RESEARCH ARTICLE

Resistant bacteria in children with community-acquired febrile illness in a tertiary hospital in Nigeria

Abstract

Background: Blood bacterial infection is a cause of serious illness in children, especially the antibiotic resistant organisms. Since there is variation in the causative organisms with different location, there is need to determine the burden in our location aside the low data recorded. This study determined prevalence of bacteraemia, resistance pattern of implicated organisms and the role of Procalcitonin (PCT) in children with Community Acquired Bacteraemia (CAB) at a tertiary hospital in Nigeria. It is to enhance focus on antibiotic stewardship in clinical practice.

Methods: Children clinically suspected to have bacteraemia at presentation during 13 months of the period of study were recruited. Their blood samples were cultured and assayed for serum procalcitonin. Antibiotic resistance was determined on isolated bacteria, and polymerase chain reaction was used to confirm implicated genes. The data generated were analyzed using appropriate descriptive and inferential statistics.

Results: A total of 343 children ≤ 14-years were evaluated, and 94 (27.4%) had bacteraemia. The most common organisms were Staphylococcus aureus (n=66; 70.2%), *Stenotrophomonas maltophilia* (n=7; 7.4%), and coagulase negative staphylococci (n=6; 6.4%). More than fifty percent of all the isolates were multidrug-resistant. Twenty-one of 21 *Staphylococcus aureus* had *mecA* gene and three Gram-negative isolates had at least one of *bla*CTX-M/*bla*SHV/*bla*TEM genes. Elevated serum procalcitonin level was significantly associated with bacteraemia (χ^2=21.652, ρ=<0.001), sensitivity of 83.0% and negative predictive value of 87.3% (80.4-92.0). Congenital malformation was most associated with community acquired bacteraemia.

Conclusion: Nearly 30% of children suspected with bacteraemia in the studied population had positive blood-culture. The most isolated pathogen was *Staphylococcus aureus*; and a third of the pathogens were multi-drug resistant. Procalcitonin assay is useful in excluding bacteraemia in febrile children. Resistant bacteria pathogens are not uncommon in the community.

Keywords: multi-drug resistance, extended spectrum beta-lactamase, *meca* genet

Introduction

Bacterial infections are common in children and are a serious cause of childhood mortality in sub-Saharan Africa [1-3]. Community Acquired Bacteremia (CAB) is due to dissemination of viable bacterial in the bloodstream from a primarily infected site, of an individual outside the period of hospital admission [1]. The diagnosis is sometimes obscured, in this environment, due to other endemic illnesses like malaria [2,4]. The gold standard for diagnosis of bacteremia is by blood culture [5]. The diagnosis and care of patients with bacteremia can be enhanced by biomarkers like Procalcitonin (PCT) [6]. Information about CAB in southwestern region of Nigeria is sparse [1-3,7-9]. Immediate treatment of CAB may increase patients' chance of survival, whereas delay may increase the morbidity and mortality [10]. In most cases, bacteremia is due to infections of the respiratory, gastrointestinal tracts, central nervous system and soft-tissues. The initial site of infection may be obscured (primary bacteremia), despite testing with the best tests available [11]. It is especially so in malnourished or HIV-infected children [1-3,8,9]. Other risk factors for CAB are age, malaria, low birth weight, overcrowding, deficiencies of minerals and vitamins, inadequate immunization, breast feeding, adverse obstetrics history, congenital anomaly, poor socio-economic status, and care givers' inadequate health education [1,3,8,12-17]. Commonly implicated organisms are *Staphylococcus aureus, Streptococcus pneumonia, Haemophilus influenzae, Klebsiella pneumoniae*

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and *Salmonella typhi* [3,8,14,18,19]. Asides low data on epidemiologic patterns of CAB in our location, the emergence and dissemination of multidrug-resistant bacteria causing difficult-to-treat infections, requires attention [1,3,8,9].

