FUDMA Journal of Sciences (FJS)
ISSN online: 2616-1370
ISSN print: 2645 - 2944
Vol. 9 No. 3, March, 2025, pp 22 - 28
DOI: https://doi.org/10.33003/fjs-2025-0903-2871

INCIDENCE OF ANTIBIOTIC RESISTANCE AMONG UROLOGICAL BACTERIA FROM PATIENTS WITH URINARY TRACT INFECTION AT A SELECTED HOSPITAL IN SOUTHWESTERN NIGERIA

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ABSTRACT

Uropathogenic bacteria are known to be significant pathogens responsible for urinary tract infections (UTIs). UTIs are among the most prevalent infectious diseases, affecting millions of people worldwide, and are a significant healthcare burden. This study determined the antibiotics susceptibility patterns of uropathogenic bacterial isolates obtained from UTIs at a selected hospital in Ekiti-State, Nigeria. Fifty Gram-negative (8 *E. coli*, 25 *K. pneumoniae* and 17 *P. aeruginosa*) and 6 Gram-positive (6 *S. aureus*) bacterial isolates were obtained from patients referred to the laboratory. Each isolate was identified accordingly using conventional biochemical tests. All bacteria recovered were subjected to antibiotic susceptibility tests using the agar disk diffusion method. The bacteria were further tested presumptively for the formation of biofilms. All 50 (100%) the Gram-negative bacteria were resistant to ceftazidime. They also showed resistance to vancomycin 49 (98%) and cefuroxime 48 (96%). Furthermore, the Gram-negative bacteria showed the least resistance to chloramphenicol 17 (34%) and ciprofloxin 23(46%). All the *S. aureus* strains showed elevated resistance against the antibiotics tested. Thirty five multiple antibiotic resistance patterns were observed among the isolates. The research has shown that multidrug resistant bacteria in UTI constitutes a healthcare problem and efforts must be made to enforce strict antibiotic treatment regimen to prevent the emergence and spread of antibiotic resistant bacteria in clinical settings.

Keywords: Antibiotic, Multidrug resistance, Antibiotic resistance, Uropathogens

INTRODUCTION

Uropathogenic bacteria include both Gram-positive *Bacillus* spp., *Staphylococcus aureus* and Gram-negative *Klebsiella pneumoniae* and *Escherichia coli* that are known to be significant pathogens responsible for urinary tract infections (UTIs) and other infections. UTIs are among the most prevalent infectious diseases, affecting millions of people worldwide, and are a significant healthcare burden (Flores-Mireles *et al.*, 2015). Bacteria are known to be the leading cause of UTIs, particularly in healthcare settings and among hospitalized patients (Paczosa and Mecsas, 2016). One of the most common bacterial diseases in humans is ~~(~~UTI~~s)~~. In healthcare settings, it is known to be affecting individuals of all ages and genders (Flores-Mireles *et al.*, 2015). In UTI, *Klebsiella pneumoniae* has emerged as a significant causative agent of UTIs, particularly in nosocomial settings and among hospitalized patients (Paczosa and Mecsas, 2016). Also, Gram-positive bacteria like *Staphylococcus aureus* are frequently present in UTIs. *Escherichia coli*, a Gram-negative bacterium, is the most predominant causative agent of UTIs, responsible for approximately 80% of community-acquired and also average rate of about 40% of hospital-acquired cases (Ramírez-Castillo *et al.*, 2018).

