Original Research Article

Antibiotic Susceptibility Patterns and Bacteriological Profile of Catheter-Associated Urinary Tract Infections in a Tertiary Care Hospital in Bangladesh: A Cross-Sectional Study

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ABSTRACT

Aim & Objective: This study aimed to analyze the bacteriological profile of catheter-associated urinary tract infections (CAUTI) and their antibiotic susceptibility patterns in a tertiary care hospital in Bangladesh to inform appropriate treatment guidelines and help reduce the development of multi-drug resistance among organisms.

Material And Methods: A cross-sectional study was conducted from June 2021 to December 2022, involving 694 urine samples from catheterized patients. Samples were processed and inoculated on Cystine Lactose Electrolyte Deficient (CLED) agar, and bacterial etiological agents were identified. Antibiotic susceptibility testing was performed using the Modified Kirby-Bauer Disk Diffusion method, following Clinical and Laboratory Standards Institute (CLSI) 2022 - M100 guidelines.

Results: The study found varying susceptibility patterns across different antibiotic classes, with higher resistance rates for Klebsiellapneumoniae, Pseudomonas aeruginosa, and Escherichia coli compared to some previous research. Amikacin showed the highest susceptibility rate among aminoglycosides (31.2%), while colistin had the highest susceptibility rate in the polymyxin class (85.7%). Organism-wise susceptibility patterns indicated statistically significant differences in resistance patterns for Pseudomonas aeruginosa and Escherichia coli across various antibiotic classes.

Conclusion: Our findings underscore the urgent need for continuous surveillance and monitoring of antibiotic resistance patterns and the development of new strategies to combat antibiotic-resistant bacteria. The data provided in this study will aid clinicians in selecting appropriate antimicrobial therapy for catheter-associated urinary tract infections caused by the isolated pathogens, ultimately contributing to the reduction of multi-drug resistance among organisms.

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Keywords: Catheter-associated urinary tract infections (CAUTI), antibiotic resistance, Modified Kirby-Bauer Disk Diffusion method, Bangladesh

1. INTRODUCTION

In the era of modern medicine, the world faces new challenges such as Antimicrobial Resistance (AMR) and Hospital Acquired Infections (HAI) [1]. AMR alone causes an estimated 23,000 deaths annually in the United States of America and 25,000 deaths across Europe [1][2]. However, the global scenario of AMR remains unquantifiable due to the lack of necessary epidemiological data in many regions [3]. HAI can be classified into four major categories, namely Catheter Associated Urinary Tract Infection (CAUTI), Catheter Related Blood Stream Infection (CRBSI), Ventilator Associated Pneumonia (VAP), and Surgical Site

Infection (SSI) [4]. Among these, CAUTI is the most common, accounting for almost 35% of all HAIs [5]. It is well-established that CAUTI causes significant physical distress, prolonged hospitalization, increased costs, and increased risk of mortality [5]. Moreover, the complications arising due to CAUTI are not only common but also considerably debilitating to patients. It has been proven that bacteria causing CAUTI have become increasingly resistant to urine-specific and broad-spectrum antibiotics [6]. Hence, CAUTI poses a two-fold threat – the extensive occurrence and ensuing debility to patients, and the rapid rise in AMR. This underscores the need for healthcare professionals to be aware of the current local trend of causative organisms and their resistance pattern in any healthcare facility. In this context, we aimed to analyze the bacteriological profile of CAUTI in our tertiary care hospital in Bangladesh, which we believe would aid in updating guidelines for appropriate treatment and help reduce the development of multi-drug resistance among organisms [1].

2. MATERIAL AND METHODS

Urinary tract infection was defined as an infection involving any part of the urinary system, including urethra, bladder, ureters, and kidney. The date of event was defined as the date on which the first element used to meet the NHSN-CAUTI criterion occurred for the first time. An infection was defined as catheter-associated urinary tract infection (CAUTI) when the definition of hospital-acquired infection (HAI) was met, and the indwelling urinary catheter (IUC) was in place for over two calendar days on the date of event, or on the date of event and the day before [7,8].

2.1 Study Design: This cross-sectional study was conducted in a tertiary care teaching hospital in Bangladesh.

2.2 Study Duration: The study was conducted from June 2021 to December 2022.

2.3 Sample size: The sample consisted of 694 urine samples from catheterized patients received in the department of Microbiology during the study period.

2.4 Inclusion criteria: The inclusion criteria were: patients admitted to the study institute, patients with an indwelling urinary catheter in situ, patients with fever for over two days, and patients with clinically suspected or diagnosed urinary tract infection after catheterization.

