DOI: 10.22625/2072-6732-2026-18-2-71-79

NASAL METHICILLIN–RESISTANT *STAPHYLOCOCCUS AUREUS* CARRIAGE IN TERTIARY HOSPITALS: EVIDENCE OF HOSPITAL–ACQUIRED TRANSMISSION IN NIGERIA

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Носительство метициллин-резистентного золотистого стафилококка в носовой полости в больницах третьего уровня: доказательства внутрибольничной передачи инфекции в Нигерии

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Abstract

Methicillin-resistant staphylococcus aureus (MRSA) nasal carriage is a significant source of infection and transmission in hospital environments. Effective infection control and antimicrobial stewardship are hampered in low-and middle-income countries by a lack of local monitoring data. This study investigated the prevalence, antimicrobial resistance pattern and genetic determinants of MRSA in patients and healthcare in two tertiary hospitals in Nigerian. A total 1, 309 nasal swabs specimens were collected from in-patients, healthcare workers and out-patients from two different tertiary hospitals. Staphylococcus aureus was identified and isolated using standard biochemical methods. The MRSA were phenotypically detected using Brilliance MRSA chromagar and cefoxitin and latter subjected to antimicrobial susceptibility testing following the standard Kirby—Bauer disk diffusion method. PCR-specific primers were used to screen for mecA and pvl genes in ten randomly selected MRSA. Out of the 1,309 nasal samples collected, 575 S. aureus representing 43.9% were isolated from the nasal samples of which 96 (17%) were MRSA, 81 from in-patients/out-patients and 15 from health care workers. The in-patients and doctors habour the highest number of MRSA, 73/81 and 8/15 respectively. All the MRSA isolates resistant to cefoxitin were also found to be resistant to tetracycline, amoxicillin, and amoxicillin-clavulanic acid. The mecA and pvl genes were detected in five of the isolates. However, pvl gene was detected in one isolate without corresponding detection of mecA gene. The high frequency of MRSA carriage among patients and healthcare personnel underscores the potential for hospital-acquired transmission and highlights the need for strengthened infection control and antibiotic stewardship in Nigerian tertiary hospitals.

Резюме

Носительство метициллин-резистентного золотистого стафилококка (MRSA) в носовой полости является значительным источником инфекции и передачи инфекции в больничных условиях. Эффективный инфекционный контроль и рациональное использование антибиотиков затруднены в странах с низким и средним уровнем дохода из-за отсутствия данных местного мониторинга. В этом исследовании изучались распространенность, характер антимикробной резистентности и генетические детерминанты MRSA у пациентов и медицинских работников в 2 больницах третьего уровня в Нигерии. Всего было собрано 1309 образцов мазков из носовой полости у стационарных пациентов, медицинских работников и амбулаторных пациентов из 2 разных больниц третьего уровня. Золотистый стафилококк был идентифицирован и выделен с использованием стандартных биохимических методов. MRSA были фенотипически обнаружены с использованием хромагара Brilliance MRSA и цефокситина, после чего проводилось тестирование на чувствительность к антимикробным препаратам по стандартному методу дисковой диффузии Кирби — Бауэра. Для скрининга генов mecA и pvl в 10 случайно выбранных образцах MRSA использовались ПЦР-специфические праймеры. Из 1309 собранных образцов из носовой полости было выделено 575 штаммов S. aureus, что составляет 43,9%, из которых 96 (17%) были MRSA, 81 — от стационарных/амбулаторных пациентов и 15 — от медицинских работников. Наибольшее количество MRSA было обнаружено у стационарных пациентов и врачей — 73/81 и 8/15 соответственно. Все изоляты MRSA, устойчивые к цефокситину, также оказались устойчивыми к тетрациклину, амоксициллину и

амоксициллину-клавулановой кислоте. Гены tecA и pvl были обнаружены в 5 изолятах. Однако ген pvl был обнаружен в 1 изоляте без соответствующего обнаружения гена tecA. Высокая частота носительства MRSA среди пациентов и медицинского персонала подчеркивает потенциал внутрибольничной передачи инфекции и необходимость усиления инфекционного контроля и рационального использования антибиотиков в нигерийских больницах третьего уровня.