The earlier studies done in our location of study showed that the leading cause of bacteremia in young children is Gram negative bacteria in Ilesa [12], while Ile-Ife documented Gram positive bacteria [13,20,21]. These isolated organisms were sensitive to the commonly used antibiotics then, this included quinolones and third-generation cephalosporin [20,21] although one of the studies from Ile-Ife detected *in vitro* resistance some of the isolates [13]. With the increasing incidence of community acquired resistant bacteria pathogens, there could have been alterations in what was documented. Besides, a regular surveillance is important in determining the epidemiologic pattern of bacteria pathogens to maintain a rational antibiotic use. This will also assist in reducing morbidity and mortality, associated with community acquired bacteremia. As at the time of this study initial antibiotics chosen for the treatment of bacteremia-related cases in this locality is mainly the combination of gentamicin with ceftriaxone or ampicillin for new born and infants; while in older children, it is cefuroxime with or without gentamicin.

The aim of this study was to determine the prevalence of bacteremia, resistance pattern of the causative organisms and role of procalcitonin in children with CAB seen at a university teaching hospital in southwestern Nigeria.

Methodology

Study site

This study was conducted at Obafemi Awolowo University Teaching Hospitals Complex (OAUTHC), a tertiary hospital in Ile-Ife, Osun State, Nigeria. Osun State is situated in the tropical rain forest zone, covering an area of approximately 14,875 sq km and lies between latitude 7˚30′0″ N and longitude 4˚30′0″ E. It provides services through six health care units, two of which have inpatient services-Ile-Ife Hospital Unit and the Wesley Guild Hospital with 535 and 212 bed complements respectively. Approval for the study (Approval number-IRB/IEC/0004553 and Protocol number-ERC/2015/04/06) was obtained from the Ethical Review Committee of OAUTHC. The patients were recruited between August 2015 and August 2016 at the children emergency and neonatal wards.

Sampling

All patients with febrile illness suspected of having a community acquired bacteremia, based on pediatrician assessment, were recruited. Children with diagnosis not related to sepsis, those admitted for more than 48 hours before developing fever, children who were discharged from hospital and re-presented with fever within 48 hours and children whose parent (s) or guardian (s) did not give consent were all excluded from the study. Demographic information and clinical details of each patient was recorded on forms specific for this study. The venipuncture site was cleaned with 70% alcohol and povidone-Iodine, then one to three milliliters of venous blood were drawn and introduced aseptically into two blood culture bottles (by BD PeadPlus bottle; Becton Dickinson). Also, three drops of plasma were added into the well of procalcitonin rapid diagnostic kit (StrongStep® PCT Rapid Test).

Processing

The PCT rapid kit was read after 15 minutes and interpreted based on the manufacturer recommendation. Readings >0.5 were taken as a case of sepsis. The blood culture samples were incubated using the BD Bactec™ 9050 Blood Culture System; Becton Dickinson. The Gram-negative organisms were identified with morphology, microscopy and Microbact GNB 24E, identification kit by Oxoid, while Gram-positive organisms were identified with morphology, microscopy, catalase, coagulase and optochin testing. Susceptibility testing was done using the following antibiotic discs: ampicillin (10 µg), ceftriaxone (30 µg), ceftazidime (30 µg), cefotaxime (30 µg), cefepime (30 µg), co-amoxiclav (20/10 µg), cefuroxime (30 µg), ciprofloxacin (5 µg), gentamicin (10 µg), imipenem (10 µg), levofloxacin (5 µg), cotrimoxazole (1.25/23.75 µg), piperacillin/tazobactam (110 µg), ampicillin/sulbactam (30 µg), aztreonam (30 µg) and azithromycin (15 µg) by modified Kirby-Bauer disk diffusion technique in line with the Clinical Laboratory Science Institute (CLSI) guidelines [22].

Phenotypically positive isolates for Extended Spectrum Beta-Lactamase (ESBL) producing bacteria and Methicillin-Resistant *Staphylococcus aureus* (MRSA) were subjected to molecular confirmation. The DNA extraction was conducted by the boiling method and the resulting DNA suspension was used as a template DNA for Polymerase Chain Reaction (PCR) based detection [23]. The

ESBL genes tested for were blaTEM, blaSHV and blaCTX-M, while the MRSA gene tested for was mecA. The primers used, as shown in **TABLE 1**, were commercially synthesized by Inqaba biotechnical Industries (Pty) Ltd. (South Africa) [24-26]. The procedure was followed according to the specification of the manufacturer.

