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Prevalence of Antibiotic-Resistant Gram-Negative Bacteria among Patients with Urinary Tract Infection at a Facility in Ado Ekiti, Ekiti-State, Nigeria

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Abstract

Urinary Tract Infections (UTIs) constitute a huge public health burden especially in developing countries. This study was carried out to determine the current incidence of antibiotic resistance among Gram-negative bacteria recovered from urine of patients with UTI. This study used a cohort study design wherein one hundred and twenty one (121) mid-stream urine samples were collected and cultured onto sterile Cysteine Lactose Electrolyte Deficient medium (CLED) and MacConkey agar plates. All bacteria recovered were tested for resistance to the selected antibiotics as follows: ceftazidime (30 µg), ceftriaxone (30 µg), gentamicin (1 0µg), ampicillin (10 µg), meropenem (10 µg), ertapenem (10 µg), tetracycline (30 µg), norfloxacin (10 µg) and pefloxacin (5 µg). Twenty (20) isolates were chosen for detection of extended spectrum beta-lactamase producers using the double disk synergy test (DDST). All the bacteria were tested for biofilm production and haemolysis. Among the one hundred and twenty-one (121) mid-stream urine samples collected from patients, forty-six (46) samples grew significant bacteria. The bacteria recovered were Klebsiella pneumonia17 (37.0%), Klebsiella oxytoca 2 (4.3%), Escherichia coli (32.6%) and Proteus mirabilis (26.0%). Overall, the bacteria showed the highest resistance to pefloxacin (97.8%) and least resistance to meropenem (34.7%). The bacteria also showed high multiple resistance. All the bacteria subjected to DDST were confirmed as extended-spectrum beta-lactamase ESBL producers. Forty (43.6%) bacteria were designated as strong biofilm producers while 17.4 % bacteria showed hemolysis. The findings obtained in this study have ramifications for clinical management of UTI and public health public health in general. There should be strict enforcement of antibiotic stewardship.

Keywords: Gram-negative bacteria, Urinary tract infection(s), Antibiotic, Resistance, Biofilm.

INTRODUCTION

The UTI is the infection that infects the whole or parts of the urinary tract in humans (Shih *et al.,* 2019; Tan & Chlebicki, 2016). The major classes of UTI are the non-complicated UTI, which are as a result of compromised immune status of infected individuals and compromised UTIs which are active invasion of the urinary tract by pathogenic organisms (Bono *et al.,* 2023; Eliakim-Raz *et al.,* 2018; Jancel, 2002). UTIs have constituted a serious economic and public health burden in terms of mortality, morbidity, increased cost of treatment and healthcare and increased days of hospitalization (Li *et al.,* 2022; Yang *et al.,* 2022). In addition, UTIs are reputed to be the most common infection globally and Nigeria has its share of the global burden (Huang *et al.,* 2022; Shih *et al.,* 2019). The epidemiology of UTI spans across different age groups that includes children, adults, the elderly, pregnant women and overall immuno-

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compromised individuals (Çağ et al., 2021; Lawani et al., 2015; Okonko et al., 2009; Shih et al., 2019). UTI is also associated with certain risk factors and co-morbidities which include diabetes among the different age groups (Yenehun Worku *et al.,* 2021). Other risk factors for UTI are associated with pregnancy, frequent sexual intercourse, family history, conformed history of UTI (Eliakim-Raz et al., 2018; Storme et al., 2019).

As stated earlier, Nigeria also has its share of the global burden of UTI shared across different geographical locations and different age groups. A study carried out at Ile Ife Nigeria confirmed more than one thousand cases of UTI across five years (Ako-Nai *et al.,* 1993). UTI is more common among female patients in Nigeria, as confirmed by different studies carried out in different parts of the country (Obiogbolu *et al.,* 2009; Okonko *et al.,* 2009; Oli *et al.,* 2017). UTI has also been reported in core rural settings in Nigeria with associated mortality and morbidity in such settings (Oladeinde *et al.,* 2011). The array of scientific evidence confirming UTI in different settings, age groups and hospital environments in Nigeria is a serious cause for concern.

