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PREVALENCE OF MULTIDRUG RESISTANT UROPATHOGENIC *ESCHERICHIA COLI* EXTENDED SPECTRUM BETA LACTAMASE PRODUCERS FROM URINE SAMPLES IN A STATE HOSPITAL, OTA, NIGERIA

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ABSTRACT
The global spread of Extended Spectrum Beta-Lactamases (ESBLs) by members of the Enterobacteriaceae family is one of the major threats in current clinical issues. In this study, a total of one hundred (100) urine samples from both male and female patients aged between 20-60 clinically suspected to have urinary tract infection were screened for extended spectrum Beta Lactamase Uropathogenic *Escherichia coli* using standard microbiological procedures. Of the 100 urine samples obtained, only 70% showed significant growth while 30% had no significant growth. Antimicrobial susceptibility screening revealed that all the uropathogenic *E. coli* isolated had varying susceptibility patterns and most were multidrug resistant. All uropathogenic *E. coli* isolated were hundred percent resistant to cloxacillin and augmentin, while 75 and 68.75% were resistant to cefuroxime and erythromycin respectively. However, the uropathogenic *E. coli* was highly sensitive to cefotaxime (81.25%), gentamicin (75%), and oflaxacin (75%). The double disk synergy test for extended spectrum beta lactamase (ESBL) divulged that majority of the uropathogenic *E. coli* isolated were positive for extended spectrum beta lactamase (87%). On account of the high occurrence of ESBL multidrug resistant uropathogenic *E. coli* in urine samples from this study, there is a need for immediate action in the area of routine diagnosis, surveillance and control as recommended by Center for Disease and Control (CDC), to address the threat posed by multidrug resistant ESBL producers before its catastrophic consequences become inevitable.

KEYWORDS: Extended spectrum Beta-Lactamase, Uropathogenic *Escherichia coli*, Cephalosporins, Multidrug resistant, Urine.

INTRODUCTION
The global spread of Extended Spectrum Beta Lactamases (ESBLs) by members of the Enterobacteriaceae family is one of the major threats in current clinical issues (Caini *et al*., 2013; Muhammad *et al*., 2013; Pokhrel *et al*., 2014). These classes of beta-lactamases are of particular concern because genes coding for their production are located on plasmids which not only contain genes that confer resistance to other antimicrobial agents but are also acquired easily among bacterial species, through lateral gene transfer (Qureshi *et al*., 2012; Reuland *et al*., 2013). It is no doubt that ESBLs are the most isolated beta-lactamases with very broad resistance patterns due to their ability to confer resistance to other classes of antibiotics, asides cephalosporins (Reuland, *et al*., 2013). The extended spectrum β-lactamase (ESBL) classified as a serious threat by Centre for Disease and Control (CDC, 2013), is one of the main enzymatic resistance weapon used by members of the Enterobacteriaceae to develop multiple resistance against many beta-lactam antibiotics (Dhillon and Clark, 2012). Over 300 different beta-lactamase types has long been isolated, following its discovery in *Klebsiella pneumoniae* in 1983, with Escherichia coli (*E. coli*) and *Klebsiella* species being the most common carriers (Nijhuis *et al*., 2012; Mohanalakshmi *et al*., 2014). The emergence and continuous increase in the rate of multidrug resistance among the Enterobacteriaceae over the last decade is even more challenging as they limit effective therapeutic options against the infections they cause (Nathwani *et al*., 2014). Most important multidrug resistant Enterobacteriaceae are those capable of producing extended spectrum beta lactamases (Vahdani *et al*., 2012). The current leading cause of many nosocomial bacterial infections are the extended spectrum beta-lactamase producing Enterobacteriaceae (Qureshi *et al*., 2012). Many members of the Enterobacteriaceae family capable of producing ESBLs also bear multiple resistances to other non-beta-lactamase antibiotics. The extended spectrum beta-lactamase producing *E. coli* are among the major threat that rapidly disseminates multidrug resistance within Gram negative organisms (Raji *et al*., 2013). Not only worrisome is the fact that they have developed resistance to 3rd generation cephalosporins through ESBL production, they are also multidrug resistant, which is even a more challenging threat as it reduces the effectiveness of antibiotic therapy (Yusuf *et al*., 2013). *Escherichia coli* are by far the most common uropathogen responsible for not less than 80% of community-acquired urinary tract infections (UTIs) and 40% of healthcare-associated UTI (Yusuf *et al*., 2013) and urinary tract infections caused by ESBL producing *E. coli* causes an increase in mortality rate and medical cost (Linhares *et al*., 2013).Differing antimicrobial resistance patterns has been displayed from several studies on extended spectrum producing *E. coli*. Ejaz *et al*. (2013) reported the resistance pattern of extended spectrum producing *E. coli* to be cefotaxime (100%), ceftazidime (99.4%) and cefuroxime

