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## High Proportion of slime and metalloβ-lactamase (MβL) producing multi-drug resistant bacteria from patients at referral hospitals in Uyo: A Three-Year Retrospective Study

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### Abstract

Bacteriological examination of 510 clinical samples (mid-stream urine (n=194), stool (n=146) and wound swab (n=170) from patients at referral hospitals between 2016 and 2018 was carried out using standard bacteriological techniques. The antibiotic susceptibility profile, slime and metallo-β-lactamase (MβL) production among the isolated bacteria were determined by disc diffusion, Congo Red Agar (CRA) / Tube Method and Imipenem / ethylenediamine-tetra-acetic acid disc methods, respectively. A total of 564 bacteria constituting eight genera were isolated from mid-stream urine (n=194), stool (n=146) and wound (n=170) specimens. *Escherichia coli* (37.3%) was the predominant species while *Acinetobacter* spp (7.1%) and *Citrobacter freundii* (7.1 %) were the least occurring species. The results showed that ≥ 46.8 %, 37.9 % and ≥ 34.0 % isolates were resistant to Imipenem; Ampicillin and Ceftriaxone., respectively. Out of 564 isolates obtained, 59.4% were multidrug resistant strains with multiple antibiotic resistant indices ranging from 0.38 to 0.63. Of 270 Imipenem resistant isolates, 64.4% and 65.9% isolates were positive for MβL production by the double disc synergy test and combined double disc test, respectively. The percentages of slime producing isolates using CRA in decreasing order were *K. pneumoniae* (82.9%) > *Acinetobacter* spp (77.8%) > *E. coli* (64.2%) > *P. aeruginosa* (62.5%) > *P. mirabilis* (51.7 %) > *Salmonella* spp (45.0%) > *Enterobacter* spp (36.8%) > *C. freundii* (33.3%). Quantitative assessment of the 352 isolates revealed 20% as weak, 34% as moderate and 47% as strong slime producers. This study therefore showed the necessity to continuously assess the antibiotic susceptibility profiles of bacterial slime producers and also to consider the use of non-carbapenem antibiotics for treatment of infectious diseases.

**Key Words:** Slime, Metalloβ-lactamase, Resistant, Isolates, Antibiotics, Imipenem.

## Introduction

Microorganisms make use of different mechanisms for their survival in the environment and in humans (Hall-Stoodley *et al.*, 2004). Slime production by bacteria is one of the mechanisms by which microorganisms adhere to and colonize smooth artificial surfaces such as indwelling prosthetic devices and catheters. Slime is a viscous, loosely bound, extracellular material comprising exopolysaccharides, glycoproteins and glycolipids (Akinjogunla *et al.*, 2018). Studies have shown that slime-producing bacteria have a higher colonization capacity than the non-slime-producing isolates (Ammendolia *et al.*, 1999; Arslan and Özkarde, 2007). Thus, bacterial slime plays a role in the establishment and severity of infections (Ammendolia *et al.*, 1999), aids in bacterial resistance to phagocytosis and opsonization and protects bacteria from antibiotics and unfavourable environmental conditions (Akyar *et al.*, 1998). Some strains of *Staphylococcus* spp., *Acinetobacter* spp., *Escherichia coli* and *Pseudomonas aeruginosa* have been reported as slime producers (Ammendolia *et al.*, 1999; Arslan and Özkarde, 2007). Bacterial slime has been associated with intravenous-catheter-related bacteremia and other prosthetic device infections (Rupp and Archer, 1994).

Antibiotic resistance by bacteria is a serious threat to management of patients' illnesses