The increasing prevalence of antibiotic resistance in bacteria has become a worldwide public health issue that presents several difficulties in the effective management and treatment of UTIs (Lerminiaux and Cameron, 2019). The widespread and indiscriminate uses of antibiotics, together with the capacity of bacteria to use horizontal gene transfer pathways to acquire and spread resistance genes, has contributed to the rapid emergence and spread of multidrug-resistant (MDR) and extensively drug-resistant (XDR) bacterial strains (Shrivastava *et al.*, 2018). Antibiotic susceptibility is defined as the ability of an antibiotic to act effectively by inhibiting or killing a particular bacterial strain. Antibiotic resistance among uropathogenic bacteria is mediated by various mechanisms, including the production of extended-spectrum beta-lactamases (ESBLs), carbapenemases, and other enzymes that inactivate antibiotics, as well as the acquisition of efflux pumps and modifications in the target sites of antibiotics (Munita and Arias, 2016). These processes confer resistance to several antibiotic classes, drastically reducing the range of available treatments and raising morbidity, death, and medical expenses (Gandra *et al.*, 2014). In Nigeria, several studies have reported alarmingly high rates of antibiotic resistance among urologic bacterial isolates, with a significant prevalence of infections by MDR and XDR strains (Mohd-Asri *et al.*, 2021).

Monitoring antibiotics susceptibility patterns is crucial for guiding appropriate antibiotic therapy and detecting the emergence and spread of antibiotic resistance (Said *et al.*, 2021). Understanding local antibiotics resistance patterns is crucial for guiding appropriate empiric therapy, developing evidence-based treatment guidelines, and implementing effective infection control measures. Failure to address the problem of antibiotic resistance in uropathogenic bacteria can lead to treatment failures, prolonged hospital stays, increased risk of complications, and higher healthcare costs (Bassetti *et al.*, 2018).

Although the study area has been of interest in the surveillance of antibiotic resistant bacteria among individuals with UTIs, the fact that multiple resistance patterns of bacteria varies over time, therefore, makes it imperative to routinely conduct surveillance of antibiotic_resistant bacteria in the study environment. Hence, this study was aimed to determine the current prevalence of multiple antibiotic resistance uropathogenic bacteria and their antibiotic susceptibility

patterns among individuals who reported at a teaching hospital in Ado Ekiti, Ekiti State, and Southwestern Nigeria.

MATERIALS AND METHODS

Description of study location

The study was carried out and samples collected from a healthcare facility within the metropolis. This facility offers comprehensive inpatient and outpatient services to the general public. It also offers specialized and referral services to the population.

Sample collection and processing

Bacterial samples were obtained from routine mid-stream urine samples collected from patients that were referred to the microbiology laboratory between January and March, 2024. The routine samples were collected in sterile urine sample bottles and processed immediately in the laboratory. The urine samples were streaked in Cysteine Lactose Electrolyte Deficient medium (CLED), mannitol salt agar and MacConkey agar simultaneously. The colony counts were taken on the CLED and bacterial counts equivalent to 10^5 cfu/mL were regarded as significant bacteriuria. Colonies were presumptively selected and streaked from the corresponding MacConkey and mannitol salt agar plates and were subcultured into fresh agar plates to get the pure cultures of the bacteria. Standard biochemical tests such as indole, methyl red, citrate utilization, Voges-Proskauer, oxidase test and sugar fermentation tests were carried out to identify the bacterial isolates (Cappuccino and Sherman, 2019). All bacteria were kept in sterile nutrient agar slants and refrigerated at 4^OC until further use. Fifty Gram-negative isolates (8 *E. coli*, 25 *K. pneumoniae*, and 17 *P. aeruginosa*) and six Gram-positive bacteria that were *S. aureus* were recovered from the samples (Figure 1). Slant bottles that were frequently used for long-term preservation and transportation of bacterial cultures, were employed to hold each isolate. Until additional examination, the slants were stored in a refrigerator at 4°C.