Antibiotics are the mainstay of treatment for UTIs in different parts of the world including Nigeria (Abbott et al., 2022; Langenstroer et al., 2022; Mohamed et al., 2023). The common antibiotics that are used for the treatment and management of UTIs include the fluoroquinolones, third generation cephalosporins and other types of beta lactams (Bader *et al.,* 2020). Other novel antibiotics such as pivmecillinam and mecillinam have been used for treatment of UTIs in different setting (Hansen *et al.,* 2022; Jensen *et al.,* 2022). The heavy dependence on the use of antibiotics for the treatment and management of UTI has raised concerns due the emergence of antibiotic resistant bacteria (Haindongo *et al.,* 2022). This growing incidence of UTI caused by antibiotic resistant bacteria has added layers of complication for the treatment of UTIs (Mohamed *et al.,* 2023). The common antibiotic resistant bacteria implicated in UTI are extended-spectrum beta-lactamase (ESBL) producing *Escherichia coli* and *Klebsiella pneumoniae.* Related studies in Nigeria have confirmed that the incidence of antibiotic resistant bacteria in UTI is increasing (Oli *et al.,* 2017). Furthermore, the emergence of some bacterial uropathogens that show resistance to third generation cephalosporins, carbapenems and polymyxins in different clinical environments in Nigeria has posed a serious cause for concern due to the risk of prolonged treatment complications that may be associated with such resistant strains (Iregbu & Nwajiobi-Princewill, 2013).

In view of the reported prevalence of antibiotic resistant UTIs globally and in different clinical environments in Nigeria, it is equally necessary to gain some knowledge of possible prevalence of the infection in sub-urban areas in Nigeria, where healthcare facility is located. Therefore, this study was conducted to ascertain the present frequency of several antibiotic resistant Gram-negative bacteria and their current patterns of antibiotic resistance among people who reported at a tertiary healthcare facility in Ekiti-State, Nigeria. The findings obtained would enable the design of mitigatory and treatment measures that will be useful to curtail the presence of uropathogens in the clinical setting under view.

MATERIALS AND METHODS

Study Location and Sample Collection

Urine samples were collected at a healthcare facility in Ado-Ekiti, Ekiti-State, Nigeria. Recently urinated midstream samples were taken from inpatients and outpatients between March 2018 and July 2018 (Table 1). One hundred and twenty one (121) samples were collected. Out of this number, forty-six (46) urine samples grew bacteria. The distribution of the samples according to the wards and units is shown in Table 2. Ethical permission was obtained before samples were collected.

Table 1: Demographic characteristics of patients with significant urine bacterial growth

Demographic details	**(n = 46)**
Sex	
Male	22 (47.8%)
Female	24 (52.2%)
Age	
≥70 yrs	8 (17.3%)
41-70 yrs	16 (34.8%)
41-70 yrs	16 (34.8%)
11-40 yrs	21 (45.7%)
≤10 yrs	1 (2.2%)
Outpatients/inpatients	
Inpatients	15 (32.6%)
Outpatients	31 (67.4%)

Table 2: Total number of samples according to hospital units

Patient type	**Unit**	**Number**
Outpatients	OPD	28
	A/E	12
	O/G	5
	Clinic/MED	1
	ANC	2
Inpatients		
	Urology	1
	FMW	1
	FSW	2
	MSW	3
	ARD	-
	ICU	-
	ORTHO	-
	PALPI	3
	CHEW	3
	MMW	3
	OHW	1
	ANW	3
	HDU	1
	ER	1
	CW	2
	Others	49
Total		**121**

Note: A/E- Accident and Emergency Department, O/G- Obstetrics and Gynecology Department ANC-Antenatal Care, OPD- Surgical Out-patient Department, MSW- Male Surgical Ward FMW- Female Surgical Ward ARD- Ascites Reinfusion Dialysis ICU- Intensive Care Unit Ortho- Orthopedic.