worldwide. Bacteria have developed various mechanisms of resistance to antibiotics such as production of beta-lactamases, alteration of penicillin-binding proteins and plasmid enzymatic modification (Akinjogunla *et al.*, 2011). Metallo-β-lactamases (MβLs) are zinc-dependent enzymes, belonging to Ambler's Class B, which hydrolyze a variety of beta-lactam antibiotics such as penicillins, cephalosporins and carbapenems, and require divalent cation (zinc) as a cofactor for enzyme activity (Bush *et al.*, 1995; Navon-Venezia *et al.*, 2006). These β-lactamase enzymes are produced by bacteria, especially Gram-negative bacteria, and the clinical infections with MβL-producing isolates are associated with high morbidity and mortality (Deshmukh *et al.*, 2011). Carbapenem resistance due to MβL production has been recently reported among clinical isolates of *E. coli*, *P. aeruginosa* and *Klebsiella* spp. (Navon-Venezia *et al.*, 2006; Villegas *et al.*, 2007). Therefore, the presence of MβL-producing bacteria in the hospital environment has put the use of the beta-lactam antibiotics especially carbapenems under threat (Thompson, 2010). This study was therefore designed to determine the occurrence of slime and MβL-producing producing MDR bacterial isolates in clinical specimens from 2016 to 2018 in Uyo, Nigeria.

## Materials and methods

### Collection of specimens

Five hundred and ten (510) clinical specimens consisting of mid-stream urine (n =97), stool (n =73) and wound swab (n =85) were aseptically collected using sterile wide-mouth vials (100mL) and swab sticks from patients at referral hospitals in Uyo, Akwa Ibom State. The Hospital Ethics Review Committee approval and verbal informed consent of patients were obtained prior to samples collection. The clinical specimens were carefully labelled to reflect the date and time of collection and were immediately transported to the Microbiology Laboratory, University of Uyo, for bacteriological analysis.

### Bacteriological Analysis of Samples

The methods described by Jena *et al.* (2013) was used for the isolation of urinary bacterial isolates. One millilitre (1 mL) of each well mixed mid-stream urine (MSU) specimens was inoculated onto plates of cysteine lactose electrolyte deficient agar (CLED) and MacConkey agar (MCA) without salt. Each of the wound swabs was immersed into a test tube containing 9 mL of sterile distilled water; 0.1 mL was pipetted and surface-inoculated on plates of MCA and blood agar. One gram of each stool specimen was serially diluted and one millilitre (1 mL) of each aliquot was inoculated on plates of MCA and Eosine Methylene Blue (EMB) agar. All the plates were aerobically incubated for

24hrs at 37°C. After incubation, plates with positive bacterial growths were subcultured onto plates of nutrient agar and incubated for 24 hrs at 37°C. Thereafter, pure cultures of isolates were streaked onto nutrient agar slants, incubated for 24 hrs at 37°C and stored in the refrigerator at 4°C until identification. All isolates were Gram stained and subjected to various conventional biochemical tests using standard methods as described in Cheesbrough (2006).

### Antibiotic susceptibility testing

*In vitro* susceptibility testing of all the bacterial isolates to Ampicillin (AMP, 10  $\mu$ g), Imipenem (IMP, 10  $\mu$ g), Meropenem (MER, 10  $\mu$ g), Ceftriaxone (CTX, 30  $\mu$ g), Streptomycin (STP, 10  $\mu$ g), Ceftazidime (CTZ, 30  $\mu$ g), Ciprofloxacin (CIP, 5  $\mu$ g) and Gentamycin (GEN, 10  $\mu$ g) (Oxoid, UK) was determined by the disc diffusion method (CLSI, 2009). Briefly, 10  $\mu$ L of each bacterial isolate, prepared directly from an 18-hr agar plate and adjusted to 0.5 McFarland Standard, was spread-plated on Mueller Hilton Agar (MHA). The antibiotic discs were aseptically placed on the surfaces of the culture plates with sterile forceps, and the plates were incubated at 37°C for 18 hrs. Thereafter, inhibitory zones were observed and measured in millimeters (mm). The interpretation of the measurement as sensitive and resistant was determined based on the criteria of CLSI (2009).

### **Determination of multiple antibiotic resistance**

#### **Index**

Multiple antibiotic resistance (MAR) index was determined using the formula  $MAR = x/y$ , where 'x' was the number of antibiotics to which test isolate displayed resistance and 'y' was the total number of antibiotics to which the test isolates has been evaluated for sensitivity (Akinjogunla *et al.*, 2010). Isolates that were resistant to three or more antibiotic classes were taken to be multiple antibiotic resistant (Jan *et al.*, 2002).