The PCR products were electrophoresed, and the amplified bands were visualized under ultraviolet light with an UVitech transilluminator (Aveburg, Cambridge UK). The position of the amplified product was estimated by the position of 100 base pair molecular weight marker (Bio Lab Scientific Ltd., Toronto, Canada). All the data generated were entered into Microsoft Excel and processed using Statistical Package for the Social Sciences (SPSS) version 20.

Results

Three hundred forty-three infants and children aged 1 hour to 14 years [Median (IQR); 5 wks (2 days-34 months)] were evaluated, male: female ratio was found to be 1.1:1.0. The percentage of subjects recruited decreased progressively with age, from 49.3% in neonates to 7.6% in adolescents. The most common diagnosis was sepsis 142 (44.8%) and other illnesses include soft-tissue infection 26 (8.2%) and pneumonia 23 (7.3%). Ninety-four (27.4%) of the 343 patients had proven bacteremia. The number of cases seen during the harmattan season was 60 which yielded 13.8% of the positive cases. While in the rainy season 283 cases yielded 86.2% of the total positive cases. The frequency of patients is higher in the younger age group, especially the neonates, but the fraction of those with bacteremia within the different groups is higher in the older children. The case fatality rate among recruited patients was 12.8%. There is was no significant association of bacteremia with gender, age, season, socio-economic class or final outcome the illness.

Seventy-eight of the 94 bacteremia subjects had positive serum procalcitonin assay for bacterial infection. Procalcitonin assay was significantly associated with bacteraemia (χ^2=21.652, ρ=<0.001). The sensitivity is equal to 83.0% while the specificity is equal to 44.2%; also the positive predictive value and negative predictive values were 35.9% (29.9-42.5) and 87.3% (80.4-92.0) respectively. The organisms isolated from patients' blood cultures are listed in **TABLE 2**. Only 98 of the 343 blood culture pairs yielded the same organisms/pair. Ninety-four (27.4%) of these pairs were considered clinically significant community-acquired organisms while 4 (1.2%) were considered contaminants. Of the clinically significant organisms isolated, 75 (79.8%) were Gram-positive, and 19 (20.2%) were

TABLE 1. Sets of primers used to identify ESBL and mecA genes.

Genes	Primers		
	Forward	Reverse	Amplification at
bla_{SHV}	CGCCTGTGTATTATCTCCCT	CGAGTAGTCCACCAGATCCT	293 bp region
bla_{TEM}	TTTCGTGTCGCCCTTATTCC	ATCGTTGTCAGAAGTAAGTTGG	403 bp region
bla_{CTX-M}	CGCTGTTGTTAGGAAGTGTG	GGCTGGGTGAAGTAAGTGAC	569 bp region
*mec*A	AGTTCTGCAGTACCGGATTTGC	ATCGATGGTAAAGGTTGGC	530 bp region

TABLE 2. Organisms isolated from blood cultures.

Isolate	Frequency (%)		
Staphylococcus aureus	66 (70.2)	Gram-positives	Clinically significant organisms
Coagulase negative staphylococci	6 (6.4)		
Steptococcus pnaeumoniae	2 (2.1)		
Viridans group of streptococci	1 (1.1)		
Stenotrophomonas maltophilia	7 (7.4)	Gram-negatives	
Acinetobacter baumanii	2 (2.1)		
Acinetobacter haemolyticus	1 (1.1)		
Proteus mirabilis	1 (1.1)		
Escherichia coli	2 (2.1)		
Citrobacter sedlaki	1 (1.1)		
Hafnia alvei	2 (2.1)		
Salmonella Arizonae	1 (1.1)		
Salmonella Typhi	2 (2.1)		
Total	94 (100)		
Gram-positive bacilli	3 (75.0)	Contaminants	
Fungi	1 (25.0)		
Total	4 (100)		

Gram-negative. The most prevalent organism was *Staphylococcus aureus* (70.2%), followed by *Stenotrophomonas maltophilia* (7.4%) and coagulase-negative staphylococci (CoNS; 6.4%). The organism *Staphylococcus aureus* was seen to be predominant in all age groups.