Culture Procedure

Ten microliters (10 µl) was pipetted per urine sample and transferred to sterile MacConkey agar and Cysteine Lactose Electrolyte Deficient medium (CLED) and thereafter incubated for

24 hours at 37 °C. For each sample, colony counts equivalent to ≥ 10^5 CFU/mL on CLED was considered as bacteriuria. Colonies were presumptively selected from the corresponding MacConkey agar plates and were sub-cultured into fresh agar plates. Standard biochemical assays were used to identify the bacteria, and they were all kept on nutrient agar slants for future tests (Cheesbrough, 2006).

Antibiotic Susceptibility Tests and Detection of Extended-Spectrum Beta-Lactamase Producers

All bacterial isolates underwent antibiotic disk diffusion for susceptibility testing, which in accordance with the Clinical Laboratory Science Institute's interpretation standards. (Patel, 2017). A few colonies of the bacteria were inoculated onto sterile normal saline that had been modified to meet the 0.5 turbidity criterion after being cultured overnight on sterile Mueller Hinton agar plates. Ertapenem (10 mg), meropenem (10 mg), ceftazidime (30 mg), ceftriaxone (30 mg), gentamicin (10 mg), ampicillin (10 mg), tetracycline (30 mg), norfloxacin (10 mg), and pefloxacin (5 mg) were all used (Oxoid, UK). Multiple drug resistance (MDR) refers to isolates that are resistant to at least two different classes of antibiotics. All tests for antibiotic susceptibility were conducted using the *E. coli* ATCC 25922 as the control. Using the common double disk synergy test, 20 ESBL producers that displayed decreased susceptibility to either ceftazidime, ceftriaxone, or any of the carbapenems was discovered. In this experiment, disks containing amoxicillin-clavulanic acid were positioned in the middle of Mueller-Hinton agar plates containing the bacterial uropathogens. This disk was surrounded by third generation cephalosporins, ceftazidime and ceftriaxone disks placed 20 mm measured from the center of the agar where amoxicillin-claviculanic disk is located. Bacteria that showed enhanced inhibition zone were recognized as ESBL producers.

Detection of Biofilm Formation

All the bacteria recovered as specified were examined for biofilm production using the Congo red agar method. On agar plates with Congo red added, all bacteria were cultivated before being incubated for 24 hours at 37 °C. Black crystalline colony formations were interpreted as evidence that the bacterial isolates had formed biofilms. Grey colonies indicated intermediate biofilm producers, while red colonies indicated non-biofilm producers (Melo *et al.,* 2013).

Detection of Hemolytic Activity

All bacteria were inoculated on Mueller-Hinton agar plates containing 5% blood. The plates were incubated at 35 °C for 24 hours to identify those with hemolytic activity of all the bacteria (Ruiz *et al.,* 2002*).* The plates were subsequently checked for characteristic hemolytic patterns for interpretation (Desai *et al.,* 2021).

RESULTS

Forty-six (46) Gram-negative bacteria were obtained from urine samples across the different wards and units (Table 3). The bacteria recovered were *Escherichia coli, Klebsiella pneumoniae, Klebsiella oxytoca* and *Proteus mirabilis.* The bacteria recovered from the different wards and units are shown in (Table 4) with the outpatient department (OPD) emerging as the unit where the highest number of bacteria was isolated. The *K. pneumonia* had the highest frequency of isolation from samples, followed by *Escherichia coli (*Table 3). Many of the Gram-negative bacteria isolated showed reduced susceptibility to different antibiotics. Overall, resistance to pefloxacine was highest in this healthcare facility, followed by reduced susceptibility to ampicillin and tetracycline respectively (Table 5). The frequency of resistance demonstrated against the different antibiotics among the different organisms is shown in (Table 6). In this study, multiple antibiotic resistance to antibiotics was considered as resistance of a bacterium to two or more antibiotics of different classes and bacteria recovered also showed considerable level of multiple antibiotic resistance (Table 7). Twenty different bacterial isolates were selected for ESBL production on the basis of their reduced susceptibility to caftazidime, ceftriaxone and multiple antibiotic resistance patterns. They were all confirmed to be ESBL producers based on their patterns observed with the double disk synergy test (Table 8). Eight bacterial isolates showed hemolysis among the bacteria that were recovered from the second location (Table 9). Majority of the bacteria produced biofilms (Table 10).