Ключевые слова: *метициллин-резистентный золотистый стафилококк (MRSA), антибиотикорезистентность, золотистый стафилококк, медицинские работники, пациенты.*

Key words: *Methicillin-resistance Staphylococcus aureus (MRSA), antibiotic resistance, Staphylococcus aureus, health care workers, patients.*

Introduction

For almost a century, *Staphylococcus aureus* has been identified as a significant contributor to human illness (1). Although chromosomal mutation and antibiotic modification are also significant, it was found that resistance was acquired through horizontal gene transfer from within and across strains. The majority of deadly infections were initially cured by penicillin, but by the mid-1940s, just a few years after it was first used in clinical settings, resistance had been found in hospitals, and within ten years, penicillin resistance had grown to be a serious issue in the community (2). In order to address the rise in penicillin resistance, semisynthetic penicillinase resistant methicillin was developed in 1961. However, reports of methicillin-resistant isolates quickly followed its introduction (3), which alarmed medical professionals. The effectiveness of treatment for infections caused by methicillin-resistant *S. aureus* (MRSA) is more detrimental than those resulting from methicillin-sensitive strains (4). Methicillin-resistant *Staphylococcus aureus* (MRSA) continues to be a major global cause of bacterial infections that are difficult to cure and a persistent risk to patient safety in both community and medical settings. Antimicrobial resistance is widely acknowledged as a serious worldwide public health issue that significantly increases morbidity and death while weakening the efficacy of common practices and therapies (5,6).

Nasal carriage of *S. aureus*, especially MRSA, is a predictor of clinical infection and a significant reservoir for subsequent transmission. Carriage surveillance is a key component of infection-prevention measures since healthcare workers (HCWs) can be both recipients and carriers of MRSA between wards and patients. There is an urgent need for local data to direct control efforts because surveillance and stewardship deficiencies have been associated with higher and varied MRSA prevalence in tertiary care settings in low- and middle-income countries, particularly Nigeria (7,8). From a molecular perspective, the *mecA* gene, which codes for the modified penicillin-binding protein PBP2a and provides decreased affinity for β-lactam antibiotics, is most frequently responsible for resistance to methicillin and similar β-lactams. The lukS-PV/lukF-PV genes encode the Panton-Valentine leukocidin (PVL) toxin, which is often linked to community-acquired strains that cause severe skin and soft-tissue infections as well as, on occasion, necrotizing pneumonia. Therefore, the presence or lack of *mecA* and pvl genes offers clinically useful information about virulence potential and resistance mechanisms (9,10). The purpose of this study was to describe the antimicrobial susceptibility pattern and genetic determinants of methicillin-resistant MRSA in patients and healthcare professionals who visit tertiary hospitals in two significant Nigerian cities in South Eastern Nigeria.

Methodology

Sample collection

A total one thousand three hundred and nine (1, 309) nasal swabs specimens were collected from in-patients, healthcare workers and out-patients from two different hospitals; University of Nigeria Teaching Hospital (UNTH), Enugu and Alex Ekwueme Federal University Teaching Hospital (AE-FUTHA) Abakaliki both in South East Nigeria. The study included: patients that have spent at least 3 days on admission in the hospital, healthcare workers who were involved in direct management of patients or their specimens, out-patients who were not on admission. All the subjects were not on any antibiotics for at least 7 days before sample collection. The study excluded: patients admitted less than 3 days before sample collection, out-patients who have been on hospital admission 12 months preceding sample collection, patients and healthcare workers who were on antibiotics 7 days or less prior to specimen collection. All the specimens collected were transported to the laboratory units of the department of medical microbiology UNTH and AE-FUTHA for immediate culture, biochemical and morphological characterization.