Antibiotic Susceptibility Test

Antibiotic susceptibility testing was carried out on all isolates using the agar disk diffusion method. Mueller Hinton Agar (MHA) was prepared according to the manufacturer's procedure. The agar was poured into well-labeled petri dishes and allowed to solidify. A loop of 24 hours old bacterial culture was inoculated into 5 ml Mueller-Hinton broth and incubated at 37°C for 4 hours. The inocula for each bacterium was standardized to match the 0.5 McFarland standard (Khan *et al.,* 2019). A sterile swab was dipped into the standardized bacterial suspension and used to inoculate freshly prepared sterile Mueller Hinton agar plates (Balouiri *et al.,* 2016). Antibiotic discs were placed onto the surface of the inoculated agar. The antibiotics (Biomark) were: cefuroxime (10µg), ampicillin (10µg), vancomycin (30µg), ceftazidime (15µg), tetracycline (30µg), cotrimoxazole (25µg), gentamicin (10µg), augmentin (30µg), erythromycin (5 µg), meropenem 15µg), cephalexin (10 µg), ciprofloxacin (5µg), cefotaxime (30µg), ceftriaxone (30µg), amikacin (30µg) and chloramphenicol (10µg). The plates were incubated at 37°C for 18-24 hours. After incubation, the zones of inhibition were measured in millimeters and compared with the clinical standard laboratory institution's guidelines (CLSI, 2017) to classify the results as sensitive, intermediate and resistance. Resistance of the isolates to antibiotics in two or more distinct classes of antibiotics was referred to as multiple drug resistance (MDR).

Detection of Biofilm Formation

All bacteria were subjected to a biofilm test to detect biofilm formation among bacteria from the different samples. The Brain heart infusion agar (BHI) fortified with Congo red was used for the detection of biofilm producers. The bacteria were inoculated into the agar plates and were incubated at 37°C for 24 hours. After incubation, the plates were inspected for the presence of characteristic biofilm appearance. The colonies with characteristic red appearance on the agar plates were identified as potential biofilm producers (Khan *et al.,* 2019).

Statement of ethical approval

This study was approved by the ethical committee before samples were taken for analysis. Permission was obtained from the hospital and laboratory personnel.

RESULTS AND DISCUSSION

All bacteria were identified using conventional biochemical tests (Table 1). Fifty six isolates were recovered (n = 56). Among the bacteria recovered, 50 isolates comprising of *E. coli* (8), *Pseudomonas aeruginosa* (17), and *Klebsiella pneumonia* (25) were the Gram-negative bacteria, while 6 isolates of *S. aureus* were the only Gram-positive (Table 1). All Gram-negative bacteria were resistant to ceftazidime. One isolate each was susceptible to vancomycin, ceftriaxone and cefotaxime while others were resistant to other antibiotics. The results showed that bacteria demonstrated the highest susceptibility to chloramphenicol (Table 2). Results also showed that the frequencies of resistance across the Gram-negative bacteria were evenly distributed (Table 2). All the six strains of *S. aureus* showed resistance to all antibiotics except erythromycin and cephalexin (Table 3). Multiple antibiotics resistance among the bacteria showed prominently. Thirty five different antibiotic resistance patterns were observed with different frequencies of occurrence. However, the most commonly observed resistance phenotypes were Crx-Van-Ctr-Ctx-Cpz-Tet-Gen-Mem-Cot-Amk, Crx-Van-Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Cip-Amk and Crx-Van-Chl-Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Cip-Amk. In addition, several phenotypes occurred only once among the bacterial isolates (Table 4). The multiple antibiotic resistance further indicated that most of the bacteria showed resistance to multiple antibiotics (Table 5).

Table 1: Occurrence of uropathogenic bacteria from patients with UTI (n=56)

S/N	Bacterial identities	Frequencies
1	*Staphylococcus aureus*	6 (10.7%)
2	*Pseudomonas aeruginosa*	17 (30.1%)
3	*Klebsiella pneumoniae*	25 (44.6%)
4	*Escherichia coli*	8 (14.3%)
	TOTAL	56 (100.0%)

Table 2: Resistance to antibiotics by each of the Gram-negative uropathogenic bacteria (*n*=50)