Table 3: Frequency of organisms recovered from urine samples

Bacteria	**No (%) (n= 46)**
K. pneumoniae	17 (40)
K. oxytoca	2 (4.3)
E. coli	15 (32.6)
P. mirabilis	12 (26.1)
TOTAL	**46**

Table 4: Frequency of bacterial isolates according to wards and units

Wards/Units	***K. pneumoniae*** **(n=17)**	***K. oxytoca*** **(n=2)**	***E. coli*** **(n=15)**	***P. mirabilis*** **(n=12)**
OPD	9 (52.9%)	2 (100.0%)	10 (66.6%)	5 (41.6%)
A/E	2 (11.8%)	0 (%)	0 (%)	2 (16.7%)
O/G	0 (%)	0 (%)	2 (13.3%)	1 (8.3%)
ANC	0 (%)	0 (%)	0 (%)	1 (8.3%)
MED	1 (5.9%)	0 (0%)	0 (%)	0 (%)
HDU	1 (5.9%)	0 (%)	0 (0%)	0 (%)
MSW	0 (0%)	0 (0%)	2 (13.3%)	0 (0%)
FMW	0 (0%)	0 (0%)	0 (0%)	1 (8.3%)
CW	2 (11.8%)	0 (0%)	0 (0%)	0 (0%)
FSW	0 (0%)	0 (0%)	0 (0%)	1 (8.3%)
PALPI	0 (0%)	0 (0%)	1 (6.7%)	0 (0%)
MMW	2 (11.8%)	0 (0%)	0 (0%)	1 (8.3%)

Key: A/E- Accident and Emergency Department, O/G- Obstetrics and Gynecology Department ANC-Antenatal Care, OPD- Surgical Out-patient Department, MSW- Male Surgical Ward FMW- Female Surgical Ward ARD-Ascites Reinfusion Dialysis ICU- Intensive Care Unit Ortho- Orthopedic.

Table 5: Overall antibiotic susceptibility to individual antibiotics among bacterial isolates

	n =46	
Antibiotic	**Susceptible (%)**	**Resistant (%)**
Meropenem	30 (65.2)	16 (34.8)
Ertapenem	29 (63)	17 (37)
Ceftazidime	20 (43.5)	26 (56.5)
Ceftriaxone	16 (34.8)	30 (65.2)
Norfloxacin	13 (28.3)	33 (71.7)
Gentamicin	8 (17.4)	38 (82.6)
Ampicilin	2 (4.3)	44 (95.7)
Tetracycline	5 (10.9)	41 (89.1)
Pefloxacin	1 (2.2)	45 (97.8)

Table 6: Individual antibiotic resistance among bacterial isolates

Antibiotic	*K. pneumonia* (n= 17)	*K. oxytoca* (n= 2)	*E. coli* (n= 15)	*P. mirabilis* (n= 12)
Ertapenem	7 (41.2)	0	3 (20.0%)	6 (50.0%)
Meropenem	8 (47.1)	1 (50%)	1 (6.7%)	6 (50.0%)
Ceftazidime	15 (88.2)	-	2 (13.3 %)	7 (58.3%)
Ceftriaxone	17 (100)	-	3 (20.0%)	9 (75.0%)
Gentamicin	16 (94.1)	1 (50%)	9 (60.0%)	11 (91.7%)
Ampicilin	17 (1000	2 (100%)	13 (86.7%)	11 (91.7%)
Tetracycline	15 (88.2)	1 (50%)	13 (86.7%)	12 (100.0%)
Norfloxacin	13 (76.5)	-	11 (73.3%)	8 (66.7%)
Pefloxacin	16 (94.1)	2 (100%)	13 (86.7%)	11 (91.7%)