(93.3%). Another study carried out in India by Mukherjee *et al*. (2013) showed a resistance profile of ESBL producing *E. coli* to be 67.5%, 62.5% and 55% for cefotaxime, ceftriaxone and ceftazidime respectively. A review study carried out by Denisuik *et al*. (2013) showed that ESBL producing *E. coli* had a resistance of 97% to ceftriaxone and 56.2% to ceftazidime. Aminzadeh *et al*. (2013) showed that ESBL producing *E. coli* displayed 95.9%, 95.9% and 95.9% resistant to ceftriaxone, cefotaxime and cefixime respectively. However, Nitrofurantoin has been reported from most studies to be effective for infections caused by extended spectrum producing *E. coli* (Aminzadeh *et al*., 2013; Ejaz *et al*., 2013; Linhares *et al*., 2013; Mukherjee *et al*., 2013; Sharma *et al*., 2013). The aim of this Study is to evaluate the resistance pattern of Extended Spectrum Beta Lactamase Uropathogenic *Escherichia coli* isolated from patients in a State Hospital, Ota, Nigeria.

MATERIALS & METHODS

Study population

The study population involved patients attending a State Hospital in Ota, Nigeria from January to May, 2014. A total of one hundred (100) patients clinically suspected to have urinary tract infection were involved in this study which comprised of both male and female patients aged between 20- 60 years.

Sample collection and processing

Early morning midstream urine was obtained from each patient into sterile screw- capped universal bottles. The specimens were labeled accordingly, transported to the laboratory and processed immediately.

Microbial analysis

Samples were cultured on Cysteine lactose electrolyte deficient (CLED) agar, MacConkey agar and Eosin methylene blue (EMB) media plates using a calibrated sterile platinum wire loop (4.0 mm in diameter) to deliver 0.01 ml of the urine sample on the agar plates. The plates were incubated aerobically at 37°C for 24 hours and then examined for bacterial growth. On CLED agar, yellow colonies observed were regarded as *Escherichia coli* while smooth pink colonies on MacConkey agar plates and very dark colonies with a metallic green sheen on Eosin methylene blue (EMB) agar plate were suspected to be *Escherichia coli* (Cheesbrough, 2004). Isolates were then characterised biochemically as described by Cowan and Steel (1993) and Cheesbrough (2000).

Antimicrobial susceptibility testing

Antimicrobial susceptibility testing was conducted using Kirby Bauer disk diffusion method, according to Clinical and Laboratory Standards Institute guidelines (CLSI, 2013).The following commonly prescribed antibiotics with their specific concentrations were used Ceftazidime (30 µg), cefuroxime (30µg), gentamicin (10µg), ceftriaxone (30µg), erythromycin (15µg), cloxacillin (5µg), oflaxacin (5µg), cefotaxime (30µg) and augmentin (30µg). Antibiotic discs were placed on Mueller-Hinton agar (MHA) plates seeded with isolate suspended in sterile distilled water according to 0.5 McFarland turbidity standards. Plates were incubated appropriately and results were interpreted using Clinical and Laboratory Standards Institute (CLSI) breakpoints (CLSI, 2013).

Detection of Extended Spectrum Beta Lactamase (ESBL) producers

Isolates showing resistance to third generation cephalosporins (ceftazidime, cefuroxime, ceftriaxone and cefotaxime) were further screened for ESBL production using double disc synergy test (DDST). Discs of augmentin (20 µg amoxycillin + 10 µg clavulanate) were placed on the surface of the MHA already seeded with the isolates. Discs of cefotaxime (30 µg) and ceftazidime (30 µg) were also placed 16 to 20 mm apart from the augmentin disc (centre to centre). Plates were incubated at 37 °C overnight and results were interpreted according to the standards established by the Clinical and Laboratory Standards Institute (CLSI, 2013).