S/N	Antibiotics	*P. aeruginosa*	*K. pneumoniae*	*E. coli*	Total
1	Crx	16_(32.0%)	25 (50.0%)	7 (14.0%)	48 (96.0%)
2	Van	16 (32.0%)	25 (50.0%)	7 (14.0%)	48 (96.0%)
3	Chl	7 (14.0%)	8 (16.0%)	2 (4.0%)	17 (34.0%)
4	Ctr	16 (32.0%)	25 (50.0%)	8 (16.0%)	49 (98.0%)
5	Ctx	17 (34.0%)	25 (50.0%)	7 (14.0%)	49 (98.0%)
6	Cpz	17 (34.0%)	25 (50.0%)	8 (16.0%)	50 (100.0%)
7	Tet	9 (18.0%)	23 (46.0%)	7 (14.0%)	39 (78.0%)
8	Cot	9 (18.0%)	20 (40.0%)	2 (4.0%)	31(62.0%)
9	Gen	13 (26.0%)	22 (44.0%)	6 (12.0%)	41(82.0%)
10	Mem	14 (28.0%)	24 (48.0%)	7 (14.0%)	45 (90.0%)
11	Cip	8(16.0%)	13(26.0%)	2(4.0%)	23(46.0%)
12	Amk	10(20.0%)	20(40.0%)	6(12.0%)	36(36.0%)

Keys/Legends

Crx = Cefuroxime, Amp = Ampicillin, Van = Vancomycin, Cpz = Ceftazidime, Tet = Tetracycline, Cot = Cotrimoxazole, Gen = Gentamicin, Aug = Augmentin, Ery = Erythromycin, Mem = Meropenem, Cp = Cephalexin, Cip = Ciprofloxacin, Ctx = Cefotaxime, Ctr = Ceftriaxone, Amk = Amikacin, Chl = Chloramphenicol

Table 3: Overall resistance of *Staphylococcus aureus* to antibiotics (*n*=6)

S/N	Antibiotics	Resistance (%)
1	Ampicillin	6 (100.0%)
2	Meropenem	6 (100.0%)
3	Erythromycin	3 (50.0%)
4	Tetracycline	6 (100.0%)
5	Cotrimoxazole	6 (100.0%)
6	Cefuroxime	6 (100.0%)
7	Gentamicin	6 (100.0%)
8	Ciprofloxacin	6 (100.0%)
9	Augmentin	6 (100.0%)
10	Vancomycin	6 (100.0%)
11	Ceftazidime	6 (100.0%)
12	Cephalexin	5 (80.0%)

Table 4: Result of antibiotics resistance patterns of uropathogenic bacteria

S/N	No of antibiotics	Resistance pattern	*K. pneumoniae*	*E. coli*	*P. aeruginosa*	*S. aureus*	Total
1	4	Ctr-Cpz-Tet-Mem	-	1	-	-	1
2	6	Ctr-Ctx-Cpz-Amk-Crx-Van	-	1	-	-	1
3		Crx-Van-Ctr-Ctx-Cpz-Mem	-	-	1	-	1
4		Van-Ctr-Ctx-Cpz-Gen-Amk	-	-	1	-	1
5	7	Crx-Van-Ctr-Ctx-Cpz-Tet-Gen	1	-	-	-	1
6		Crx-Van-Chl-Ctx-Cpz-Cot-Gen	-	-	2	-	2
7		Crx-Van-Ctr-Ctx-Cpz-Mem-Amk	-	-	1	-	1
8	8	Crx-Van-Ctr-Ctx-Cpz-Tet-Mem-Amk	1	-	-	-	1
9		Crx-Van-Ctr-Ctx-Cpz-Cot-Gen-Mem	1	-	-	-	1
10	9	Crx-Van-Ctr-Ctx-Cpz-Tet-Mem-Cip-Amk	1	-	-	-	1
11		Crx-Van-Ctr-Ctx-Cpz-Cot-Gen-Mem-Cip	1	-	-	-	1
12		Crx-Van-Ctr-Ctx-Cpz-Tet-Cot-Mem-Amk	1	-	-	-	1
13		Crx-Van-Ctr-Ctx-Cpz-Tet-Gen-Mem-Amk	1	-	-	-	1
14		Ctr-Ctx-Cpz-Tet-Gen-Mem-Amk-Crx-Van	-	2	-	-	2
15		Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Crx-Van	-	1	-	-	1
16		Crx-Van-Ctr-Ctx-Cpz-Cot-Gen-Mem-Amk	-	-	1	-	1
17		Crx-Van-Chl-Ctr-Ctx-Cpz-Gen-Mem-Cip	-	-	1	-	1
18		Crx-Van-Chl-Ctr-Ctx-Cpz-Tet-Cot-Mem	-	-	1	-	1
19		Crx-Van-Chl-Ctr-Ctx-Cpz-Tet-Gen-Mem	-	-	1	-	1
20	10	Crx-Van-Ctr-Ctx-Cpz-Tet-Gen-Mem-Cot-Amk	4	1	-	-	6
21		Crx-Van-Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Cip	1	-	-	-	2
22		Crx-Van-Chl-Ctx-Cpz-Tet-Cot-Gen-Mem-Cip	1	-	-	-	1