More than 50% of the isolates were resistant to at least three antibiotics from the different classes of antibiotics (multidrug-resistant), including the commonly used antibiotics [27]. **TABLE 3** shows the antibiotic resistance patterns of the isolated Gram-negative bacteria. High rates of resistance were present in *Stenotrophomonas maltophilia*, *Acinetobacter baumanii, Acinetobacter haemolyticus* and *Proteus mirabilis*, whereas *Salmonella Typhi, Salmonella Arizonae* and *Citrobacter sedlaki* had the lowest rates of resistance. Three Gram-negative bacteria were phenotypically positive for ESBL production. Thirty-three percent of the Gram-negative isolates had ESBL genes as shown in **FIGURE 1**. The genes identified with PCR were blaSHV/TEM/CTX-M (in S. maltophilia), blaCTX-M/TEM (in H. alvei) and blaCTX-M (in A. haemolyticus).

The antibiotic resistance pattern of Gram-positive isolates is shown in **TABLE 4**. *Staphylococcus aureus* had high rates of resistance to ampicillin, penicillin, cefuroxime, ceftriaxone, ceftazidime, cefepime, tetracycline, co-trimoxazole and azithromycin. Nineteen (28.8%) of the Gram positive bacteria identified as *Staphylococcus*

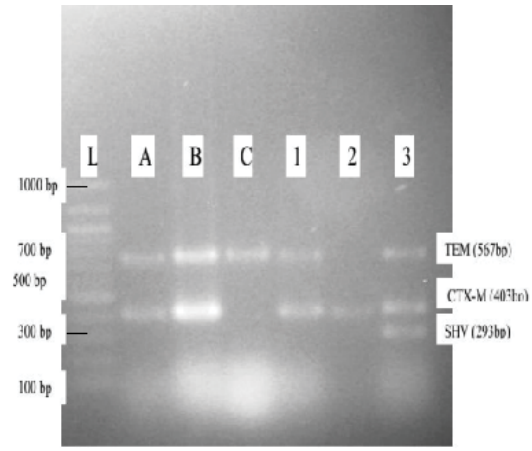

FIGURE 1. Agarose gel of CTX-M, TEM and SHV PCR products. L=100 bp ladder; A,B and C=positive controls; Number 1-3 correspond to samples: 1=Hafnia alvei (CTX-M and TEM), 2=*Acinetobacter haemolyticus* (CTX-M), 3=*Stenotrophomonas maltophilia* (CTX-M, TEM and SHV).

TABLE 3. Resistance pattern of the isolated Gram-negative bacteria.