RESULTS

Of 100 urine samples obtained during this study, only 70% showed significant growth while 30% had no significant growth. Most of the organisms isolated were Gram negative organisms, with a few Gram positive organisms present (Table 1 and Table 2) *Escherichia coli* and *Klebsiella pneumoniae* were the most predominant uropathogen with about 22.54%, followed by *Staphylococcus saprophyticus* (19.72%), *Enterococcus sp.* (5.63 %) *Proteus* (4.23 %), *Neisseria* and *Serratia* were (1.41 % each), as shown below (Figure 1).

Though antimicrobial susceptibility test revealed that all the uropathogenic *E. coli* isolated had varying susceptibility patterns (Table 3), most were multidrug resistant (Table 4). All uropathogenic *E. coli* isolated were resistant to cloxacillin (100%) and augmentin (100%) while 75% and 68.75% were resistant to cefuroxime and erythromycin respectively (Figure 2). However, high sensitivity was generally displayed towards certain antibiotics which include cefotaxime (81.25%), gentamicin (75%) and oflaxacin (75%). Majority of the uropathogenic *E. coli* isolated were positive for extended spectrum beta lactamase (ESBL), with prevalence percentage of about 87% (Figure 3).

TABLE 1: Colonial and biochemical characteristics for Identification of bacteria isolated from male patient samples obtained from State Hospital, Ota

Samples	CC	GR	Shape	H_2S	G	IND	MOT	CIT	CAT	MR	VP	K	A	Identification
M1	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M2	Mucoid yellow	-	Rod	-	+	-	-	+	+	-	+	A	A	*Klebsiella pneumoniae*
M3	White	+	cocci	-	-	-	-	-	+	ND	ND	K	A	*Staphylococcus saprophyticus*
M4	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M5	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M6	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M7	Yellow	+	Cocci	-	-	-	-	-	+	ND	ND	K	A	*Staphylococcus saprophyticus*
M8	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M9	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M10	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M11	Green	-	Rod	-	-	-	+	+	+	-	-	K	K	*Pseudomonas aeruginosa*
M12	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M13	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M14	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M15	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M16	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M17	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M18	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M19	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M 20	Yellow	-	Rod	-	-	+	+	-	+	+	-	A	A	*Escherichia coli*
M21	White	+	Cocci	-	-	-	-	-	+	+	-	K	A	*Staphylococcus saprophyticus*
M22	Yellow	-	cocci	-	-	-	-	-	-	ND	ND	K	A	*Neisseria species*
M23	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M24	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
M25	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil

KEY- CC: Colony characteristics GR: Gram reaction K: Alkaline A: Acid H_2S: Hydrogen sulphide G: Gas. IND: Indole MOT: Motility, CIT: Citrate, CAT: Catalase ND: Not done MR: Methyl red VP: Voges-proskauer **(-)**: negative (+): positive

TABLE 2: Colonial and biochemical characteristics for Identification of bacteria isolated from female patient samples obtained from State Hospital, Ota

Samples	CC	GR	Shape	K	A	H_2S	G	IND	MOT	CIT	CAT	MR	VP	Identification
F1	Small mucoid	+	cocci	A	A	+	+	+	-	-	-	ND	ND	*Enterococcus Faecalis*
F2	Green	-	Rod	K	K	-	-	-	+	+	+	-	-	*Pseudomonas Aeruginosa*
F3	White	+	Cocci	K	A	-	-	-	-	-	+	ND	ND	*Staphylococcus saprophyticus*
F4	White	+	Cocci	K	A	-	-	-	-	-	+	ND	ND	*Staphylococcus saprophyticus*
F5	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F6	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F7	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F8	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F9	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F10	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F11	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F12	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F13	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F14	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F15	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F16	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F17	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F18	White	+	Cocci	K	A	-	-	-	-	-	+	ND	ND	*Staphylococcus saprophyticus*
F19	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F20	White	+	Cocci	K	A	-	-	-	-	-	+	ND	ND	*Staphylococcus saprophyticus*
F21	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F22	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F23	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F24	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil

F25	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F26	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F27	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F28	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F29	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F30	Small yellow	+	Cocci	A	A	+	+	+	-	-	-	ND	ND	*Enterococcus faecalis*
F31	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F32	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F33	White	+	Cocci	K	A	-	-	-	-	-	+	ND	ND	*Staphylococcus saprophyticus*
F34	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F35	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F36	Small Yellow	+	Cocci	A	A	+	+	+	-	-	-	ND	ND	*Enterococcus faecalis*
F37	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F38	Small Yellow	+	Cocci	A	A	+	+	+	-	-	-	ND	ND	*Enterococcus faecalis*
F39	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F40	Blue Grey	-	Rod	K	A	+	+	+	+	+	+	+	-	*Proteus spp*
F41	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F42	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F43	Blue Grey	-	Rod	K	A	+	+	+	+	+	+	+	-	*Proteus spp*
F44	White	+	Cocci	K	A	-	-	-	-	-	+	ND	ND	*S. saprophyticus*
F45	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	- -	+	*Klebsiella pneumoniae*
F46	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F47	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F48	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F49	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F50	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F51	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil	Nil
F52	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F53	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F54	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F55	Yellow	-	Rod	A	A	-	+	+	+	-	+	+	-	*Escherichia coli*
F56	Green	-	Rod	-	-	-	+	+	+	-	-	K	K	*Pseudomonas aeruginosa*
F57	White	+	Cocci	K	A	-	-	-	-	-	+	ND	ND	*Staphylococcus saprophyticus*
F58	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F59	Red	-	Rod	A	A	-	+	-	+	+	+	-	+	*Serratia spp*
F60	Mucoid Yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F61	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F62	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F63	Green	-	Rod	-	-	-	+	+	+	-	-	K	K	*Pseudomonas aeruginosa*
F64	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F65	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F66	Green	-	Rod	-	-	-	+	+	+	-	-	K	K	*Pseudomonas aeruginosa*
F67	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F68	White	+	Cocci	K	A	-	-	-	-	-	+	ND	ND	*Staphylococcus saprophyticus*
F69	Blue grey	-	Rod	K	A	+	+	+	+	+	+	+	-	*Proteus spp*
F70	White	+	Cocci	K	A	- -	-	-	-	-	+	ND	ND	*Staphylococcus saprophyticus*
F71	White	+	Cocci	K	A	-	-	-	-	-	+	ND	ND	*S. saprophyticus*
F72	Mucoid yellow	-	Rod	A	A	-	+	-	-	+	+	-	+	*Klebsiella pneumoniae*
F73	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F74	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*
F75	Yellow	-	Rod	A	A	-	+	-	+	+	+	-	+	*Enterobacter spp*

KEY- CC: Colony characteristics GR: Gram reaction K: Alkaline A: Acid H_2S: Hydrogen sulphide G: Gas. IND: Indole MOT: Motility, CIT: Citrate, CAT: Catalase ND: Not done MR: Methyl red VP: Voges-proskauer (**-**): negative (+): positive

TABLE 3: Resistance, Intermediate and Sensitivity patterns of uropathogenic *E. coli*

Samples	CAZ	CRX	GEN	CTR	ERY	CXC	OFL	AUG	CTX
F5	20 (S)	R	R	R	20 (S)	R	12 (R)	R	R
F8	18 (S)	12 (R)	17 (S)	12 (R)	20 (S)	18 (R)	21 (S)	R	30 (S)
F9	R	R	23 (S)	R	R	R	30 (S)	R	12 (R)
F10	8 (R)	R	7 (R)	19 (I)	R	R	R	R	29 (S)
F14	R	15 (I)	20 (S)	21 (S)	20 (S)	R	21 (S)	R	37 (S)
F15	17 (I)	17 (I)	22 (S)	21 (S)	R	R	20 (S)	R	36 (S)
F22	16 (I)	16 (I)	19 (S)	19 (I)	R	R	10 (R)	R	34 (S)
F26	19 (S)	14 (R)	15 (S)	14 (I)	R	R	33 (S)	R	31 (S)
F28	14 (R)	R	20 (S)	23 (S)	R	R	24 (S)	R	35 (S)
F29	14 (R)	12 (R)	16 (S)	19 (I)	R	R	30 (S)	R	32 (S)
F34	22 (S)	20 (S)	R	18 (I)	12 (R)	R	R	R	33 (S)
F35	18 (S)	14 (R)	R	22 (S)	R	R	30 (S)	R	31 (S)
F55	R	R	22 (S)	5 (R)	15 (I)	R	25 (S)	R	17 (I)
F52	18 (S)	R	17 (S)	18 (I)	R	R	21 (S)	R	33 (S)
F37	18 (S)	13 (R)	17 (S)	20 (S)	R	R	33 (S)	R	34(S)
M20	R	R	22(S)	6 (R)	26(S)	R	21(S)	R	20(S)