### **Phenotypic detection of metallo-betalactamase**

#### **Using combined double disc test**

The metallo-betalactamase (MβL) producing Gram negative bacterial (GNB) isolates was determined using Combined Double Disc Test (CDDT). Ten microlitres (10 μL) of each GNB isolates, prepared directly from an overnight agar plate, adjusted to 0.5 McFarland Standard, was spread-plated on MHA. A disc of imipenem (10 μg) and imipenem-EDTA disc (imipenem disc impregnated with 5 μL of EDTA) were placed 20 mm apart on the plates. After incubation for 18 hr at 37°C, a difference of  $\geq 7$  mm between inhibitory zones of the imipenem and imipenem-EDTA discs indicated MβL production (Deshmukh *et al.*, 2011; Sachdeva *et al.*, 2017).

### **Phenotypic detection of metallo-betalactamase using double disc synergy test (DDST)**

The production of MβL by GNB isolates was determined using the Double Disc Synergy Test (Deshmukh *et al.*, 2011; Sachdeva *et al.*, 2017). Ten microlitres (10 μg) of each GNB isolate prepared directly from an agar plate incubated for 18 hours and adjusted to 0.5 McFarland Standard was spread-plated on MHA. Imipenem (10 μg) and EDTA discs (a blank filter paper disc impregnated with 10 μL of 0.5M EDTA solution) were placed 20 mm apart on the plates. After incubation for 18 hr at 37°C, an enlarged inhibitory zone towards the EDTA disc was considered MβL positive.

### **Phenotypic detection of slime using congo red**

#### **Agar method**

Slime production by GNB isolates was evaluated by the Congo red agar (CRA) method previously described by Akinjogunla *et al.* (2018). The medium was prepared with 37 g/L brain heart infusion (BHI) broth, 50 g/L sucrose, 10 g/L agar and 0.8 g/L Congo red. Plates of CRA were surface-inoculated with test isolates and incubated aerobically for 24 hrs at 37 °C. A positive result was indicated by black colonies with a dry crystalline consistency.

### **Phenotypic detection of slime using tube method (Quantitative Assessment)**

Slime production by GNB isolates was determined using the Tube Method (TCM) of Hassan *et al.*

(2011) with slight modification. Briefly, a loopful of each GNB isolate from 24 hrs agar plate was inoculated onto a test tube containing 10 mL BHI broth supplemented with 2% sucrose. The tubes were incubated aerobically for 24 hrs at 37 °C. After incubation, the contents of each tube were poured out, each tube washed with phosphate buffer saline (pH 7.3), dried and stained with crystal violet (0.1%). Excess stain in each tube was washed off with deionized water and tubes dried in an inverted position. A positive result for slime formation was indicated when a visible film lined the wall and bottom of the tube; quantification was as follows: 0: absent; 1: weak; 2: moderate and 3: strong.

#### Statistical analysis

The Statistical Package for Social Sciences (IBM SPSS Version 22.0. Armonk, NY: IBM Corp.) was used for data analysis. The significant difference between metallo-betalactamase and non-metallo-betalactamase producing bacterial isolates at  $p \leq 0.05$  were determined using chi-square ( $\chi^2$ ) test. Descriptive data were presented as percentages.

#### Results

A total of 564 bacteria, belonging to eight genera, were isolated from MSU (n=194), Stool (n=146) and wound (n=170) specimens within the study period (Table 1). *Escherichia coli* was the predominant bacterial isolate constituting 37.3% (190/564), followed by *P. aeruginosa* and *K.*

*pneumoniae* with 18.8% (96/564) and 13.7% (70/564), respectively. Of the 58 isolates identified as *P. mirabilis*, 30 were isolated from wound swabs, 18 from MSU, while 10 were from stool specimens. *Salmonella* spp, *Enterobacter* spp, *C. freundii* and *Acinetobacter* spp constituted 7.8%, 7.5%, 7.1% and 7.1% of the total bacterial isolates (n=564), respectively (Table 1).