Staphylococcus aureus isolation and identification

The specimens were inoculated on Mannitol salt agar (MSA), Blood agar (BA) and Chocolate agar (CA) for the isolation of *S. aureus* and incubated at 35° C for 24 hours. These isolates were identified by the conventional methods as described by Cheesbrough,

2006 (11). Smooth colonies that appeared whitish on BA, greyish on CA and yellowish with yellow zones on MSA were subjected to Gram staining, catalase, coagulase, urease, oxidase, indole, citrate and lactose fermentation tests. Positive isolates were re-screened on Chromagar orientation for a characteristic grey color of *S. aureus* in this medium. Standard strain of *S. aureus* (ATCC 25923) was used as a control. The stock culture of each biochemically confirmed isolate was stored in nutrient agar slants at 4° C prior to use. During use, the cultures were successively activated by sub-culturing into Mannitol salt agar and thereafter into nutrient agar plates for a period of 3 days to ensure there were no contaminants (12).

For molecular identification, genomic DNA from the isolates was extracted using Zymo Research Quick-DNA Fungal/Bacteria Miniprep kit (Cat. D6005), according to the procedure outlined by Nawrot *et al.,* 2010 (13). DNA quality was assessed on agarose gel and then visualized under a UV transilluminator. The bacterial 16S rRNA gene was amplified. The universal primer pair used is shown in Table 1, while the generated electrophoresis bands are seen in figure S1. Representative amplicons were selected, sequenced and deposited in GenBank

Phenotypic detection of MRSA and antimicrobial susceptibility testing

Antibiograms of *S. aureus* against cefoxitin and 17 other antibiotics was determined by disc diffusion method according to Clinical Laboratory Standard Institute (CLSI) recommendation (CLSI, 2012) on Mueller-Hinton agar plates (14). The following antibiotic discs were purchased from Oxoids Chemical, (Cambridge, UK) and used**:** cefoxitin (FOX 30 mg), vancomycin (VA 30 mg), erythromycin (E 15 mg), ciprofloxacin (CIP 5 mg), gentamycin (CN 10 mg), tetracycline (TE 30 mg)**,** ceftriaxone (CRO 30 mg)**,** imipenem (IPM 10 mg), amoxicillin (AML 25 mg), amoxicillin/Clavulanic acid (AMC 30 mg), tazobactam/Piperacillin (TZP 30 mg), linezolid (LZD 30 mg), azithromycin (AZM 15 mg), sulphamethoxazole/trimethoprim (SXT 25 mg), cefuroxime (CXM 30 mg), clindamycin (DA 2 mg), mupirocin (MUP 5 mg), and ceftaroline (CFT 30 mg). The antibiotics were aseptically placed on the surface of the inoculated Mueller-Hinton agar plate using sterile forceps. For quality control, *S. aureus* ATCC 25923 was used. The plates were incubated at 37°C for 24 hours, and the inhibition zone diameters (IZDs) produced by the antibiotic disks were measured, recorded and compared to the standard breakpoints. A colony of an organism suspected to be MRSA was smeared and streaked out on Brilliance MRSA chromagar, along with a known MRSA colony and incubated at 35°C for 24 h (15). Thereafter the culture plate was observed and MRSA colonies displayed deep blue coloration (Brilliance blue).

Amplification and detection of mecA and pvl genes

The primers used are presented in Table 1. PCR was carried out in a total volume of 25 µl containing 10 µl of genomic DNA, 13 µl of distilled H_2O, 1 PCR Ready-To-Go bead (the bead contains 2.5 units of Taq DNA polymerase, 10 mM Tris-HCl (pH 9.0), 50 mMKCl, 1.5 mM $MgCl_2$, and 200 M of each of dNTP), 1.0 µl each of forward and reverse primer (100 mM). For quality control, *S. aureus* ATCC 25923 was used. All amplification reactions were performed in a Biorad PCR system, for 36 cycles as follow: For the *mecA* primer, the cycling conditions were as follows: initial denaturation for 5 min at 94°C; 35 cycles of denaturation for 30 sec at 94°C, annealing for 30 sec at 53°C, and extension for 1 min at 72°C; and a final extension for 5 min at 72°C. For *pvl* gene, the cycling conditions were as follows: initial denaturation for 5 min at 94°C; 35 cycles of denaturation for 40 sec at 94°C, annealing for 40 sec at 53°C, and extension for 1 minutes at 72°C; and a final extension for 10 min at 72°C (16).

