Antibiotic Resistance Pattern of Uropathogens in a Tertiary Care Hospital in Calabar, Nigeria

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Authors' contributions

This work was carried out in collaboration among all authors. Authors BEE and EAO were involved in the conception and design of the study. Author BEE drafted the initial manuscript. Authors BEE, DE, PO, BEM and BAA were involved in laboratory work and wrote manuscript. Authors EAO, IU, CN and SEE conducted a critical review of the manuscript. All authors have read and approved the final manuscript.

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ABSTRACT

Introduction: Urinary tract infection is a major reason for hospital visits and a common clinical condition encountered by clinicians. The causative agents of urinary tract infection and their resistant pattern vary globally. The aim of this study was to highlight the profile of pathogens

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associated with urinary tract infections in our locality. The objective was to investigate the resistant pattern of these microbial isolates from patients with urinary tract infection and offer recommendations for effective treatment.

Materials and methods: We retrospectively analyzed the urine culture and antimicrobial sensitivity reports of patients with suspected urinary tract infection at the University of Calabar Teaching Hospital, Calabar, Nigeria, from September 2019 to August 2020. Methicillin resistance was detected by disk diffusion method using 30 µg ceftazidime disk. Production of Extended spectrum beta lactamases was detected by the Combination disk and the double-disk synergy method.

Results: Of 979 urine culture and sensitivity reports, 306 (31.26%) were positive for microbial growth. Two microbial isolates each were recovered from urine samples of 5 patients giving a total number of 311 isolates from 306 patients. 45.75% of positive results were in males. The predominant isolate was *Escherichia coli* (n=97, 31.19%). Extended Spectrum Beta Lactamases (ESBL) producing strains comprised 10.08% (10/238) of Gram-negative group of organisms, while 47.39% (145/306) of all bacterial isolates in our study were multi drug resistant (MDR). 14.29% (6/42) of *S. aureus* isolates were methicillin resistant *S. aureus*, while 33.33% (2/6) of methicillin resistant *S. aureus* (MRSA) were multi drug resistant.

Conclusion: Urinary tract infection caused by antimicrobial resistant organisms is common among studied patients. This emphasizes the need for urine culture and sensitivity tests in the management of urinary tract infection.

Keywords: Antibiotic; resistance; susceptibility; infection; uropathogens.

1. INTRODUCTION

Urinary tract infections (UTI) are defined by the presence of a growth of more than 10^5 colony forming units (CFU) of bacteria per ml of urine for asymptomatic individual and $\sim 10^3$ CFU/ml for symptomatic individual [1,2]. In urine samples obtained by supra pubic aspiration or catheterization and in samples from a patient with an indwelling catheter, colony count of 10^2 - 10^4 CFU/ml generally signifies urinary tract infection [1]. UTI are one of the commonest clinical conditions encountered by physicians and accounts for 1-6% of all medical visits [3]. It is the second most common reason for empirical antibiotic treatment and a major reason for antibiotic usage globally [4]. Therefore, the need for periodic monitoring of causative agents in a given locality and their resistance pattern is necessary to ensure appropriate and successful treatment.

2. MATERIALS AND METHODS

This is a retrospective study, conducted at University of Calabar Teaching Hospital Calabar, Nigeria. Study population comprised patients aged between 1 and 88 years who attended the hospital with complaints of UTI symptoms. A total of 979 urine culture reports were analyzed. Urine specimens were inoculated on Blood agar and McConkey agar plates or Cysteine lactose electrolyte deficient agar plates (Himedia) using 2mm calibrated loops (0.002ml) and were

incubated aerobically at 37°C for 24-48 hours. Culture plates showing growth of >20 colonies ($>10^5$ CFU/ml) colonies were considered as Significant bacteriuria and were subjected to standard biochemical tests (Catalase, Coagulase, Indole, Citrate, Urea and Kligler iron agar) for identification of isolates. Besides conventional biochemical tests, Oxoid Microbact TM GNB kit and Analytical profile index 20E were also used for the identification of culture isolates [5,6]. Antimicrobial sensitivity testing was done using the Kirby- Bauer disc diffusion method. Interpretation of results as 'Sensitive' or 'Resistant' or 'Intermediate' was done according to the Clinical and Laboratory Standard Institute (CLSI) guidelines [7]. Antibiotics against which sensitivity was tested in this study included ampicillin, amoxiclav, amikacin, ceftazidime, cefuroxime, ceftriaxone, ceftazidime, cefepime, cefixime, cefotaxime, ciprofloxacin, imipenem, meropenem, levofloxacin, piperacillin/tazobactam, gentamicin and nitrofurantoin. Quality control as per CLSI standards was done for antimicrobial susceptibility tests to confirm the potency of antibiotics [7]. Detection of ESBL production in Gram negative bacteria was done as per CLSI guidelines, by Phenotypic Confirmatory Disc Diffusion Test (PCDDT) and/or the Double Disc Synergy Test (DDST). A zone diameter of more than 5mm for Ceftazidime-clavulanate (30/10 mcg) compared to ceftazidime (30 mcg) was considered positive for ESBL (PCDDT). DDST was done using a combination of antibiotics including Aztreonam