KEY- CAZ: Ceftazidime CRX: Cefuroxime GEN: Gentamicin CTR: Ceftriaxone ERY: Erythromycin CXC: Cloxacilin OFL: Oflaxacin AUG: Augmentin CTX: Cefotaxime F: Female M: Male

TABLE 4: Multidrug resistance pattern of *E. coli* strain

Isolate code	Resistance Pattern	Number (%)
I1	CRX- GEN- CTR-CXC- OFL-AUG-CTX	1(6.25)
I2	CRX-CTR-CXC-AUG	1(6.25)
I3	CAZ-CRX-CTR-ERY-CXC-AUG-CTX	1(6.25)
I4	CRX-GEN-ERY-CXC-OFL-AUG	1(6.25)
I5	CAZ-CXC-AUG	1(6.25)
I6	ERY-CXC-AUG	1(6.25)
I7	ERY-CXC-OFL-AUG	1(6.25)
I8	CRX-ERY-CXC-AUG	4(25)
I9	CAZ-CRX-ERY-CXC-AUG	2(12.5)
I10	GEN-ERY-CXC-OFL-AUG	1(6.25)
I11	CRX-GEN-ERY-CXC-AUG	1(6.25)
I12	CAZ-CRX-CTR-CXC-AUG	2(12.5)

KEY-CAZ: Ceftazidime CRX: Cefuroxime GEN: Gentamicin CTR: Ceftriaxone ERY: Erythromycin CXC: Cloxacilin OFL: Oflaxacin AUG: Augmentin CTX: Cefotaxime

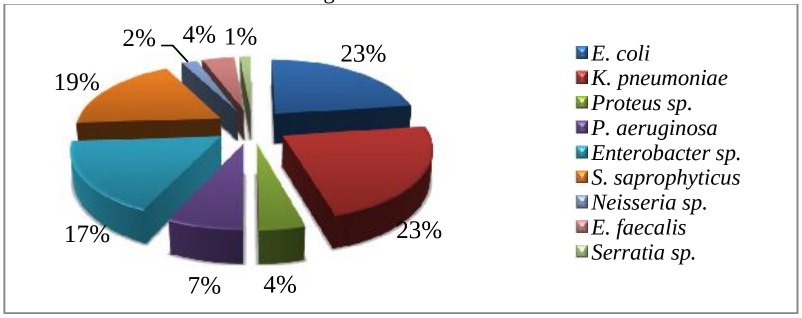
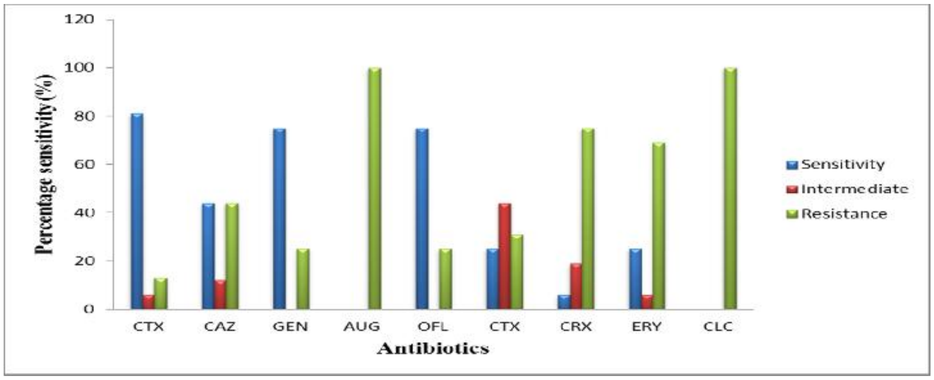


FIGURE 1: Distribution of Bacterial isolates from urine samples



KEY- CAZ: Ceftazidime CRX: Cefuroxime GEN: Gentamicin CTR: Ceftriaxone ERY: Erythromycin CLC: Cloxacilin OFL: Oflaxacin AUG: Augmentin CTX: Cefotaxime

