%), Levofloxacin Levobac (100.0%), Co-trimoxazole (62.5%), Doxycycline (50.0%), Ceftazidime (50.0%) and Aztreonam (50.0%).

Most sensitive antibiotics for *Klebsiella spp* were Imipenem (100.0%), Meropenem (100.0%), Amikacin Amibac (90.9%), Ciprofloxacin Civox

(90.0%), Netilmicine (85.7%), Cefepime (83.3%), Levofloxacin Levobac (83.3%), Gentamicine gentabac (81.8%), Co-trimoxazole (80.1%), Ceftriaxone (80.0%), Aztreonam (75.0%), Cephixime (75.0%) and Ceftazidime (72.7%). Most resistant antibiotic for *Klebsiella spp* was Cephadrine (66.7%) followed by ceftazidime (27.3%), Cefixime (25.0%) and ceftriaxone (20.0%).

DISCUSSION

This study reveals *Escherichia coli* (58.6%) as the most prevalent organism among UTI patients in a private chamber setting, consistent with findings from several other studies where *E. coli* predominates in UTIs across diverse patient populations. For instance, research in hospital settings similarly reports *E. coli* as the leading causative organism, reflecting its common role in urinary tract infections due to its presence in the gut and its ability to easily colonize the urinary tract [10, 11]. However, while this study shows *E. coli* as responsible for nearly 60% of cases, some studies indicate even higher frequencies, suggesting possible variability based on healthcare settings or patient demographics.

Klebsiella spp. emerged as the second most common pathogen in this study (20.7%), a finding also reflected in other UTI research, although with some variation in frequency. In hospital-based studies, *Klebsiella* spp. often ranges between 15-25%, aligning with the rate observed here. However, some studies conducted in larger urban hospitals report slightly higher prevalence, possibly due to differences in patient population, exposure to broad-spectrum antibiotics, or environmental factors [12]. The private outpatient setting, as studied here, may cater to relatively less severe cases, potentially impacting the type and resistance profiles of infecting organisms seen in comparison to larger hospitals.

Antibiotic sensitivity patterns in this study show high susceptibility of *E. coli* to Imipenem (100%) and Meropenem (96%), with significant effectiveness also observed for Nitrofurantoin (92.3%) and Amikacin (81.5%). This is in line with other research showing carbapenems as among the most effective antibiotics against *E. coli* in UTI cases, highlighting their reliability in cases of resistant infections. Conversely, high resistance to Ciprofloxacin (48.5%) and Cefixime (48%) indicates substantial resistance concerns, a pattern commonly seen in global studies where fluoroquinolones face reduced efficacy due to widespread usage and resulting resistance.

The sensitivity profile for MSSA in this study also shows strong susceptibility to Imipenem, Meropenem, and Cephixime (100%), while resistance to Ciprofloxacin and Levofloxacin is notably high (100%). These findings echo similar resistance patterns found in studies from hospital settings, where MSSA has shown rising resistance to fluoroquinolones but retained susceptibility to carbapenems and newer-generation cephalosporins [13-15]. This resistance in MSSA to fluoroquinolones poses challenges, especially in settings with frequent empirical antibiotic use, underscoring the importance of susceptibility testing for effective UTI management.

In the case of *Klebsiella* spp., this study reports 100% sensitivity to Imipenem and Meropenem, aligning with broader findings on carbapenem efficacy against this pathogen. Sensitivity to Ciprofloxacin and Netilmicin was also high, contrasting with some hospital-based studies where *Klebsiella* has shown higher resistance to fluoroquinolones, possibly due to the selection pressures of a hospital environment. However, Cephadrine showed high resistance (66.7%) among *Klebsiella* strains, highlighting the need to avoid certain cephalosporins for empiric treatment and instead consider alternative options with demonstrated effectiveness.

CONCLUSION

In conclusion, this study highlights *Escherichia coli* as the predominant organism causing UTIs in a

private outpatient setting, followed by *Klebsiella* spp. and MSSA, with significant implications for antibiotic selection. The high sensitivity of *E. coli*, MSSA, and *Klebsiella* spp. to carbapenems like Imipenem and Meropenem underscores their effectiveness as treatment options, especially in cases of resistant infections. However, elevated resistance rates to commonly used antibiotics, such as Ciprofloxacin and Cefixime, emphasize the need for routine susceptibility testing and cautious use of these agents to mitigate further resistance development. Overall, these findings underscore the importance of antibiotic stewardship in both private and hospital settings to ensure effective treatment outcomes for UTI patients.

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