The results of the antibiotic resistant profiles of clinical bacterial isolates obtained between 2016 and 2018 are presented in Table 2. The results showed that > 46.8% isolates were resistant to Imipenem and Meropenem (carbapenem class of beta-lactam); 37.9% isolates were resistant to Ampicillin (penicillin class), > 34.0% isolates showed resistance to Ceftriaxone and Ceftazidime (cephalosporin class); 22.3% isolates were resistant to Ciprofloxacin (fluoroquinolone class), while > 19.1% bacterial isolates were resistant to Gentamycin and Streptomycin (aminoglycoside class). Table 3 shows the MAR indices of bacterial isolates from clinical specimens within the study period. Of the 564 bacterial isolates obtained, 72 (12.8%) were sensitive to all the 8 antibiotics tested, 92 (16.3%) were single drug resistant isolates, 65(11.5%) isolates were resistant to 2 antibiotics, while 335 (59.4%) isolates demonstrated multidrug resistant (MDR) phenotypes. The MAR indices of *Acinetobacter* spp and *Enterobacter* spp ranged

from 0.38 to 0.63 ( $\leq 5$  antibiotics) and 0.38 to 0.75 ( $\leq 6$  antibiotics), respectively. The MAR indices of *Salmonella* spp and *C. freundii* ranged between 0.38 and 0.88, while 14 isolates comprising *E. coli* (n=7), *K. pneumoniae* (n=2), *P. aeruginosa* (n=4) and *P. mirabilis* (n=1) had the highest MAR index of 1.0 (Table 3).

Out the 270 Imipenem resistant bacterial isolates from the clinical specimens, 174 (64.4%) isolates were positive for MβL production by DDST. Of the 174 phenotypically detected MβL producing bacterial isolates, *E. coli* had (70), *K. pneumoniae* (16), *P. aeruginosa* (32), *Salmonella* spp (10), *P. mirabilis* (14), *Enterobacter* spp (10), *C. freundii* (10) and *Acinetobacter* spp (12). Out the 270 Imipenem resistant bacterial isolates from the clinical specimens, 178 (65.9%) isolates were positive for MβL production by CDDT. More than 74.0% *E. coli* and *Acinetobacter* spp obtained from the clinical specimens were MβL producers, while  $< 57.1\%$  *K. pneumoniae*, *Salmonella* spp and *P. mirabilis* were positive for MβL production by CDDT (Table 4). There was no significant difference ( $p > 0.05$ ) between MβL producers and non- MβL producers using DDST and CDDT (Table 4).

The occurrence of slime producing bacterial isolates in clinical specimens using Congo Red Agar (CRA) is presented in Table 5. The results

showed a statistically significant difference ( $p < 0.05$ ) between the slime producers (342, 60.6%) and non-slime producers (222, 39.4 %). The percentage proportion of slime producing bacterial isolates using CRA in decreasing order was *K. pneumoniae* (82.9%)  $>$  *Acinetobacter* spp (77.8%)  $>$  *E. coli* (64.2%)  $>$  *P. aeruginosa* (62.5%)  $>$  *P. mirabilis* (51.7 %)  $>$  *Salmonella* spp (45.0%)  $>$  *Enterobacter* spp (36.8%)  $>$  *C. freundii* (33.3%) (Table 5). Three hundred and fifty-two (62.4 %) bacterial isolates from clinical specimens produced extracellular material (slime) using tube method (TCM). The quantitative assessment of the 352 slime producers revealed 70 (19.9%) as weak (+), 118 (33.5%) as moderate (++) and 164 (46.6%) as strong (+++) slime producers. The proportion of slime producing bacterial isolates from clinical specimens was significantly ( $p=0.0002$ ) greater than non-slime producers using TCM (Table 6).

**Table 1: Occurrences of bacterial isolates in clinical specimens from patients at referral hospitals**

Bacterial Isolates	No (%) of Occurrence			Total No (%)
	Urine (n =194)	Stool (n =146)	Wound (n =170)	
<i>Escherichia coli</i>	72 (37.1)	90 (61.6)	28 (16.5)	190 (37.3)
<i>Klebsiella pneumoniae</i>	26 (13.4)	24 (16.4)	20 (11.8)	70 (13.7)
<i>Pseudomonas aeruginosa</i>	38 (19.6)	16 (10.9)	42 (24.7)	96 (18.8)
<i>Salmonella</i> spp	22 (11.3)	18 (12.3)	0 (0.0)	40 (7.8)
<i>Proteus mirabilis</i>	18 (9.3)	10 (6.8)	30 (17.6)	58 (11.4)
<i>Enterobacter</i> spp	12 (6.2)	14 (9.6)	12 (7.1)	38 (7.5)
<i>Citrobacter freundii</i>	8 (4.1)	20 (13.7)	8 (4.7)	36 (7.1)
<i>Acinetobacter</i> spp	18 (9.3)	6 (4.1)	12 (7.1)	36 (7.1)
Total	214	198	152	564 (100)