(30mcg), Amoxicillin-Clavulanic acid (20/10mcg), Ceftriaxone (30mcg), Ceftazidime (30mcg) and Cefotaxime (30mcg). The development of zone of inhibition towards the Clavulanate disc was indicative of a potential ESBL positive organism [6,7]. Detection of methicillin resistance was done as per CLSI guidelines [7].

3. RESULTS

A total of 979 urine culture sensitivity reports were analyzed retrospectively out of which 306 were positive for microbial growth. Two microbial isolates each were recovered from urine samples of 5 patients giving a total number of 311 isolates from 306 patients. Among the 306 reports, 166 (54.25%) belonged to females. The age range was 1 to 88 years with a mean of 36.4 years. Table 1 summarizes the age distribution of patients and the number of cultured isolates per age group. The predominant culture isolates in our study were; *E. coli* (n=97, 31.2%) and *Staphylococcus aureus* (n=36, 11.58%). Gram-negative bacilli were a total of 238 (77.78%) and accounted for most of the culture isolates. Gram positive cocci were a total of 68 (21.86%), while 5 (1.61%) culture reports were positive for *Candida spp.* as shown in Table 2.

4. DISCUSSION

The sex distribution of patients in our study is consistent with studies previously done in many centers with a higher prevalence of UTI in females (54.23%) compared to males [8]. The high prevalence of UTI in females compared to males is related to the anatomical and microflora differences between the male and female genitourinary systems [1,9]. Women are more susceptible than men because of short straight anatomy of the urethra and termination of female urethra beneath the labia resulting in colonization of the urinary tract by colonic Gram-negative bacilli. Pregnancy also increases the risk of UTI in females due to positional changes within the urinary tract caused by the enlarged uterus. Associated hormonal changes in pregnancy also causes susceptibility to urinary tract infections in pregnant women. Other factors include decreased ureteric tone and peristalsis, temporary incompetence of the vesicoureteral valves and bladder catheterization [9,10]. Social activities in females like sexual activity, douching and child birth also increase the risk of urethral contamination as the bacteria could be pushed into the urethra during sexual intercourse as well

as bacteria being massaged up the urethra into the bladder during child birth [9,10].

The incidence rate (31.26%) of UTI in our study was much higher compared to a previous study (7.7%) from the same center carried out by Jumbo et. al, 2011 [8]. Both studies were retrospective in nature, but of varied duration. Our study spanned a duration of one year while the previous study covered a duration of five years [8]. The higher incidence from our study despite the short duration may be attributed to improved infrastructure and laboratory services, increased skilled man power, a better working environment and the drive to attain international best practices.

The predominant isolate in our study was *E. coli*. Its prevalence (37.19%) in this study was similar to other reports [11,12]. Globally, more than 80% of UTI are caused by uropathogenic *Escherichia coli* and *Klebsiella species* specifically, *K. pneumoniae* and *K. oxytoca*, both in the community and nosocomial settings [13,14]. *E. coli* is the etiological agent in 60–90% of UTI, while *Klebsiella species* accounts for 3–20% of cases [13,14].

Age group 16–44 years had the highest frequency of UTI (61.74%) probably due to increased sexual activity as corroborated from other studies (Table 1) [8,12]. The commonest etiological agents causing UTI in the younger age group (1–15) were *E. coli* (n=3), *P. aeruginosa* (n=2), *Acinetobacter spp.* (n=2), and *Enterococcus spp.* (n=2). Amongst the elderly (≥65), the predominant isolates were; *E. coli* (n=18), *Morganella morganii* (n=7), and *Staphylococcus spp.* (n=5). Within age groups 16–44 and 45–64, all culture isolates were implicated except for *Acinetobacter spp.* which were not implicated as causative agents of UTI for age group 45–64. This may be explained by the varied distribution of uropathogens across age groups as documented in previous studies [15,16].