Statistical analysis

Statistical analysis using the ANOVA and turkey post-hoc multiple comparison test tools for the comparative evaluation of categorical variables was performed with the SPSS 20.0 version statistical software package. Results were only considered to be statistically significant if the *p*-value was less than 0.05 ($p < 0.05$).

Table 1

Oligonucleotide primer sequences used in the study

Genes	Primer sequences (5′-3′)	Amplicon size (bp)	References
16S rRNA	27F: AGAGTTTGATCMTGGCTCAG	1500	[30]
	1525R: AAGGAGGTGWTCCARCCGCA		
mecA	F: TCCAGATTACAACTTCACCAGG	162	(Asghar, 2014)
	R: CCACTTCATATCTTGTAACG		
pvl	F:ATCATTAGGTAAAATGTCTGGACATGATCCA	433	(Asghar, 2014)
	R: GCATCAAGTGTATTGGATAGCAAAAGC		
	R: CTTCAAGTATGACGGGCTGA		

Results

Out of the 1,309 nasal samples collected from the hospitals, 926 (70.7%) and 382 (29%) were collected from the in-patients/out-patients and health care workers respectively. From both hospitals, the highest number of samples were collected from the female adults' in-patients and the laboratory scientists. A total of 575 *S. aureus* representing 43.9% were isolated from the nasal samples of which only 96 (17%) were MRSA, 81 from in-patients/out-patients and 15 from health care workers (Table 2 and 3). Within the patient's population, the in-patients harbor the highest number of *S. aureus* colonization and MRSA in both hospitals. Also, within the health care workers, the medical doctors carry the highest number of MRSA in both hospitals, followed by the nurses.

In Table 4, all the MRSA isolates resistant to cefoxitin were also found to be resistant to tetracycline, amoxicillin, and amoxicillin-clavulanic acid. Addition-

Table 2

Isolation of *S. aureus* from in–patients and out–patients

Demography	Nasal samples	*S. aureus* number (%)	p-value	MRSA number (%)	p-value
AEFUTHA					
Female adult in-patients	203	79 (39)	0.2862	16 (8)	0.4252
Male adult in-patients	122	40 (33)		13 (11)	
Female adult out-patients	39	16 (41)	0.0048	0 (0)	
Male adult out-patients	18	5 (28)		0 (0)	
Female Pediatrics in-patient	24	10 (42)	0.3587	2 (8)	0.4894
Male Pediatrics in-patients	23	6 (26)		0 (0)	
Female Pediatrics out-patient	14	2 (14)	0.6887	1 (7)	0.35
Male Pediatrics out-patients	26	6 (23)		0 (0)	
Total	**469**	**164 (35)**		32 (6.8)	
UNTH					
Female adult in-patients	141	73 (52)	0.0044	19 (13)	0.3441
Male adult in-patients	126	43 (34)		12 (10)	
Female adult out-patients	59	32 (54)	0.8515	3 (5)	
Male adult out-patients	56	32 (57)		3 (5)	
Female Pediatrics in-patient	28	21 (75)	0.0375	6 (21)	0.5174
Male Pediatrics in-patients	35	16 (46)		5 (14)	
Female Pediatrics out-patient	5	1 (20)	0.4167	1 (20)	0.4164
Male Pediatrics out-patients	7	0 (0)		0 (0)	
Total	457	218 (47.7)		49 (10.7)	
Subtotal	**926**	**382 (41.3)**		**81 (8.7)**	