**Table 2: Antibiotic resistance profiles of clinical bacterial isolates from patients at referral hospitals**

Bacterial Isolates	Year	No of Isolates	Number (Percentage) of Isolates Resistant to Antibiotics							
			AMP	GEN	IMI	CTX	CTZ	STP	MER	CIP
<i>E. coli</i>	2016	52	20 (38.5)	14 (26.9)	28 (53.8)	18 (34.6)	20 (38.5)	12 (23.1)	26 (50.0)	14 (26.9)
	2017	62	22 (35.5)	10 (16.1)	34 (54.8)	18 (29.0)	26 (41.9)	10 (16.1)	34 (54.8)	18 (29.0)
	2018	76	30 (39.5)	16 (21.1)	38 (50.0)	26 (34.2)	26 (34.2)	14 (18.4)	36 (47.4)	16 (21.1)
<i>K. pneumonia</i>	2016	18	6 (33.3)	4 (22.2)	8 (44.4)	6 (33.3)	4 (22.2)	4 (22.2)	8 (44.4)	2 (11.1)
	2017	22	10 (45.4)	4 (27.3)	10 (45.4)	8 (36.4)	10 (45.4)	2 (9.1)	10 (45.4)	4 (27.3)
	2018	30	12 (40.0)	4 (13.3)	14 (46.7)	12 (40.0)	10 (33.3)	4 (13.3)	16 (53.3)	6 (20.0)
<i>P. aeruginosa</i>	2016	26	12 (46.2)	8 (30.8)	14 (53.8)	14 (53.8)	12 (46.2)	8 (30.8)	14 (53.8)	8 (30.8)
	2017	40	16 (40.0)	6 (15.0)	18 (45.0)	16 (40.0)	16 (40.0)	6 (15.0)	16 (40.0)	6 (15.0)
	2018	30	10 (33.3)	2 (6.7)	12 (40.0)	8 (26.7)	8 (26.7)	6 (20.0)	16 (53.3)	4 (13.3)
<i>Salmonella</i> spp	2016	10	4 (40.0)	2 (20.0)	4 (40.0)	4 (40.0)	2 (20.0)	2 (20.0)	4 (40.0)	2 (20.0)
	2017	10	4 (40.0)	2 (20.0)	4 (40.0)	4 (40.0)	4 (40.0)	4 (40.0)	4 (40.0)	2 (20.0)
	2018	20	6 (30.0)	4 (20.0)	8 (40.0)	8 (40.0)	6 (30.0)	4 (20.0)	10 (50.0)	4 (20.0)
<i>P. mirabilis</i>	2016	14	6 (42.9)	6 (42.9)	8 (57.1)	4 (28.6)	10 (71.4)	2 (14.3)	6 (42.9)	6 (42.9)
	2017	30	10 (33.3)	6 (20.0)	14 (46.7)	10 (33.3)	8 (26.7)	6 (20.0)	12 (40.0)	8 (26.7)
	2018	14	4 (28.6)	2 (14.3)	6 (42.9)	6 (42.9)	8 (57.1)	4 (28.6)	8 (57.1)	2 (14.3)
<i>Enterobacter</i> spp	2016	10	4 (40.0)	2 (20.0)	4 (40.0)	0 (0.0)	4 (40.0)	0 (0.0)	4 (40.0)	2 (20.0)
	2017	16	8 (50.0)	6 (37.5)	8 (50.0)	4 (25.0)	6 (37.5)	2 (12.5)	6 (37.5)	6 (37.5)
	2018	12	4 (33.3)	0 (0.0)	4 (33.3)	4 (33.3)	2 (16.7)	4 (33.3)	4 (33.3)	0 (0.0)
<i>C. freundii</i>	2016	18	6 (33.3)	4 (22.2)	8 (44.4)	4 (22.2)	2 (11.1)	8 (44.4)	6 (33.3)	6 (33.3)
	2017	8	2 (25.0)	0 (0.0)	4 (50.0)	2 (25.0)	4 (50.0)	2 (25.0)	4 (50.0)	2 (25.0)
	2018	10	4 (40.0)	0 (0.0)	4 (40.0)	2 (40.0)	4 (40.0)	0 (0.0)	4 (40.0)	0 (0.0)
<i>Acinetobacter</i> spp	2016	4	2 (50.0)	0 (0.0)	2 (50.0)	0 (0.0)	2 (50.0)	0 (0.0)	2 (50.0)	0 (0.0)
	2017	12	4 (33.3)	2 (16.7)	6 (50.0)	6 (50.0)	4 (33.3)	2 (16.7)	4 (33.3)	4 (33.3)
	2018	20	8 (40.0)	4 (20.0)	10 (50.0)	8 (40.0)	8 (40.0)	6 (30.0)	10 (50.0)	4 (20.0)