Table 7: Multi-Drug Resistance among bacterial isolates

Number of drug groups	*K. pneumonia* (n= 17)	*K. oxytoca* (n= 2)	*E. coli* (n= 15)	*P. mirabilis* (n= 12)
3	-	-	7 (46.7%)	-
4	-	-	4 (26.7%)	2 (16.7%)
5	8 (47.1%)	1 (50.0%)	2 (13.3%)	3 (25.0%)
6	7 (41.2%)	0	1 (6.7%)	7 (58.3%)
Total	**15**	**1**	**14**	**12**

Table 8: Multiple-antibiotic resistance phenotypes among bacterial isolates

No. of antibiotics	Resistant patterns	KP	KO	EC	PM	Total (%)
2	Tet/Amp	0	0	2	0	2 (4.5)
	Amp/Pef	0	1	0	0	1 (2.25)
3	Tet/Pef/Amp	0	0	2	0	2 (4.5)
4	Pef/Nor/Amp/Etp	0	0	1	0	1 (2.25)
	Pef/Gen/Tet/Amp	0	0	0	2	2 (4.5)
	Pef/Gen/Tet/Nor	0	0	3	0	3 (6.81)
5	Pef/Gen/Tet/Amp/Mer	0	1	0	0	1 (2.25)
	Pef/Gen/Tet/Amp/Nor	0	0	3	0	3 (6.81)
6	Pef/Gen/Tet/Amp/Caz/Cro	1	0	0	0	1 (2.25)
	Pef/Gen/Tet/Amp/Cro/Mer	1	0	0	0	1 (2.25)
	Pef/Gen/Tet/Amp/Cro/Nor	1	0	1	0	2 (4.5)
7	Pef/Gen/Tet/Amp/Caz/Cro/Nor	5	0	1	3	9 (20.5)
	Pef/Gen/Tet/Amp/Cro/Mer/Etp	0	0	0	1	1 (2.25)
8	Pef/Gen/Tet/Amp/Caz/Cro/Nor/Etp	1	0	0	0	1 (2.25)
	Pef/Gen/Tet/Amp/Caz/Cro/Mer/Etp	1	0	0	0	1 (2.25)
	Pef/Gen/Amp/Caz/Cro/Nor/Mer/Etp	1	0	0	0	1 (2.25)
	Pef/Gen/Tet/Amp/Caz/Cro/Nor/Etp	1	0	1	1	3 (6.81)
9	Pef/Gen/Tet/Amp/Caz/Cro/Nor/Etp/Mer	4	0	0	5	9 (20.5)
	Total					**44**

Key: Gen- Gentamicin, Pef- Pefloxacin, Nor- Norfloxacin, Tet-Tetracycline, Etp -Ertapenem, Caz-Ceftazidime, Cro-Ceftriaxone, Amp- Ampicilin, Mer- Meropenem. *KP- Klebsiella pneumoniae, KO- Klebsiella oxytoca, PV- Proteus vulgaris, EC- Escherichia coli*

Table 9: Hemolytic patterns among bacterial isolates

Type of Haemolysis	*K. pneumonia* (n= 17)	*K. oxytoca* (n= 2)	*E. coli* (n= 15)	*P. mirabilis* (n= 12)
Beta	2 (11.8)	1 (50)	3 (20)	1 (8.3)
Alpha	-	-	-	1 (8.3)
Non-Hemolytic	15 (88.2)	1 (50)	12 (80)	10 (83.4)

Table 10: Biofilm producers among bacterial isolates

Biofilm production	*K. pneumonia* (n= 17)	*K. oxytoca* (n= 2)	*E. coli* (n= 15)	*P. mirabilis* (n= 12)
Strong	10 (58.8%)	-	11 (73.3%)	2 (16.6%)
Weak	7 (41.2%)	2 (100%)	3 (20.0%)	5 (41.7%)
Non-biofilm	-	-	1 (6.7%)	5 (41.7%)

DISCUSSION

This present study aimed to isolate Gram-negative bacteria implicated in cases of UTIs in a healthcare facility in Ekiti State and also to find out the current prevalence of multiple drug-resistant bacteria responsible for UTI in the specific clinical setting. The isolations were carried out on routine urine samples among outpatients and inpatients that reported to the different wards and the laboratory. The urine samples collected demographically spanned sexes, different age groups and different wards in the location (Table 1).