Table 3

Isolation of *S. aureus* from health care workers

Health care workers	Nasal samples	*S. aureus* number (%)	p-value	MRSA number (%)	p-value
AEFUTHA					
Lab. scientists	58	26 (45)	0.6286	0 (0)	0.035
Doctors	46	22 (48)		3 (7)	
Nurses	46	20 (43)		0 (0)	
Orderlies	25	8 (32)		0 (0)	
Total	**175**	76 (43)		3 (1.7)	
UNTH					
Lab. technicians	6	5 (83)	0.5774	1 (17)	0.7666
Health attendants	14	10 (71)		2 (14)	

Continuation of the Table 3

Health care workers	Nasal samples	*S. aureus* number (%)	p-value	MRSA number (%)	p-value
Lab. scientists	74	43 (58)		1 (1)	
Doctors	51	28 (55)		5 (10)	
Physiotherapists	11	6 (55)		0 (0)	
Radiographers	6	4 (67)		1 (17)	
Nurses	32	15 (47)		2 (6)	
Orderlies	14	6 (43)		0 (0)	
Total	**208**	117 (56)		12 (5.8)	
Subtotal	382	**193 (50.5)**		15 (3.9)	

Table 4

Antimicrobial resistance pattern of isolated MRSA (n=96)

Antibiotics	Patients, UNTH (n = 49) (%)	Patients, AE-FUTHA (n = 32) (%)	HCW UNTH (n = 12) (%)	HCW AE-FUTHA (n = 3) (%)
Tetracycline	49 (100)	32 (100)	11 (92)	3 (100)
Amoxicillin	49 (100)	32 (100)	12 (100)	3 (100)
Cefoxitin	49 (100)	32 (100)	12 (100)	3 (100)
AMC	49 (100)	32 (100)	12 (100)	3 (100)
Cefuroxime	48 (98)	31 (97)	12 (100)	3 (100)
Erythromycin	46 (94)	32 (100)	10 (83)	3 (100)
STX	46 (94)	32 (100)	11 (92)	3 (100)
Ciprofloxacin	41 (84)	30 (94)	11 (92)	3 (100)
Ceftriaxone	43 (88)	26 (81)	11 (92)	3 (100)
Aztreonam	42 (82)	30 (94)	5 (42)	3 (100)
TZP	38 (78)	22 (69)	10 (83)	3 (100)
Clindamycin	31 (64)	13 (41)	9 (75)	2 (67)
Gentamicin	21 (44)	14 (44)	5 (42)	2 (67)
Imipenem	16 (34)	4 (13)	0 (0)	0 (0)
Vancomycin	5 (12)	1 (3)	0 (0)	0 (0)
Mupirocin	4 (10)	1 (3)	2 (17)	0 (0)
Linezolid	5 (12)	5 (16)	3 (25)	0 (0)
Ceftaroline	3 (8)	0 (0)	0 (0)	0 (0)

SXT — Sulphamethoxazole/Trimethoprim, TZP — Tazobactam/Piperacillin, AMC — Amoxycillin/Clavulanic Acid, HCW — Health care workers, UNTH- University of Nigeria Teaching Hospital, AE-FUTHA, Alex Ekwueme Federal University Teaching Hospital.

ally, all isolates from health workers in AE-FUTHA extended resistance to cefuroxime, Sulphamethoxazole/trimethoprim, ciprofloxacin, ceftriaxone, aztreonam and tazobactam/piperacillin while more than 69% of other isolates were found to be resistance to the other group of antibiotics. Resistance to imipenem, vancomycin, mupirocin, linezolid and ceftaroline were very low in all the isolates, except isolates from AE-FUTHA health workers which showed susceptibility.

Figures 1 and 2 shows the amplification of *mecA* and *pvl* genes from 10 selected MRSA isolates resistant to cefoxitin and positive with Brilliance MRSA chromagar. The *mecA* and *pvl* genes were detected in five of the isolates. However, *pvl* gene was detected in one isolate without corresponding detection of *mecA* gene. For quality control, *S. aureus* ATCC 25923 was used as negative control strain lacking the genes. For positive control for the *mecA* gene, ATCC 33591 and ATCC 43300 were used. For positive control for the *pvl* gene, ATCC 49775 was used.