Analysis of antimicrobial susceptibility results of culture isolates revealed high resistance to antibiotics (ciprofloxacin, levofloxacin and ceftriaxone) commonly used for the empirical treatment of UTI. *Klebsiella spp.* were highly resistant to ceftriaxone (70%), ceftazidime (63%), gentamicin (63%), ciprofloxacin (57%) and amoxicillin-clavulanic acid (66%). This finding was in keeping with previous studies [17]. *Klebsiella spp.* produce various enzymes including extended spectrum beta lactamases,

metallo-beta-lactamases, oxacillinases, and carbapenemases that target beta lactam antibiotics. These enzymes are encoded on plasmids and are usually taken up by the process of conjugation [1,18]. *Enterobacter spp.* showed high resistant to ceftriaxone (67%), cefuroxime (62.5%) and cefdinir (62.5%). *Enterobacter spp.* ESBLs and carbapenemases, including VIM, OXA, metallo- β -lactamase-1 and *Klebsiella pneumoniae* carbapenemases [18]. Additionally, they cause opportunistic infections in immunocompromised patients and are also associated with nosocomial infections [18]. The highest resistance to antibiotics in our study was seen in *Acinetobacter spp.* especially to ceftriaxone (75%). Antibiotic resistance in *Acinetobacter. spp.* is also mediated by carbapenemases including imipenem metallo β -

lactamases, encoded by *blaIMP*, and oxacillinase serine β lactamases, encoded by *blaOXA* [16-18]. The lowest observed resistance was against imipenem; 4.12%, 7% and 12%, for *E. coli*, *Klebsiella spp.* and *Enterobacter spp.* respectively. A similar finding was reported in a previous study done by Iregbu et. al in a tertiary hospital, Abuja, Nigeria [12]. The total prevalence of Gram-positive organisms in our study was 21.86%, slightly higher than reports from previous studies [8]. This is consistent with the fact that there's been a surge in *Staphylococcus aureus* associated UTI attributed to increased instrumentation like bladder catheterization and receptive anal intercourse [19-21]. Tables 3 and 4 summarized the resistance rates of Gram positive and Gram-negative isolates to tested antibiotics.

Table 1. Age distribution of cases of UTI

Age group (years)	Number of isolates	Percentages
1-15	12	3.86
16-44	192	61.74
45-64	63	20.26
≥65	44	14.15
Total	311	100

Table 2. Frequency of culture isolates

Isolates	Number of Isolates	Percentage
<i>Escherichia coli</i>	97	31.19
<i>Staphylococcus aureus</i>	36	11.58
<i>Enterococcus spp.</i>	23	7.40
<i>Morganella morganii</i>	19	6.11
<i>Providencia alcalifaciens</i>	19	6.11
<i>Klebsiella oxytoca</i>	18	5.79
<i>Proteus vulgaris</i>	15	4.82
<i>Providencia rettgeri</i>	11	3.54
<i>Pseudomonas aeruginosa</i>	11	3.54
<i>Klebsiella pneumoniae</i>	10	3.22
<i>Enterobacter cloacae</i>	10	3.22
<i>Proteus mirabilis</i>	9	2.89
<i>Providencia stuartii</i>	6	1.93
MRSA	6	1.93
<i>Citrobacter freundii</i>	5	1.61
<i>Candida spp.</i>	5	1.61
CoNS	3	0.96
<i>Acinetobacter iwoffii</i>	2	0.64
<i>Acinetobacter baumannii</i>	2	0.64
<i>Enterobacter agglomerans</i>	2	0.64
<i>Klebsiella ozaenae</i>	2	0.64
Total	311	100

MRSA, Methicillin resistant *S. aureus*; CoNS, Coagulase negative *Staphylococcus spp.*