23		Crx-Van-Ctr-Ctx-Cpz-Tet-Gen-Mem-Cip-Amk	-	-	1	-	1
24		Crx-Van-Ctr-Ctx-Cpz-Mem-Cot-Gen-Cip-Amk	-	-	1	-	1
25		Crx-Van-Ctr-Ctx-Cpz-Tet-Cot-Gen-Cip-Amk	-	-	1	-	
26		Crx-Van-Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Cip	-	-	1	-	
27		Amp-Mem-Tet-Cot-Crx-Gen-Cip-Aug-Van-Cpz	-	-	-	1	1
28		Crx-Van-Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Amk	-	-	1	-	1
29	11	Crx-Van-Chl-Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Amk	2	-	-	-	2
30		Crx-Van-Chl-Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Cip	1	-	1	-	2
31		Crx-Van-Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Cip-Amk	5	-	-	-	5
32		Chl-Ctr-Ctx-Cpz-Tet-Gen-Mem-C`Ip-Amk-Crx-Van	-	2	1	-	3
33		Amp-Mem-Tet-Cot-Crx-Gen-Cip-Aug-Van-Cpz-Cp	-	-	-	2	2
34	12	Crx-Van-Chl-Ctr-Ctx-Cpz-Tet-Cot-Gen-Mem-Cip-Amk	4	-	1	-	5
35		Amp-Mem-Ery-Tet-Cot-Crx-Gen-Cip-Amk-Van-Cpz-Cp	-	-	-	3	3
		TOTAL	**25**	**8**	**17**	**6**	**56**

KEYS/LEGENDS: Crx-Cefuroxime, Van- Vancomycin, Chl- Chloramphenicol, Ctr- Ceftriaxone, Ctx- Cefotaxime, Cpz- Ceftazidime, Tet- Tetracycline, Cot- Cotrimoxazole, Gen- Gentamycin, Mem- Meropenem, Cip- Ciprofloxacin, Amk- Amikacin

Table 5: Result for Multiple Antibiotic Resistance Index (MARI)

S/N	MARI	Frequencies
1	0.33	1
2	0.50	3
3	0.58	4
4	0.67	2
5	0.75	11
6	0.83	13
7	0.92	14
8	1	8

The emergence and spread of resistant strains of uropathogenic bacteria is well known to have caused a lot of compromise to individual and public health (Clegg and Murphy, 2017). The prevalence of this urinary tract infection is known to be high among women, while it shows some commonality among different demographic groups. The results presented in this study proved there are uropathogenic bacteria that are implicated in UTI among individuals that reported within the location at the specific period (Clegg and Murphy, 2017).