Discussion

In this study, we evaluated the frequency and antimicrobial resistance pattern of MRSA from health care

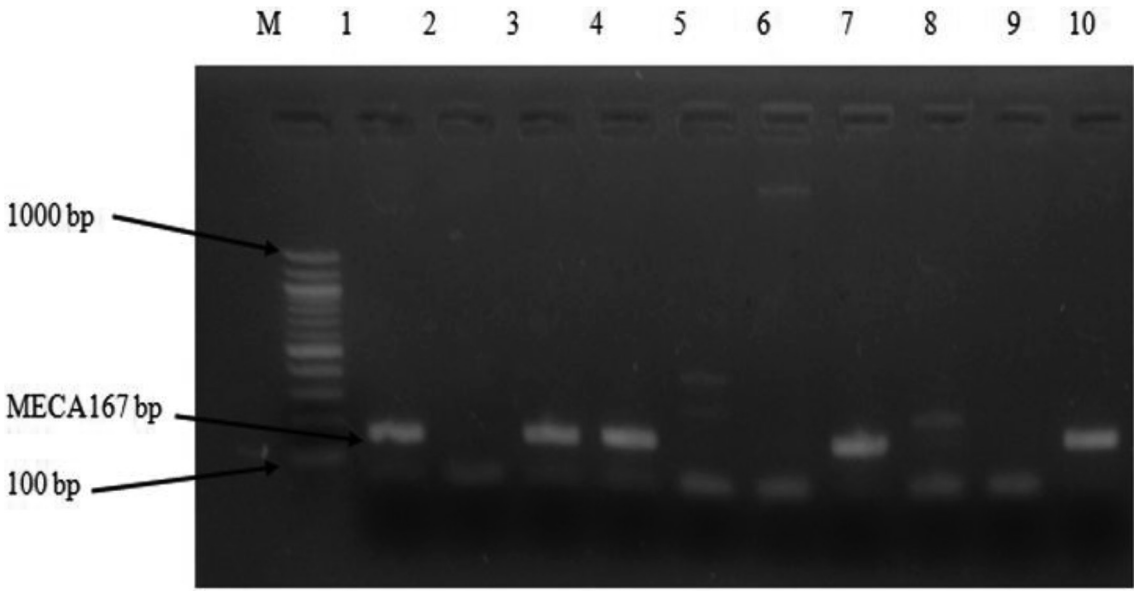

Fig. 1. Gel documentation showing amplified *mecA*. Positive isolates: Lanes 1, 3, 4, 7, 10: Lane M: 100-bp DNA ladder