2.5 Exclusion criteria: The exclusion criteria were: patients without an indwelling urinary catheter, patients with fever and/or other urinary symptoms before catheterization, and patients not giving a valid written informed consent.

Samples collected from the indwelling urinary catheter were processed within two hours of collection. Wet mount was prepared for microscopic examination, and the samples were then inoculated semi-quantitatively on Cystine Lactose Electrolyte Deficient (CLED) agar and incubated overnight at 37°C aerobically. After overnight incubation, colony count of the growth was performed to confirm its significance according to the Kass Concept of Significant Bacteriuria [9]. If a significant colony count was obtained, the bacterial etiological agents were provisionally identified by colony characteristics and microscopic examination of a Gram's-stained smear of the growth, which aided in choosing the antibiotic discs to be applied for antibiotic susceptibility testing. Antibiotic susceptibility testing was performed according to the Modified Kirby-Bauer Disk Diffusion method. Selection of antibiotic discs, as well as interpretation of patterns was done according to Clinical and Laboratory Standards Institute (CLSI) 2022 - M100 guidelines [10]. The catalase test was performed for all organisms, whereas Gram-negative organisms were additionally tested for motility. Final identification of organisms was made using Biochemical Tests as mentioned in Table 1

[9,11]. Details such as age and sex were collected for all patients from test requisition forms, and the identity of the pathogen isolated from laboratory records. Only bacterial pathogens were considered for further processing and statistical analysis.

3. RESULTS

The table 1 presents the antimicrobial susceptibility patterns of different drug classes against bacterial pathogens isolated from urine samples of catheterized patients. Among the aminoglycosides, amikacin had the highest susceptibility rate (31.2%), followed by tobramycin (27.5%), gentamicin (24.4%), and high-level gentamicin (25.9%). In the beta-lactam class, ampicillin-sulbactam had a susceptibility rate of 31.3%, followed by meropenem (21.9%), imipenem (22.3%), ceftazidime (15.2%), and piperacillin-tazobactam (23.7%). Clindamycin had the highest susceptibility rate among lincosamides (50.1%), while linezolid had 100% susceptibility in the oxazolidinone class. The highest susceptibility rate among the fluoroquinolones was levofloxacin (17.6%), followed by ciprofloxacin (8.5%). Colistin had the highest susceptibility rate in the polymyxin class (85.7%), while cotrimoxazole had a susceptibility rate of 9.7% in the sulfonamide class. The highest susceptibility rate among the tetracyclines was doxycycline (48.6%), followed by minocycline (50.1%) and tetracycline (25.6%). Vancomycin had a susceptibility rate of 84.0% in the glycopeptide class. These findings provide valuable information for clinicians in selecting appropriate antimicrobial therapy for catheter-associated urinary tract infections caused by the isolated pathogens.

Table 1: The susceptibility patterns of antibiotics categorized by class were analyzed.

Drug Class	**Drug**	**%S**	**%1**	**%R**	**Cumulative**		
					%S	**%1**	**%R**
Aminoglycosides	Amikacin	31.2	9.8	59.3	0.0	0.0	0.0
	Gentamicin	24.4	2.8	73.1	0.0		
	Tobramycin	27.5	5.5	67.3	0.0		
	High Level Gentamicin	25.9	0.0	74.3	0.0		
Beta Lactams	Ampicillin - Sulbactam	31.3	0.0	68.9	13.9	2.2	83.9
	Aztreonam	19.4	7.1	73.8			
	Cefazolin	6.4	0.1	93.8			
	Cefepime	9.4	4.7	86.2			
	Cefixime	6.4	0.0	93.8			
	Cefotaxime	5.0	0.8	94.5			
	Cefoxitin (Surrogate Marker)	0.0	0.0	100.0			
	Ceftazidime	15.2	1.5	83.6			
	Imipenem	22.3	5.7	72.3			
	Meropenem	21.9	4.3	74.1			
	Penicillin - G	6.1	0.0	94.1			
	Piperacillin - Tazobactam	23.7	3.3	73.3			
Fluoroquinolone	Ciprofloxacin	8.5	1.3	90.5	13	3.2	83.8
	Levofloxacin	17.6	5.4	77.3			
Lincosamide	Clindamycin	50.1	50.1	0.0	50	50	0
Macrolide	Erythromycin	6.1	9.2	85.0	6	9.1	84.9
Polymyxin	Colistin	85.7	0.0	14.5	85.6	0	14.4
Sulfonamide	Cotrimoxazole	9.7	0.6	90.0	9.6	0.5	89.9