Table 3. Antibiotic resistance pattern of Gram-negative bacterial isolates

Ant.	<i>E. coli</i>	<i>Providencia spp.</i>	<i>K. spp</i>	<i>Proteus spp.</i>	<i>M. morganii</i>	<i>E. spp.</i>	<i>P. aeruginosa</i>	<i>C. freundii</i>	<i>A. spp.</i>
% (n)									
CRO	35.05 (34)	55.56 (20)	70 (21)	29.12 (7)	40 (8)	67 (8)	45.5 (5)	20 (1)	75 (3)
CXM	27.84 (27)	30.56 (11)	47 (14)	29.12 (7)	30 (6)	50 (4)	NT	20 (1)	NT
CTZ	24.74 (24)	22.22 (8)	63 (19)	29.12 (7)	10 (2)	62.5 (5)	27.3 (3)	20 (1)	50 (2)
CN	24.74 (24)	11.11 (4)	63 (19)	16.67 (4)	10 (2)	37.5 (3)	18 (2)	20 (1)	50 (2)
Ak	NT	NT	20 (6)	NT	NT	12.5 (1)	NT	NT	50 (2)
LEV	24.74 (24)	16.67 (6)	50 (15)	29.12 (7)	NT	37.5 (3)	9.0 (1)	40 (2)	50 (2)
CIP	26.80 (26)	2.78 (1)	57 (17)	12.5 (3)	NT	50 (4)	NT	40 (2)	50 (2)
AMC	24.74 (24)	2.78 (1)	66 (20)	16.67 (4)	NT	37.5 (3)	NT	20 (1)	NT
MEP	12.37 (12)	NT	43 (13)	NT	NT	12.5 (1)	18.1 (2)	NT	NT
CFM	11.34 (11)	NT	40 (12)	NT	NT	12.5 (1)	NT	NT	50 (2)
COX	NT	NT	30 (9)	NT	NT	12.5 (1)	NT	NT	50 (2)
IMP	4.12 (4)	NT	7 (2)	NT	NT	12.5 (1)	NT	20 (1)	50 (2)
CPD	7.21 (7)	NT	10 (3)	NT	NT	NT	NT	NT	NT
AMP	16.49 (16)	NT	NT	NT	NT	12.5 (1)	NT	40 (2)	NT
NIT	16.49 (16)	22.22 (8)	17 (5)	33.33 (8)	55 (11)	12.5 (1)	NT	20 (1)	NT

Ant.	<i>E. coli</i>	<i>Providencia spp.</i>	<i>K. spp</i>	<i>Proteus spp.</i>	<i>M. morganii</i>	<i>E. spp.</i>	<i>P. aeruginosa</i>	<i>C. freundii</i>	<i>A. spp.</i>
CFX	28.87 (28)	27.78 (10)	NT	25 (6)	55 (11)	36.3 (4)	NT	20 (1)	NT
CTM	7.21 (7)	NT	NT	4.17 (1)	10 (2)	NT	NT	20 (1)	25 (1)
PTZ	16.49 (16)	19.44 (7)	NT	16.67 (4)	40 (8)	12.5 (1)	36.3 (4)	40 (2)	25 (1)

n, number of resistant isolates; % (percentage of resistance) =number of resistant isolates/total number of isolates; NT, not tested; CRO, Ceftriaxone; CXM, Cefuroxime; CN, Gentamicin; AK, Amikacin; LEV, Levofloxacin; CIP, Ciprofloxacin; AMC, Amoxicillin Clavulanate; MEP, Meropenem; CFM, Cefepime; COX, Cefoxitin; IMP, Imipenem; CPD, Cefpodoxime; AMP, Ampicillin; CTZ, Ceftazidime; NIT, Nitrofurantoin; CFX, Cefixime; CTM, Cefotaxime; PTZ, Piperacillin Tazobactam; Ant. Antibiotics

Table 4. Antibiotic resistance pattern of Gram-positive bacterial isolates

Antibiotics	<i>S. aureus</i>	CoNS	MRSA	<i>Enterococcus spp.</i>
	% (n)			
Gentamicin	13.89 (5)	33.33 (1)	0%	10.04(3)
Amikacin	2.78 (1)	33.33 (1)	NT	NT
Levofloxacin	19.44 (7)	33.33(1)	0%	10.04(3)
Ciprofloxacin	13.87 (5)	0% (0)	33.33(2)	0(0)
Erythromycin	16.67 (6)	33.33 (1)	NT	21.74(5)
Cefoxitin	2.78 (1)	NT	NT	NT
Clindamycin	0% (0)	NT	NT	NT
Nitrofurantoin	19.44 (7)	66.67(2)	0%	10.04 (3)
Penicillin	2.78(1)	33.33(1)	NT	NT
Linezolid	NT	NT	NT	17.39(4)
Vancomycin	NT	NT	NT	4.35(1)

n, number of resistant isolates; %, number of resistant isolates/total number of isolates tested; NT, not tested; CoNS, coagulase negative *S. species*; MRSA, methicillin resistant *S. aureus*; % (percentage of resistance) =number of resistant isolates/total number of isolates