FIGURE 2: Antimicrobial Susceptibility pattern of uropathogenic *E. coli* isolates in percentage

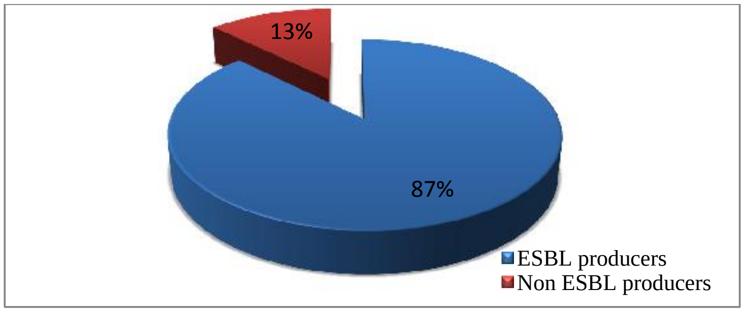


FIGURE 3: Percentage prevalence of non ESBL and ESBL producers

DISCUSSION

The extended spectrum beta lactamase producers are a serious challenge, as grouped by CDC and are one of the most current clinical issues, not only in the hospital setting but also in the community. It has been documented that some ESBL- producing Enterobacteriaceae are responsible for about 26,000 Hospital acquired infections and 1,700 mortality annually (CDC, 2013). In recent time, several studies conducted across the globe have reported ESBL producers to be multidrug resistant; thus having the ability to develop resistance to other classes of antibiotics, in addition to the third generation cephalosporins. This ability is of major concern since it leaves us with little to no therapeutic option. Most challenging of all is the fact that even with the rapid spread of multidrug resistant ESBL producers among members of the enterobacteriaceae family worldwide, many clinical settings in the developing countries are yet to incorporate the detection of ESBL producers into routine diagnosis. Continuous treatment failure with penicillins and other cephalosporins, and increase in multidrug resistance are likely to result when ESBL detection are not carried out, posing a serious challenge to physicians. The present study focuses on only extended spectrum beta lactamase producing uropathogenic *E. coli*. Out of seventy bacterial isolates that was recovered from urine samples, only sixteen were *E. coli* and 87% of these were ESBL producers (Figure 3). Most of the multidrug resistant *E. coli* isolates (94%) were from female samples. One cannot conclusively say that the higher occurrence rate based on gender is significant because this present research is not gender based and samples obtained for both gender were not equal.

From this study, all uropathogenic *E. coli* positive for ESBL production showed 100% resistance to cloxacillin and augmentin (Figure 2), two of the most commonly used penicillins for urinary tract infection treatment. It was also observed that all the *Escherichia coli* isolates were at least resistant to three antibiotics used in this study (Table 4). About 78% of the ESBL producers were also carrying resistance for other classes of antibiotics such as the macrolides (erythromycin) while only 25% were resistant to gentamycin. Though many studies have shown strong association between ESBL production and fluroquinolone resitance (Raei *et al*., 2014; Tacão *et al*., 2014), only 28% of the ESBL producers detected were resistant to ofloxacin, the most widely prescribed antibiotics for urinary tract infection. Resistance of uropathogenic *E.coli* to Ceftazidime (43.75%) is similar to the findings of Ejikeugwu *et al*. (2012), where 57.5% resistance was reported. With 25% resistance to gentamycin and ofloxacin from this study, aminoglycosides and quinolones still remains an effective therapeutic agent for urinary tract infections caused by uropathogenic *E. coli*. ESBL producers detected in this study generally showed a considerable resistance variation to the third generation cephalosporins: only about 12.5% were resistant to cefotaxime, 43.75% to ceftazidime and 31.25% to ceftriaxone. However, most were resistant to second generation cephalosporin tested, as only one (6.25%) showed a significant sensitivity. The high prevalence rates of ESBL producers in urine samples in the studied area corroborate the works of Olowe and Aboderin (2010) and Folasoge *et al*. (2014).

In conclusion, it is obvious that the occurrence of ESBL multidrug resistant uropathogenic *E. coli* in patient urine samples obtained from State Hospital, Ota is high, and therefore, there is a need for immediate action in the area of routine diagnosis, surveillance and control as recommended by Center for Disease and Control (CDC), to address the threat posed by multidrug resistant ESBL producers before its catastrophic consequences become inevitable.

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