Keys: AMP: Ampicillin, GEN: Gentamycin; IMI: Imipenem; CTX: Ceftriaxone; CTZ: Ceftazidime; STR: Streptomycin; MER: Meropenem; CIP: Ciprofloxacin.



**Table 3: Multiple antibiotic resistant index of bacterial isolates in clinical specimens from patients at referral hospitals**

MAR Index	Number / Percentage								Total No (%)
	EC	KP	PA	SS	PM	ES	CF	AS	
0.00	24(12.6)	8(11.4)	11(11.4)	3(7.5)	7(12.1)	5(13.2)	5(13.9)	9(25.0)	72(12.8)
0.13	28(14.7)	10(14.3)	15(15.6)	7(17.5)	10(17.2)	6(15.8)	9(25.0)	7(19.4)	92(16.3)
0.25	19(10.0)	7(10.0)	10(10.4)	7(17.5)	9(15.5)	4(10.5)	4(11.1)	5(13.9)	65(11.5)
0.38	43(22.6)	18(25.7)	24(25.0)	10(25.0)	8(13.8)	7(18.4)	7(19.4)	9(25.0)	126(22.3)
0.50	30(15.8)	10(14.3)	13(13.5)	3(7.5)	10(17.2)	4(10.5)	4(11.1)	3(8.3)	77(13.7)
0.63	11(5.8)	6(8.6)	6(6.3)	2(5.0)	4(6.9)	7(18.4)	2(5.6)	3(8.3)	41(7.3)
0.75	18(9.5)	4(5.7)	9(9.4)	7(17.5)	7(12.1)	5(13.2)	4(11.1)	0(0.0)	54(9.6)
0.88	10(5.3)	5(7.1)	4(4.2)	1(2.5)	2(3.4)	0(0.0)	1(2.8)	0(0.0)	23(4.1)
1.00	7(3.9)	2(2.9)	4(4.2)	0(0.0)	1(1.7)	0(0.0)	0(0.0)	0(0.0)	14(2.5)

Keys: EC: *E. coli*; KP: *K. pneumoniae*; PA: *P. aeruginosa*; SS: *Salmonella* spp; PM: *P. mirabilis*; ES: *Enterobacter* spp; CF: *C. freundii*; AS: *Acinetobacter* spp