Major findings emerged from this study that are crucial for the development of mitigatory measures that can be used to prevent further increase in emergence of antibiotic-resistant bacteria in cases of UTI. Among the bacteria recovered, *K. pneumonia* appeared as the bacterium with the highest frequency in the clinical setting, and followed closely by *E. coli*. Although UTIs are caused by different organisms, the Gram-negative bacteria however, are the most common class of organisms that are etiologically linked to UTIs (Ngbede *et al.*, 2021). This finding agrees with previous studies that have also reported that, *K. pneumonia* is a major bacterium linked with UTIs in clinical and community settings (Hyun *et al.,* 2019; Podschun & Ullmann, 1998). Although *K. pneumonia* did occur most frequently in this study, others studies (e.g. Cunha et al., 2016)appeared to show that *E. coli* has the highest frequency of isolate among patients with UTI in different clinical settings. *E. coli* has also been reported as another common organism in UTI with higher frequency of isolation more than *Klebsiella* spp. as reported in this study. It can be implied that the specific organism isolated from UTI can vary in different healthcare settings.

An examination of total antibiotic susceptibility revealed that resistance to pefloxacine was the highest (97.8%), while resistance to ampicillin followed closely (95.7%), and tetracycline (89.1%). In this study, bacterial susceptibility to meropenem was the highest (65.2%) and ertapenem (63.0%), which are part of the carbapenems antibiotics. These findings also demonstrate that, compared to the total quantity of each bacterium that was recovered from the urine samples and tested for their susceptibility profile, isolated and tested for antibiotic resistance, various bacteria had varying proportions of antibiotic resistance to various antibiotics. According to reports, there are high levels of resistance to third-generation antibiotics and ampicillin, and there is a considerable level of reduced susceptibility to these antibiotics, especially ampicillin. (Cunha et al., 2016; Munkhdelger et al., 2017). Going by the report of (Leski et al., 2016), Gram-negative bacteria isolated and identified in this study exhibited high level of resistance to sulphonamides, chloramphenicol, and gentamicin, whereas ampicilin resistance was only mild. A similar study by Ali *et al.,* (2016) found a low prevalence of tetracycline and ampicillin resistance. It should be mentioned that just as the causes of UTIs vary depending on the geographic region and the clinical environment, so does their responsiveness to antibiotic treatment. As seen in this study, meropenem showed more activity compared to ertapenem, and resistance to the carbapenems was at its lowest level. Despite the fact that carbapenem resistance among bacterial illnesses has not yet reached a crisis level, the prevalence of carbepenem-resistant Gram-negative bacteria still poses a severe threat to healthcare. Reduced sensitivity to carbapenems is also being observed more frequently (Eshetie *et al.,* 2015). There are also indications of an increase in carbapenem resistance in primary clinical settings in Nigeria (Ngbede *et al.,* 2021; Jesumirhewe *et al.,* 2017). Bacteria recovered from UTIs are reputed to exhibit differences in their capacity to resist several antibiotics that belong to different classes (Jalil & Al Atbee, 2022).

