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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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Authors' contributions

This work was carried out in collaboration among all authors. Author SRD designed the study, performed the statistical analysis, wrote the protocol and wrote the first draft of the manuscript. Authors MSI, SI and SA managed the analyses of the study. Authors SRD, SSS and MSSS managed the literature searches. All authors read and approved the final manuscript.

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ABSTRACT

Aim and 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.

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Materials 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 *Klebsiella pneumoniae, 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.

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].

In addition to the challenges posed by Antimicrobial Resistance (AMR) and Hospital Acquired Infections (HAI), understanding the immunological aspects of these infections is crucial for comprehensive management. The immune response plays a pivotal role in combating infections and preventing their dissemination. In the case of CAUTI, the immune system recognizes the presence of bacterial pathogens in the urinary tract and mounts an inflammatory response to eliminate them. However, the bacteria causing CAUTI have evolved mechanisms to evade immune detection and clearance, leading to persistent infections and increased morbidity.

2. MATERIALS 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 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. Acinetobacter baumannii 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 *Klebsiella pneumoniae* and *Acinetobacter baumannii* 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.

The Table 3 presents the antibiotic susceptibility patterns for different organisms causing catheter-associated urinary tract infections (CAUTI). The values indicate the percentage of resistance to various antibiotics.

Among the studies mentioned, Kulkarni et al.(2014) found that Escherichia coli showed 33.34% resistance to aminoglycosides (AG), 88.89% resistance to cephalosporins (cs), and 59.26% resistance to fluoroquinolones (FQ). Klebsiella pneumoniae exhibited 54.51% resistance to AG, 100.01% resistance to carbapenems (CP), and 81.81% resistance to FQ. Pseudomonas aeruginosa showed 37.51% resistance to AG and 75.01% resistance to FQ.

In Kazi et al.(2015), Escherichia coli had 18.01% resistance to AG and 55.01% resistance to FQ. Klebsiella pneumoniae showed 50.01% resistance to AG and 100.01% resistance to CP. Pseudomonas aeruginosa exhibited 22.31% resistance to AG and 100.01% resistance to CP.

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. 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		
Pseudomona s 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	
Enterococcu s species	%R							51.62	83.88	100
	p-value							<0.001	0.008	<0.001

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

Tomar et al.(2017) found that Escherichia coli had 35.51% resistance to AG and 82.51% resistance to FQ. Klebsiella pneumoniae exhibited 75.01% resistance to AG and 93.76% resistance to FQ. Pseudomonas aeruginosa showed 23.34% resistance to AG and 33.34% resistance to FQ.

Singh et al.(2018) reported that Escherichia coli had 50.01% resistance to AG and 100.01% resistance to CP. Klebsiella pneumoniae exhibited 100.01% resistance to AG. Pseudomonas aeruginosa showed 50.01% resistance to AG.

Liu et al. (2020) found that Klebsiella pneumoniae exhibited 45.61% resistance to AG and 82.21% resistance to CP.

In the present study (2023), Escherichia coli showed 72.63% resistance to AG, 95.43% resistance to cs, and 93.51% resistance to FQ. Klebsiella pneumoniae exhibited 71.44% resistance to AG, 73.78% resistance to CP, and 94.84% resistance to FQ. Pseudomonas aeruginosa showed 46.02% resistance to AG, 90.41% resistance to cs, and 93.98% resistance to FQ.

These findings highlight the varying susceptibility patterns of different organisms causing CAUTI to different classes of antibiotics. It is evident that resistance rates differ across studies and over time. It is crucial to monitor these patterns to inform appropriate treatment guidelines and mitigate the development of multi-drug resistance among the organisms causing CAUTI.

4. DISCUSSION

In this study, the analysis of antibiotic susceptibility patterns across different classes of antibiotics was conducted, including Aminoglycosides, Beta Lactams, Fluoroquinolones, Lincosamides, Macrolides, Polymyxins, Sulfonamides, Tetracyclines, Oxazolidinones, Nitrofurans, and Glycopeptides (Table 1) [12]. Furthermore, the susceptibility patterns for specific organisms such as Klebsiella pneumoniae, Pseudomonas aeruginosa, Escherichia coli, Acinetobacter baumannii, and Enterococcus species were evaluated in relation to these antibiotic classes (Table 2) [12]. A review of previous research on antibiotic susceptibility patterns was also included (Table 3) [13-17].

However, it is important to explore the factors contributing to the observed resistance rates and discuss strategies that can help reduce the occurrence of resistance. Several factors may contribute to antibiotic resistance, including the overuse and misuse of antibiotics, inadequate infection control practices, and the presence of resistant strains in healthcare settings. Understanding these factors and implementing measures to address them is crucial in minimizing the existence of antibiotic-resistant microorganisms.

Various strategies can be employed to reduce the occurrence of antibiotic resistance. These may include implementing antimicrobial stewardship programs to promote rational antibiotic use, enhancing infection prevention and control measures, promoting hygiene practices, and educating healthcare professionals and the public about the appropriate use of antibiotics. Additionally, the development of new antimicrobial agents and alternative treatment approaches, such as phage therapy or immunotherapy, may offer potential solutions to combat antibiotic-resistant bacteria.

It is worth mentioning successful experiences from other researchers or healthcare teams in addressing antibiotic resistance. These experiences could provide valuable insights and serve as a basis for developing effective interventions in the local context. Citing and discussing such experiences can further enrich the discussion on strategies to combat antibiotic resistance.

In conclusion, while this study provides a comprehensive analysis of antibiotic susceptibility patterns, it is important to delve deeper into the factors leading to resistance and discuss strategies to minimize the existence of antibiotic-resistant microorganisms. Continuous surveillance, monitoring, and the implementation of effective measures are necessary to combat the alarming increase in antibiotic resistance rates. By considering the experiences and approaches that have shown success in other settings, healthcare professionals can develop evidence-based strategies to address the challenge of antibiotic resistance effectively [1].

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.

CONSENT AND ETHICAL APPROVAL

All participants provided informed consent before participating in the study. Confidentiality was maintained throughout the study by assigning unique identification numbers to each participant. 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.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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