**Table 4: Metallo-betalactamase (MβL)-producing bacteria in clinical specimens from patients at referral hospitals**

Method Used	Bacterial Isolates	No of IMP <sup>R</sup> Isolates	MβL Producers No (%)	Non-MβL Producers No (%)	χ <sup>2</sup>	p-value
DDST	<i>E. coli</i>	100	70 (70.0)	30 (30.0)	8.25	0.311
	<i>K. pneumoniae</i>	32	16 (50.0)	16 (50.0)		
	<i>P. aeruginosa</i>	44	32 (72.7)	12 (27.3)		
	<i>Salmonella</i> spp	16	10 (62.5)	6 (37.5)		
	<i>P. mirabilis</i>	28	14 (50.0)	14 (50.0)		
	<i>Enterobacter</i> spp	16	10 (62.5)	6 (37.5)		
	<i>C. freundii</i>	16	10 (62.5)	6 (37.5)		
	<i>Acinetobacter</i> spp	18	12 (66.7)	6 (33.3)		
	Total	270	174 (64.4)	96 (35.6)		
CDDT	<i>E. coli</i>	100	74 (74.0)	26 (26.0)	10.5	0.162
	<i>K. pneumoniae</i>	32	16 (50.0)	16 (50.0)		
	<i>P. aeruginosa</i>	44	28 (63.6)	16 (36.2)		
	<i>Salmonella</i> spp	16	8 (50.0)	8 (50.0)		
	<i>P. mirabilis</i>	28	16 (57.1)	12 (42.9)		
	<i>Enterobacter</i> spp	16	10 (62.5)	6 (37.5)		
	<i>C. freundii</i>	16	10 (62.5)	6 (37.5)		
	<i>Acinetobacter</i> spp	18	14 (77.8)	4 (22.2)		
	Total	270	178 (65.9)	92 (34.1)		

Keys: DDST: Double Disc Synergy Test; CDDT: Combined Double Disc Test; MβL: Metallobetalactamase; IMP: Imipenem

**Table 5: Slime producing bacterial isolates in clinical specimens (Congo Red Agar Method) from patients at referral hospitals**

Bacterial Isolates	No of Isolates	Slime Producers		Non-Slime Producers		$\chi^2$	p-value
		No (%)	No (%)	No (%)	No (%)		
<i>E. coli</i>	190	122 (64.2)	68 (35.8)				
<i>K. pneumoniae</i>	70	58 (82.9)	12 (17.1)				
<i>P. aeruginosa</i>	96	60 (62.5)	36 (37.5)				
<i>Salmonella</i> spp	40	18 (45.0)	22 (55.0)				
<i>P. mirabilis</i>	58	30 (51.7)	28 (48.3)	46.4		0.0001*	
<i>Enterobacter</i> spp	38	14 (36.8)	24 (63.2)				
<i>C. freundii</i>	36	12 (33.3)	24 (66.7)				
<i>Acinetobacter</i> spp	36	28 (77.8)	8 (22.2)				
Total	564	342 (60.6)	222 (39.4)				

**Table 6: Slime producing bacterial isolates in clinical specimens (Tube Method) from patients at referral hospitals**

Bacterial Isolates	No of Isolates	Slime Producers No (%)	Quantitative Assessment of Slime Producers			Non-Slime Producers No (%)	$\chi^2$	p-value
			Weak No (%)	Moderate No (%)	Strong No (%)			
<i>E. coli</i>	190	126 (66.3)	26 (20.6)	38 (30.2)	62 (49.2)	64 (33.7)		
<i>K. pneumoniae</i>	70	58 (82.9)	16 (27.6)	18 (31.0)	24 (41.4)	12 (17.1)		
<i>P. aeruginosa</i>	96	60 (62.5)	12 (20.0)	26 (43.3)	22 (36.7)	36 (37.5)		
<i>Salmonella</i> spp	40	16 (40.0)	4 (25.0)	4 (25.0)	8 (50.0)	24 (60.0)		
<i>P. mirabilis</i>	58	32 (55.2)	4 (12.5)	14 (43.8)	14 (43.8)	26 (44.8)	38.5	0.0002*
<i>Enterobacter</i> spp	38	18 (47.4)	2 (11.1)	6 (33.3)	10 (55.6)	20 (52.6)		
<i>C. freundii</i>	36	14 (38.9)	0 (0.0)	4 (28.6)	10 (71.4)	22 (61.1)		
<i>Acinetobacter</i> spp	36	28 (77.8)	6 (21.4)	8 (28.6)	14 (50.0)	9 (22.2)		
Total	564	352 (62.4)	70 (19.9)	118 (33.5)	164 (46.6)	212 (37.6)		