Antibiotic	Isolates, n (%) resistant								
	S. maltophilia	*A. baumannii.*	*A. haemolyticus*	*E. coli*	*P. mirabilis*	*C. sedlaki*	*H.alvei*	*S.enterica Arezonae*	*S.enterica Typhi*
	(n=7)	(n=2)	(n=1)	(n=2)	(n=1)	(n=1)	(n=2)	(n=1)	(n=2)
Cefoxitin	2 (28.6)	0 (0.0)	1 (100.0)	0 (0.0)	1 (100.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Ceftriaxone	3 (42.9)	0 (0.0)	1 (100.0)	0 (0.0)	1 (100.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Cefotaxime	3 (42.9)	0 (0.0)	1 (100.0)	1 (50.0)	1 (100.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Ceftazidime	2 (28.6)	1 (50.0)	1 (100.0)	0 (0.0)	1 (100.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Cefepime	3 (42.9)	1 (50.0)	1 (100.0)	0 (0.0)	1 (100.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Aztreonam	3 (42.9)	0 (0.0)	1 (100.0)	0 (0.0)	1 (100.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Gentamicin	3 (42.9)	1 (50.0)	1 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Amikacin	1 (14.3)	1 (50.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Ciprofloxacin	3 (42.9)	1 (50.0)	1 (100.0)	1 (50.0)	1 (100.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Levofloxacin	2 (28.6)	0 (0.0)	0 (0.0)	0 (0.0)	1 (100.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Tetracycline	4 (57.1)	2 (100.0)	1 (100.0)	2 (100.0)	1 (100.0)	0 (0.0)	2 (100.0)	0 (0.0)	2 (100.0)
Imipenem	2 (28.6)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Ampicilin	6 (85.7)	0 (0.0)	1 (100.0)	1 (50.0)	1 (100.0)	0 (0.0)	2 (100.0)	0 (0.0)	1 (50.0)
Piperacillin/ Tazobactam	1 (14.3)	0 (0.0)	1 (100.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Co-Amoxiclav	3 (42.9)	0 (0.0)	1 (100.0)	1 (50.0)	1 (100.0)	0 (0.0)	2 (100.0)	0 (0.0)	0 (0.0)
Ampicillin/ Sulbactam	3 (42.9)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	0 (0.0)	1 (50.0)	0 (0.0)	0 (0.0)
Co-Trimoxazole	5 (71.4)	2 (100.0)	0 (0.0)	2 (100.0)	1 (100.0)	0 (0.0)	2 (100.0)	0 (0.0)	2 (100.0)
Chloramphenicol	5 (71.4)	1 (50.0)	1 (100.0)	2 (100.0)	1 (100.0)	0 (0.0)	2 (100.0)	0 (0.0)	2 (100.0)

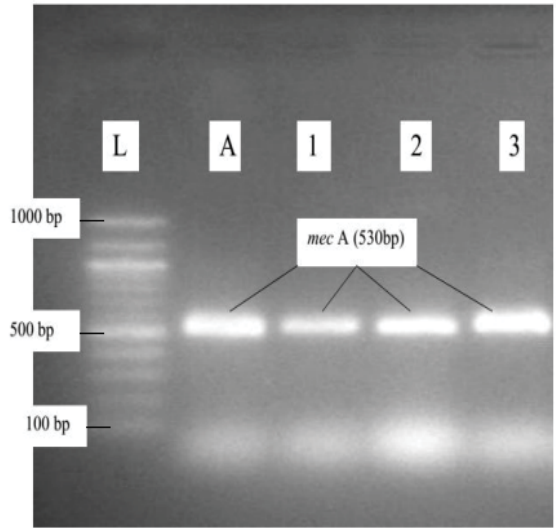

FIGURE 2. Agarose gel of mecA gene PCR products. L=100 bp ladder; A=positive control (mecA); Number 1-3 correspond to samples: 1, coagulase-negative staphylococci, 2 and 3, *Staphylococcus aureus*.

Table 4. Resistance pattern of the isolated Gram-positive bacteria.

Antibiotic	Isolates, n (%) resistant			
	S. aureus (n=66)	CoNS (n=6)	*S. pneumonia* (n=2)	VGS (n=1)
Cefuroxime	38 (57.6)	3 (50.0)	0 (0.0)	0 (0.0)
Cefoxitin	19 (28.8)	3 (50.0)		
Ceftriaxone	46 (69.7)	5 (83.3)	0 (0.0)	0 (0.0)
Ceftazidime	50 (75.8)	6 (100.0)	0 (0.0)	0 (0.0)
Cefepime	55 (83.3)	4 (66.7)	0 (0.0)	0 (0.0)
Azithromycin	38 (57.6)	3 (50.0)	0 (0.0)	0 (0.0)
Erythromycin	28 (42.4)	3 (50.0)	0 (0.0)	0 (0.0)
Gentamicin	24 (36.4)	2 (33.3)	0 (0.0)	0 (0.0)
Amikacin	7 (10.6)	0 (0.0)	0 (0.0)	1 (100.0)
Ciprofloxacin	18 (27.3)	1 (16.7)	0 (0.0)	0 (0.0)
Levofloxacin	15 (22.7)	0 (0.0)	0 (0.0)	0 (0.0)
Tetracycline	44 (66.7)	4 (66.7)	1 (50.0)	0 (0.0)
Ampicilin	49 (74.2)	4 (66.7)	0 (0.0)	0 (0.0)
Amoxicillin			0 (0.0)	0 (0.0)
Penicillin	60 (90.9)	5 (83.3)	0 (0.0)	0 (0.0)
Carbenicillin			0 (0.0)	0 (0.0)
Piperacillin/Tazobactam	18 (27.3)	2 (33.3)	0 (0.0)	0 (0.0)
Co-amoxiclav	17 (25.8)	1 (16.7)	0 (0.0)	0 (0.0)
Ampicillin/Sulbactam	11 (16.7)	1 (16.7)	0 (0.0)	0 (0.0)
Co-trimoxazole	55 (83.3)	3 (50.0)	2 (100.0)	1 (100.0)
Chloramphenicol	24 (36.4)	2 (33.3)	0 (0.0)	0 (0.0)
Clindamycin	17 (25.8)	1 (16.7)	0 (0.0)	0 (0.0)