The occurrence of uropathogenic bacteria from patients with UTI is shown in this study. The resistance of bacteria towards antibiotics has been associated with several complications in the host and even the general public (Ahmed *et al.,* 2019). This present study shows a high rate of resistance among bacteria isolated from the individuals. The highest (25, 44.6%) occurring bacterium observed in this study among patients with UTI is *Klebsiella pneumonia*. This further confirms the bacterium as the most occurring aetiological agent in UTIs in clinical and subclinical settings (Ahmed *et al.,* 2015). Several studies have reported Klebsiella *pneumonia* as the most frequently isolated bacterium in UTI. The *Pseudomonas aeruginosa* also featured prominently among the bacterial aetiology observed among the patients with UTI with 17 (30.1%) of all isolates recovered. This bacterium is also common in UTI, especially in clinical environments and their ability to form biofilms have been noted (John *et al.,* 2017).

It was also observed in this study that the proportion of resistance by each bacterium to the different antibiotics was high. Generally, the bacteria were observed to show the highest rate of resistance to the cephalosporins, especially ceftazidime (100%), cefuroxime (96%) and cefotaxime (100%). Resistance to third generation cephalosporins has been confirmed to be a serious problem in clinical environments in management of UTIs and other related infections. They have been used as the major treatment regimen for UTIs and the high rate of resistance to these groups of antibiotics have severely limited the treatment options for UTIs and other types of infections. The third generation cephalosporins always demonstrate a broad spectrum of activity and the high rate of resistance in this study implies that resistance to them could diminish their efficacy. This could lead to further complications during treatment (Mark *et al.,* 2021).

It was equally noted that the bacteria also showed resistance (90%) to meropenem, which is a prominent antibiotic among the carbapenems. The carbapenems are considered as

antibiotics of last resort, meaning that physicians resort to use the antibiotic when other drugs, especially those among the third generation cephalosporins have failed (Metis, 2016). The resistance of the bacteria to carbapenems connotes a serious public health threat with potential to further aggravate the high burden of antibiotic resistance.

However, previous studies have reported low resistance to meropenem. This shows that prevalence of resistance in various clinical settings. The study by Ahmed *et al.,* (2019) reported high susceptibility to meropenem among *Klebsiella* spp. The study also reported low resistance to ciprofloxacin (9.1%) which is slightly similar to this present study (26.0%). Ahmed *et al.* (2019) also showed low resistance among *K. pneumonia* to cephalosporins, in contrast to what was observed in this study. The *Pseudomonas aeruginosa* isolates were resistant to ceftazidime but not as high as what was obtained for *Klebsiella pneumonia.* In contrast, high prevalence of resistance to *Pseudomonas aeruginosa* have been reported (Ahmed *et al.,* 2019). This present study is in contrast to a study by Ahmed *et al.* (2019) which reported the resistance towards ceftazidime among *P. aeruginosa* goes consistently over 75%. This is most likely due to the massive use of third-generation cephalosporins and fluoroquinolones among UTIs patients. Therefore, they were increasingly recognized as important causes of UTIs and our study findings highlight the significance of this species as a leading cause of MDR infection in patients with UTIs.

The etiology of bacteria causing UTI as well as their susceptibility to antimicrobials continue to vary over time period and it is different among different countries (Bitew *et al.,* 2022). However, this present study reported a total percentage of 62.0% to cotrimoxazole in which *Klebsiella, E. coli* and *Pseudomonas aeruginosa* and isolates were observed with 40.0%, 4.0%, and 18.0%, respectively. All the *Staphylococcus aureus* isolates showed resistance to cotrimoxazole. Similarly, previous studies have reported varied resistance to cotrimoxazole among bacterial uropathogens in clinical and community settings (Ahmed *et al.,* 2019). Overall resistance to trimethoprim/ sulfamethoxazole was 49.4% and *E. coli*-specific resistance to the antibiotic was 58.3%. Recent studies also reported similar findings of such a high rate of resistance to trimethoprim/sulfamethoxazole (Sharef *et al*., 2015). The high resistance in trimethoprim/sulfamethoxazole susceptibility pattern may be due to non-judicious use and over-the-counter selling of this antibiotic. The *Escherichia coli* also featured prominently among patients with UTI in this study. This agrees with the findings of Kulkarni *et al.* (2017) which reported high prevalence of antimicrobial resistance among urinary isolates. In the study, *E. coli* was isolated from 67.5% samples and more than 35% isolates showed resistance to commonly used antibiotics in UTI.