## Discussion

The clinical and financial burden of patients and health care providers at referral hospitals with slime (pathogenic) and M $\beta$ L producing MDR bacterial isolates is enormously challenging. In our study, *E. coli* was the predominant bacterial isolate from the clinical samples, followed by *P. aeruginosa*, *K. pneumoniae*, *P. mirabilis*, *Salmonella* spp, *Enterobacter* spp, *Acinetobacter* spp and *C. freundii*. *E. coli* as the predominant bacterial uropathogen in this study was consistent with similar studies conducted by Assefa *et al.* (2008) and Akinjogunla and Divine-Anthony (2013). The isolation of *Acinetobacter* spp in stool, wound and urine samples was in conformity with results of Dijkshoorn *et al.* (2005); Howard *et al.* (2012) and Jimenez-Guerra *et al.* (2018) who isolated *Acinetobacter* spp from stool, wound and urine samples in Netherland, Ireland and Spain, respectively.

This study showed a high Imipenem, Meropenem, Ampicillin, Ceftriaxone and Ceftazidime resistant isolates. The overall resistance of isolates to Imipenem and Meropenem was  $\geq 46.8\%$  and this value was higher than  $17\%$  and  $\geq 22\%$  reported by Manoharan *et al.* (2011) and Gupta *et al.* (2006), respectively. Of the 335 MDR bacterial isolates obtained, *E. coli* had the highest percentage with  $35.5\%$ , followed by *P. aeruginosa* ( $17.9\%$ ) and

this substantiated the findings of Aly and Balkhy, (2002) who reported *E. coli* as the Gram negative bacilli (GNB) with the highest MDR profile, but contradicted Qadri *et al.* (1996) who had *P. aeruginosa* exhibiting the highest MDR profile in Riyadh, Saudi Arabia.

The rapid increasing rate of M $\beta$ L, zinc-dependent enzymes belonging to Ambler's Class B, production among bacterial isolates in the family Enterobacteriaceae has become a grave public health problem worldwide and has made use of beta-lactam antibiotics especially carbapenems for treatment of infectious diseases under threat (Bush *et al.*, 1995; Thompson, 2010). In our study, M $\beta$ L producing *K. pneumoniae*, *P. aeruginosa*, *Salmonella* spp, *P. mirabilis*, *Enterobacter* spp, *E. coli*, *C. freundii* and *Acinetobacter* spp were obtained from the clinical samples using DDST and CDDT. The phenotypic detection of M $\beta$ L production in GNB such as *E. coli*, *K. pneumoniae* and *Salmonella* spp in this study agreed with the results of Hoang *et al.*, (2013). The occurrence of M $\beta$ L producing *C. freundii* and *Acinetobacter* spp corroborated the findings of Jena *et al.* (2013) who isolated  $75\%$  *C. freundii* and  $25\%$  *Acinetobacter* spp producing M $\beta$ L from urine samples in India. More than  $63.6\%$  *P. aeruginosa* obtained in this study were positive for M $\beta$ L production and this value was higher than  $41.0\%$  and

11.1 % reported by Sadhana *et al.* (2014) and Zubair and Ireghu (2018), respectively.

Microorganisms that produce slime and form biofilms have mechanisms to synthesize several molecules that facilitate its survival in humans (Chalabaev *et al.*, 2014). In this study, varied percentages of slime producing *K. pneumoniae*, *Acinetobacter* spp., *E. coli*, *P. aeruginosa*, *P. mirabilis*, *Salmonella* spp, *Enterobacter* spp and *C. freundii* were obtained from clinical samples. The occurrence of slime producing *E. coli* and *K pneumoniae* agreed with Dadawala *et al.* (2010) and Hassan *et al.* (2011) whose findings showed slime producing *E. coli* and *K pneumoniae* in stool and urine samples in India using CRA and TCM.

### Conclusion

The study has established a high occurrence of slime- and M $\beta$ L-producing MDR bacterial isolates in Uyo. Hence, it is of necessity to consider other antibiotics besides carbapenem class of beta-lactam for treatment of infectious diseases in Nigeria. Furthermore, routine check of the antibiotic susceptibility profiles of slime-producing bacteria is necessary to support the choice of antibiotics selected for effective treatment of infectious diseases.

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