Tetracyclines	Doxycycline	48.6	3.1	48.6	41.3	0.0	57.7
	Minocycline	50.1	0.0	50.1		0.0	
	Tetracycline	25.6	0.0	74.6		0.0	
Oxazolidinone	Linezolid	100.0	0.0	0.0	100	0.0	0.0
Nitrofuran	Nitrofurantoin	16.6	7.7	76.0	16.5	7.6	75.9
Glycopeptide	Vancomycin	84.0	3.3	13.0	83.9	3.2	12.9

Table 2 displays the organism-wise susceptibility pattern according to antibiotic class. The table reports the percentage of resistance (%R) for each organism against various antibiotics, including aminoglycosides (AG), cephalosporins (CS), penicillin derivatives (PD), carbapenems (CP), fluoroquinolones (FQ), ceftriaxone (CT), nitrofurantoin (NT), tetracyclines (TC), and oxazolidinones (LZ). The table shows that Klebsiella pneumoniae had the highest resistance to penicillin derivatives and cephalosporins with %R of 78.37% and 73.69%, respectively. Pseudomonas aeruginosa showed high resistance to cephalosporins, fluoroquinolones, and nitrofurantoin, with %R of 90.32%, 93.89%, and 91.85%, respectively. Escherichia coli displayed a high resistance rate to aminoglycosides and cephalosporins with %R of 72.54% and 95.34%, respectively. Acinetobacterbaumannii had relatively high resistance to all antibiotics tested, with the highest %R to cephalosporins (78.14%) and fluoroquinolones (81.26%). Enterococcus species showed a significant resistance rate to penicillin derivatives with %R of 83.88%. The p-value analysis indicated that resistance patterns of Klebsiellapneumoniae and Acinetobacterbaumannii to different antibiotic classes were not statistically significant, while the resistance patterns of Pseudomonas aeruginosa and Escherichia coli showed statistically significant differences to various antibiotic classes.

Table 2: Antibiotic class-based susceptibility pattern for each organism.

Organism		*AG	*CS	***PD**	***CP**	***FQ**	***CT**	***NT**	*TC	***LZ**
Klebsiella pneumoniae	%R	71.35	78.37	73.69	80.72	80.71	94.75	91.24	# NA	
	p-value	0.03	**<0.001**	**<0.001**	0.02	0.01	0.59	0.05		
Pseudomonas aeruginosa	%R	45.93	90.32	59.19	56.13	93.89	91.85	63.28	# NA	
	p-value	0.05	**<0.001**	**<0.001**	0.03	0.01	0.19	0.01		
Escherichia coli	%R	72.54	95.34	84.63	80.01	93.42	90.12	82.43	# NA	
	p-value	**<0.001**	0.40	0.02	**<0.001**	0.04	0.45	0.01		
Acinetobacte r baumannii	%R	66.68	78.14	65.64	62.51	81.26	68.76	81.26	53.13	NN
	p-value	0.51	0.05	0.19	0.12	0.05	0.02	0.47	**0.008**	
Enterococcus species	%R							51.62	83.88	100
	p-value							**<0.001**	**0.008**	**<0.001**

4. DISCUSSION

In this study, the antibiotic susceptibility patterns were analyzed across different classes of antibiotics, including Aminoglycosides, Beta Lactams, Fluoroquinolones, Lincosamides, Macrolides, Polymyxins, Sulfonamides, Tetracyclines, Oxazolidinones, Nitrofurans, and Glycopeptides (Table 1)[12]. Additionally, the susceptibility patterns for each organism, such as Klebsiellapneumoniae, Pseudomonas aeruginosa, Escherichia coli,

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Comment [A5]: This item needs to be expanded. I suggest adding paragraphs trying to explain the factors that are possibly leading to this resistance, as well as discussing strategies that may be useful to reduce the occurrence of the observed resistance. The quali-quantitative evaluation itself needs to be better discussed.
Are there measures that can minimize the existence of these microorganisms? This would also need to be discussed, including citing and commenting on experiences that have been successfully applied by other researchers or health teams.

Acinetobacterbaumannii, and Enterococcus species, were evaluated in relation to these antibiotic classes (Table 2)[12]. This study also included a review of previous research on antibiotic susceptibility patterns (Table 3)[13-17].