CoNS: Coagulase-Negative Staphylococci, VGS: Viridans Group of Streptococci

aureus were Methicillin Resistant (MRSA). The six identified coagulase-negative staphylococci had a similar resistance pattern with 33.3% being methicillin-resistant coagulase-negative staphylococci (MR-CoNS).

The presence of the *mec*A gene was confirmed with PCR, as illustrated in **FIGURE 2**. All the *Staphylococcus spp*. isolates that had the *mec*A gene were sensitive to vancomycin strip (M.I.C.E-Oxoid Limited, Wade Road, Basingstoke, and Hampshire RG24 8PW, United Kingdom). The Streptococcus pneumoniae isolated were resistant to co-trimoxazole only (100%), whereas the viridians group streptococci were resistant to both cotrimoxazole (100%) and amikacin (100%).

Discussion

This study determined the prevalence and resistant pattern of bloodstream pathogens in infants and children who presented at the emergency units of Obafemi Awolowo University Teaching Hospitals Complex, Ile-Ife, Osun State, in southwestern Nigeria.

We found the prevalence of CAB to be 27.4%. This is higher than what was obtained in similar studies in Northern (18.2%), and Central Nigeria (10.8%) 2 but lower than 48.9% obtained in another study from the South-South region of Nigeria [28]. The variation in the prevalence might be ascribed to differences in methodology or, risk factors or co-morbidity, hygiene, possibly to location because regional variation has been suggested to cause this variation [2,3,12-14,21,22,29-31].

We considered the positive blood cultures of Gram-positive bacilli, like *Bacillus spp.*, and fungi to be contaminants since the patients had no clinical features of sepsis; the organisms could have been introduced into the culture bottle from contaminated skin at the time of collection [32]. The contamination rate of blood cultures in our study was very low at 8.2%, which is similar to a report from Ibadan4 and much lower than from another study in Iran [33].

Gram-positive bacteria were the most prevalent cultured pathogens, accounting for 79.8% of the cultured organisms. Some studies from Lagos and other developing countries have found similar higher prevalence of Gram-positive bacteria and lower prevalence of Gram-negative bacteria [34-36]. Conversely, studies from the northern and eastern Nigeria as well as Central Africa have recorded predominance of Gram-negative bacteria [3,28,29,37]. These differences could be due to hygiene, infrastructures or socio-economic status of the people in these regions. The species of organisms isolated from the blood of the children is not much different from that reported in other studies on bacteraemia, although there are variations in the proportion as well as predominance of organisms [2,35,36,38-41]. We found that *Staphylococcus aureus* was the predominant Gram-positive organisms. This is not an uncommon finding, as it has been reported in many studies; it could have been due to *Staphylococcus aureus* carriage on the skin, because most of the patients had soft-tissue infection initially, and some had *Staphylococcus* sepsis [34-37]. And also, CoNS has been significantly associated with both community and hospital acquired bacteremia [1]. Amongst the Gram-negative organisms isolated, *Stenotrophomonas maltophilia* predominated and this is a rather unusual finding from clinical samples of patients in this locality. Some studies done in Taiwan reported *Stenotrophomonas maltophilia* to be a cause of CAB [42,43].