Another major observation according to this study is the high frequency of bacteria that showed resistance to multiple classes of antibiotics. Forty two (42) of the bacterial isolates showed multiple resistance, equivalent to 91% of the isolated bacteria. Several reports have confirmed the growing prevalence of UTIs due to multiple antibiotic-resistant Gram-negative bacteria in core clinical and community settings (Zhanel *et al.,* 2006). A study by Mohamed *et al.* (2023) reported a high prevalence of multi-drug resistant Gram-negative bacteria as reviewed in medical records of some hospitals. Another study by Majumder *et al.* (2022) revealed that Gram-negative bacteria in some clinical settings showed high level of multiple resistance to so many antibiotics. Another study by Mahmoudi *et al.* (2014) revealed high prevalence of resistance among bacteria with *E. coli* showing the highest level of resistance to antibiotics. The predominance of multiple antibiotic resistant Gram-negative bacteria in the clinical environment implies that the bacteria will be insensitive to the antibiotics, leading to a higher rate of antibiotic treatment failure, prolonged stay in the hospital, increased risk of complications and an overall increase in the economic costs and burden of antibiotic resistant bacteria. These discoveries have important implications for public health and healthcare. The emergence of bacteria in a clinical context that are resistant to several different classes of antibiotics affects the effectiveness of antibiotic therapy and further restricts the therapeutic options for treating UTI (Saha & Sarkar, 2021).

It was observed in this present study that some of the bacteria showed resistance to the third generation cephalosporins and also carbapenems. This is a serious problem due to the high priority given to third generation cephalosporins and carbapenems which are considered as critical antibiotics within the healthcare setting. In addition, the carbapenems are often considered as antibiotics of last resort and are usually considered for use in clinical therapy when other options of antibiotics have failed in treatment. The development of ESBL by bacteria in key hospital and veterinary environments has constituted a difficult problem; and the finding in this study corresponds with this fact. Representative bacteria that were chosen for the development of ESBLs based on their multidrug resistance phenotypes and reduced susceptibility to any of ceftazidime or ceftriaxone were all verified as bacteria that produce ESBL. According to Menkem *et al.* (2023), the third generation cephalsporins are current antimicrobial options to treat bacterial infections, and this reliance on these antibiotics could enhance the development of resistance. Infections linked to healthcare in Nigeria and UTIs have also been linked to high rates of ESBL-producing bacteria (Giwa *et al.,* 2018; Nwafia *et al.,* 2019; Ogefere *et al.,* 2015). This study further confirms the emerging trend of resistance to antibiotics in the carbapenems family as evident in the resistance to meropenem and ertapenem. These antibiotics are considered as antibiotics of last resort in clinical setting and reduced susceptibility among clinical bacteria to these antibiotics portends great danger to public health.

In this study, eight bacterial isolates showed hemolysis, with potential for pathogenicity. The low frequency of hemolytic bacteria presently observed corroborates the report of Onanuga *et al.* (2016), where it was observed that some bacteria resisting antibiotics resistant in UTI cases released hemolysins. In this study, twenty-three (50.0%) of the isolated bacteria produced strong biofilms, while 17 (36.9%) bacterial isolates produced weak biofilms. The propensity of these bacteria to adhere to surfaces and hospital equipment enhanced their ability to produce chronic and recurrent bacterial infections; and also improved their ability to form biofilm. It is extremely difficult to treat bacteria that develop biofilm during infections, and greater dosages of antibiotics are needed to get rid of such germs during treatment (Flores-Mireles *et al.,* 2015). Antibiotic resistance is increased in bacterial biofilms when they are exposed to them over time.

CONCLUSION

It is observed in this study that bacteria isolated from UTI patients showed high incidence of resistance to antibiotics. This finding connotes severe implications to their health and that of the public. More importantly, some bacteria showed resistance to third generation cephalosporins and carbapenems. The overall results of this study emphasize the need for ongoing monitoring of antibiotic-resistant microorganisms in UTI cases in healthcare and community settings. It has been established that characteristics of UTIs vary according to location, etiologies and antimicrobial susceptibilities. The timely data from this ongoing surveillance will be used to inform antibiotic treatment guidelines and effective antimicrobial stewardship. It is important to use cephalosporins with caution and to pay any emerging carbapenem-resistant bacteria in clinical settings the essential attention with a view to maintaining the effectiveness of the antimicrobial agent that are frequently administered to patients to treat infections of importance.

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