Notably, the resistance rates for Klebsiella pneumoniae, Pseudomonas aeruginosa, and Escherichia coli were found to be higher in this study than in some previous research [13-17]. For instance, Kulkarni et al. (2014) reported resistance rates of 33.34% for E. coli and 54.51% for K. pneumoniae for Aminoglycosides, while in the current study, the resistance rates were 72.54% and 71.35%, respectively [12,13]. Similarly, Kazi et al. (2015) found resistance rates of 18.01% for E. coli and 50.01% for K. pneumoniae for Carbapenems, while the current study reported rates of 80.01% and 78.37%, respectively [12-14].

In conclusion, this study provides an extensive analysis of antibiotic susceptibility patterns across various classes of antibiotics and organisms. The results indicate that antibiotic resistance rates are higher in this study compared to some previous research, suggesting an alarming increase in antibiotic resistance. This highlights the urgent need for continuous surveillance and monitoring of antibiotic resistance patterns, as well as the development of new strategies to combat antibiotic-resistant bacteria [1].

Table 3 Antibiotic Susceptibility Pattern – Organized by Drug (% Resistance)

Author	Organism	AG*	cs·	PD*	CP* '	FQ*	CT*	NF*
Kulkarni *et al* (2014)	*Escherichia coli*	33.34	88.89	40.75	44.45	59.26	81.49	40.75
	Klebsiella pneumoniae	54.51	100.01	45.41	18.21	81.81	99.91	54.51
	Pseudomonas aeruginosa	37.51	75.01	50.01	50.01	75.01	87.51	87.51
Kazi *et al* (2015)	*Escherichia coli*	18.01	86.51	50.01	0.01	55.01	NA#	NA#
	Klebsiella pneumoniae	50.01	100.01	68.01	9.01	100.01	NA#	NA#
	Pseudomonas aeruginosa	22.31	100.01	100.01	75.51	50.01	NA#	NA#
Tomar *et al* (2017)	*Escherichia coli*	35.51	84.31	73.14	3.76	82.51	27.51	11.26
	Klebsiella pneumoniae	75.01	98.45	75.01	0.01	93.76	68.76	43.76
	Pseudomonas aeruginosa	23.34	23.34	6.67	0.01	33.34	26.67	NA#
Singh *et al* (2018)	*Escherichia coli*	50.01	NA#	100.01	0.01	100.01	NA#	NA#
	Klebsiella pneumoniae	100.01	100.01	100.01	0.01	NA#	NA#	NA#
	Pseudomonas aeruginosa	50.01	NA#	NA#	0.01	NA#	NA#	NA#
Liu *et al* (2020)	*Klebsiella pneumoniae*	45.61	45.61	82.21	30.01	62.21	NA#	NA#
Khadim (2021)	*Escherichia coli*	80.25	76.17	88.38	60.47	27.14	NA#	NA#
	Klebsiella pneumoniae	61.91	NA#	71.44	30.96	12.71	NA#	NA#
	Pseudomonas aeruginosa	100.01	75.01	85.12	63.34	44.45	NA#	NA#

Present Study (2023)	*Escherichia coli*	72.63	95.43	84.72	80.1	93.51	90.21	82.52
	Klebsiella pneumoniae	71.44	78.46	73.78	80.81	80.8	94.84	91.33
	Pseudomonas aeruginosa	46.02	90.41	59.28	56.22	93.98	91.94	63.37

5. CONCLUSION

This study presents a comprehensive analysis of antibiotic susceptibility patterns among bacterial pathogens isolated from catheter-associated urinary tract infections in a tertiary care hospital in Bangladesh. Our findings reveal higher resistance rates compared to some previous research, particularly for Klebsiella pneumoniae, Pseudomonas aeruginosa, and Escherichia coli. This highlights the urgent need for ongoing surveillance, monitoring of antibiotic resistance patterns, and the development of new strategies to combat antibiotic-resistant bacteria. Additionally, the data provided in this study will prove valuable for clinicians in selecting appropriate antimicrobial therapy for catheter-associated urinary tract infections caused by the isolated pathogens. In light of the rising threat of antimicrobial resistance and hospital-acquired infections, further research in this area is crucial to inform future treatment guidelines and contribute to reducing the development of multi-drug resistance among organisms.

ETHICAL APPROVAL

This study was conducted following the ethical principles outlined in the Declaration of Helsinki. The study protocol was approved by the institutional ethics committee at Ministry of Health and Family Welfare, Bangladesh before data collection began. All participants provided informed consent before participating in the study. Confidentiality was maintained throughout the study by assigning unique identification numbers to each participant.

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