It was noted in this study that all the bacteria isolated from the UTI were all presumptive biofilm producers. Biofilm formation by bacteria inside the bladder leads to recurrent infections and also increases the possibility of MDR strain causing UTI. Biofilms are aggregation of bacterial cells that are trapped within a matrix and can remain on solid surfaces, especially in hospital environments. Such biofilms also form a major component of virulence for pathogenic bacteria especially those involved in UTI. The aggregation of cells makes it difficult for antibiotics to penetrate, requiring higher concentrations of antimicrobials with high risk of adverse effect and toxicity. This study agrees with several findings that have reported that bacterial uropathogens form extensive biofilms that complicate treatment of UTIs through the development of resistance to several antibiotics (Delcaru *et al.,* 2016). Biofilms form on the surfaces of urinary catheters used in adult patients and they serve as conduits of transfer of antibiotic resistance bacterial biofilms into the bladder and other parts of the urinary tracts (Trautner, 2004).

This research work will have an important impact on the treatment and management of patients with hospital acquired UTI (HAUTI) and catheter-associated UTI (CAUTI), particularly those patients who are infected with multidrug resistant uropathogens. It should be noted that MDR in UTIs is increasing globally causing most antibiotics to lose their therapeutic value. Efforts should be intensified to ensure that clinicians realize that the possibility of multidrug resistance is high in the management of UITs. Second, the occurrence of MDR which we observed in this present study is a serious threat in the management of patients with these urinary tract infections (Ahmed *et al*., 2019).

Chloramphenicol was observed to be susceptible to most of these uropathogenic bacteria isolates in which this has proved to us that the antibiotic can effectively inhibit the growth of uropathogenic bacteria like *Klebsiella pneumoniae, Escherichia coli, Pseudomonas aeruginosa* and *Staphylococcus aureus.* This antibiotic can effectively treat UTIs caused by susceptible uropathogen in which this leads to rapid symptom resolution and cure. Strains of *Escherichia coli* that were susceptible to this antibiotic can be treated with a shorter course of chloramphenicol, thereby reducing the risk of antibiotic-related side effects. However, it is important to note that chloramphenicol use is limited due to its potential to cause serious side effects such as bone marrow suppression and grey baby syndrome (Pacifici *et al.,* 2018). Chloramphenicol is usually reserved for severe infections or when other antibiotics have failed or are observed to be ineffective. The treatment guidelines published by the European Urology Association in 2015 listed cotrimoxazole and ciprofloxacin as alternative treatment options and recommended fosfomycin, nitrofurantoin, and pivmecillinam as the first choice (Nicolle *et al.,* 2019).

CONCLUSION

This study revealed that bacterial pathogens isolated from patients with UTIs at the study location showed resistance to multiple antibiotics. More specifically, the bacteria showed elevated resistance to third generation cephalosporins which are first line antibiotics used for treatment of patients with UTIs. The antimicrobial resistance patterns of the causes of these UTI are highly variable and continuous surveillance of trends in resistance patterns of uropathogens is necessary. This research work has shown that patients who were presented with urinary tract infection in this teaching hospital are at high risk of antibiotic resistant infections. All the bacteria were potential biofilm producers which could further complicate treatment of UTIs in the study location. There should be strict antimicrobial stewardship programs to mitigate the transmission of antibiotic resistant infections and also to preserve the efficacy of existing antibiotics.

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