A major finding which gives room for concern was that more than half of the isolated organisms were multi-drug resistant. Although, multi-drug resistant organisms have been reported in sub-Saharan Africa [44-47]. With could deduce from our study that antibiotic regulation is poor, this may be a contributory factor to the multi-drug resistant pattern of the bacteria causing infections in our locality [48,20]. We also found out that, the commonly used drugs for empiric treatment of community acquired infections in this environment were often ineffective: Gram-negative organisms are now resistant to chloramphenicol, co-amoxiclav and ceftriaxone, which contradict what was earlier reported by Adejuyigbe et al, [20] in the same location as this study. Antibiotic regulation is poor in Nigeria, this leads to misuse of antibiotics and eventual resistance to them by bacteria. *Citrobacter sedlaki* and *Salmonella arizonea*, were both sensitive to all the tested antibiotics. The resistant pattern of these Gram-negative isolates, especially for *Stenotrophomonas maltophilia*, could be due to cross-resistance or the use of efflux pumps by these pathogens.

The resistance genes of the Gram-negative organism we tested for were those of ESBL genes of the 19 Gram-negative organisms, 15.8% were found to have the ESBL genes, which are fewer than reported by Kavitha, Sevitha and Sunil [35]. The only *Acinetobacter haemolyticus* isolated was blaCTX-M, while 50% of Hafnia alvie have both blaCTX-M and blaTEM, and 14.3% of *Stenotrophomonas maltophilia* have blaSHV/blaTEM/blaCTX-M. Three types of the ESBL genes were found the locality, conforming to what was found in the North Eastern Nigeria [24]. *Stenotrophomonas maltophilia* is a known ESBL producing organism that has been isolated both in clinical samples and drinking water [49-52]. In addition to multidrug-resistance ability of *Acinetobacter spp.*, they exhibit both Extended Spectrum β-lactamase and AmpC β-lactamase resistance pattern [53-57]. Also, Hafnia alvie can acquire AmpC resistance [53,58]. Plasmid transfer could account for the presence of ESBL gene in this organisms [59,60].

Since three quarters of CAB are caused by S. aureus and CoNS with half of them resistant to cefuroxime and one third to gentamicin, these antibiotics cannot be recommended in management of CAB. Up to one-third of the Gram-positive organisms, mainly *Staphylococcus aureus* and CoNS were MRSA, i.e. 28.8% and 33.3% respectively had *mec*A genes, a rate that is similar to that reported in Mangalore by Prabhu, Bhat and Rao.35 None of the MRSA or MR-CoNS bacteria isolated was found to be resistant

to vancomycin. However, due to cost and non-availability of this medication, not all the patients with MRSA infection received vancomycin therapy. Those who did not, were treated with ceftriaxone combined with gentamicin. While all the five patients treated with vancomycin recovered fully, only three (21.4%) of the 14 treated with the combination of ceftriaxone and gentamicin died, thus indicating good efficacy of this antibiotic combination. The Streptococcus pneumoniae isolated was 100% resistant to co-trimoxazole, while the *Viridians Streptococci* were resistant to amikacin and co-trimoxazole. Since these isolates occurred in only 3.2% of the patients co-trimoxazole and amikacin should not be included in the consideration of first line drugs for CAB in this locality.

Conclusion

The prevalence of CAB in the suspected infants and children utilizing this tertiary health facility in southwestern Nigeria was noted to be nearly 27.4%. The most common single agent isolated was *Staphylococcus aureus* and more than fifty percent of all the isolated pathogens were multidrug-resistant. Procalcitonin was found to be useful in excluding bacteraemia in febrile children. There is an urgent need for a review of the antibiotics in use in order to improve care. Such combinations like Piperacillin/Tazobactam, Amikacin/Levolfoxacin or Ampicillin/Sulbactam as empirical antibiotics will probably give a good outcome in the care of these patients seen at the study location.

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Conflicts of interest

None.

Disclosure

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