Table 5. Frequency and Percentage of ESBL-producing isolates

Bacterial isolates	N	% (n/24)
<i>Escherichia coli</i>	16	66.67
<i>Pseudomonas aeruginosa</i>	2	8.33
<i>Providencia rettgeri</i>	1	4.17
<i>Klebsiella pneumoniae</i>	1	4.17
<i>Enterobacter cloacae</i>	2	8.33
<i>Citrobacter freundii</i>	2	8.33
Total	24	100

ESBL, extended-spectrum β -lactamase; n, number of ESBL isolates; %, percentage of ESBL isolates

Table 6. Frequency and percentage of multidrug resistant isolates

Organisms	N	% (n/145)
<i>Escherichia coli</i>	50	34.48
<i>Staphylococcus spp.</i>	19	13.1
<i>Klebsiella spp.</i>	23	15.86
<i>Providencia spp.</i>	12	8.28
<i>Proteus spp.</i>	8	5.52
<i>Enterococcus spp.</i>	9	6.21
<i>Morganella morganii</i>	9	6.21
<i>Enterobacter spp.</i>	7	4.83
<i>Pseudomonas aeruginosa</i>	2	1.38
<i>Citrobacter freundii</i>	3	2.07
<i>Acinetobacter spp.</i>	3	2.07
Total	145	100

n, number of Multidrug resistant isolates; %, percentage of Multidrug resistant isolates

ESBL producing strains were 24 and comprised 10.08% (24/238) of the Gram-negative group of organisms. The prevalence of ESBL in our study was lower compared to a prevalence of 32.7% in a study done by Onwuezobe et. al, in a tertiary hospital, in Uyo, Nigeria [22]. Of the 24 ESBL producing strains, *E. coli* had the largest proportion (n=16), as shown in Table 5.

The production of ESBL by Gram negative organisms confers resistance to beta-lactam antibiotics through the hydrolyzation of the beta-lactam ring in beta-lactam drugs including penicillins, cephalosporins, and aztreonam, except cephamycins and carbapenems, and are usually associated with poor outcome of infections [1]. ESBL genes are encoded by plasmids which have been found to carry other genes that express resistance to drugs other than beta-lactams, such as aminoglycosides, trimethoprim, sulphonamides, tetracyclines, quinolones and chloramphenicol and as such have been implicated as a major cause of multidrug resistance [1,23,24].

The increasing rates of antimicrobial resistance of pathogenic organisms has become a public health problem. There is a startling increase in

antibiotic resistance of bacteria that cause either nosocomial infections or community acquired infections. Worthy of note are the multidrug resistant pathogens like *Klebsiella pneumoniae*, *Escherichia coli*, *Acinetobacter Baumannii* and *methicillin-resistant Staphylococcus aureus* [18]. Our study revealed a multi drug resistance rate of 47.39% (145/306) amongst bacterial isolates. Of the 145 multi drug resistant isolates, *E. coli* had the highest frequency (n=50), with a prevalence of 34.48% (50/145), Table 6. This was slightly higher than a prevalence rate of 27.3% from a study done by Maduakor et al in a tertiary hospital, in Enugu, Nigeria [25]. Higher prevalence rates of multi drug resistant *E. coli* (52.9%) have also been reported from other studies [26].

5. CONCLUSION

The spectrum of uropathogens and their antibiotic susceptibility continue to change and vary globally. The predominance of *E. coli* in our study was a finding consistent with many previous reports. Culture isolates showed high resistance to routinely used antibiotics except the carbapenems. The high resistance rates to antibiotics can be explained by the over use and

the non-judicious use of antibiotics for the treatment of UTI. The availability of these drugs over the counter without a physician's prescription has also encouraged the inappropriate use of antibiotics. Urine culture and antibiotic sensitivity testing should be done for all patients with suspected UTI especially where local antibiograms are not available.

6. LIMITATIONS OF THE STUDY

- The study was unable to state the type of UTI (uncomplicated or complicated) and associated comorbidities which may have direct implication on the cause and management of UTI due to paucity and lack of detailed clinical information from extracted records.
- The Study could not differentiate between patients from the outpatient department and patients from the inpatient department due to similar reasons stated above.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

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