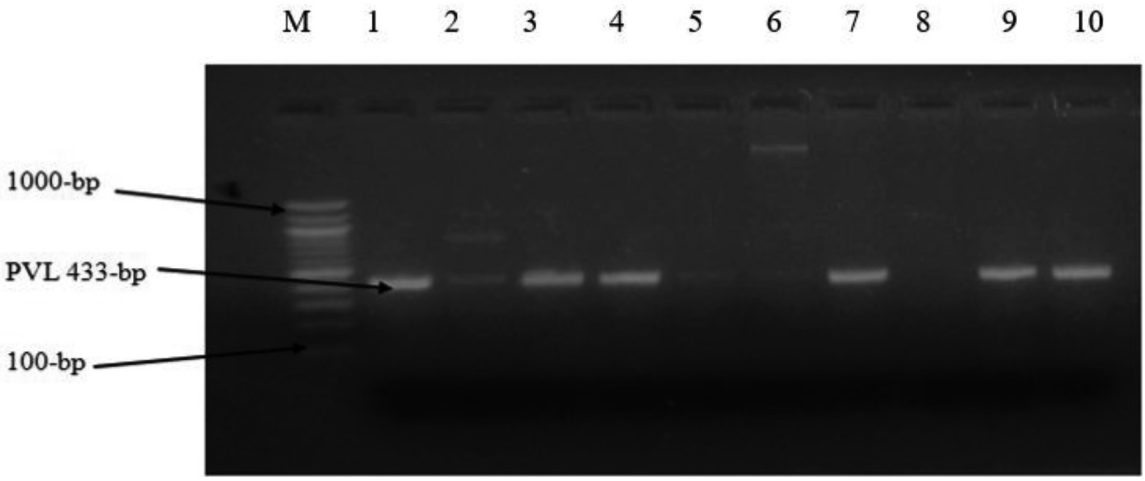

Fig. 2. Gel documentation showing amplified *pvl*. Positive isolates: Lanes 1, 3, 4, 7, 9 and 10; 100-bp DNA ladder

workers and patients from two major tertiary hospitals in Nigeria. A total of 575 (44%) *S. aureus* was isolated from 1, 309 nasal swabs specimens, out of which 96 (17%) were MRSA, 81 from in-patients/out-patients and 15 from health care workers. *S. aureus* is a commensal microorganism that typically colonizes the anterior nares of the nasal cavity of the human population (17). Consistent with our result with 44% prevalence colonization rate of *S. aureus*, different reports observed the same high frequency rates across different samples. From nasal samples of health workers in Portugal, prevalence rate of *S. aureus* colonization was reported at 39.6% (18). A higher rate was reported in Eritrea where *S. aureus* nosocomial prevalence rate was seen at 63.1% (19). Reports from other locations across Nigeria was also consistent with the result of this study. From urine samples of school pupils and clinical isolates from Abakaliki and Kano State, Nigeria, respectively, *S. aureus* colonization was reported at 88% and 50% (20,). From wounds and pus samples from Enugu State, Nigeria, the prevalence was 50% (21). This suggests that the prevalence rate of *S. aureus* depends on the environment, which may rely on the specimen sites and the degree of adherence to infection control protocols.

In this study, the prevalence rate of MRSA among the isolated *S. aureus* was 17%. Compared to results from elsewhere, a much lower rates were observed. From the nasal *Staphylococcus aureus* isolates from a Chinese Medical College Campus (22), community-acquired *Staphylococcus aureus* from Malaysia (23), nasal colonization of methicillin-resistant *Staphylococcus aureus* among healthy children in Taiwan (24), the prevalence rate of MRSA was reported at 3%, 3.2% and 7.8% respectively. In a cross-sectional study of nasal samples to as-

sess risk factors for *S. aureus* and MRSA colonization among children attending public schools in Brazil, the prevalence of MRSA was seen at 6.2% (25). Also, in a study that provided information on the susceptibility of *Staphylococcus aureus* causing skin and soft tissue infections in France, Ireland and the UK, 6%, 5% and 2% prevalence rates were reported respectively (26). These lower rates observed in these developed and emerging nations may be related to a high degree of adherence to infection control protocols. However, a higher rate (72%) was observed in systemic clinical specimens in Eritrea (19). Similarly, within Nigeria, higher rates were also mainly reported. Amongst the clinical specimens from the University of Ilorin Teaching Hospital, Southwest Nigeria (27), University of Jos, North central Nigeria (28) and National Orthopaedic Hospital, Enugu Southeast Nigeria (29), the prevalence rates were reported at 34.7%, 43% and 20.2% respectively. The only lower reported rate (10.7%) from Nigeria was from clinical isolates from a tertiary health hospital from Kano, Northwest Nigeria (30).

The result of this study showed that resistance of the MRSA ranged between 81% to 100% for tetracycline, amoxycillin, amoxicillin/clavulanic acid, cefuroxime, erythromycin, sulphamethoxazole/trimethoprim, ciprofloxacin and ceftriaxone. This result is in line with earlier reports (29, 18, 31), which may be explained by the fact that they are some of the most often prescribed antibiotics in our setting and that, aside from ceftriaxone, other antibiotics are available in tablet form, making them easy targets for drug abuse. MRSA also displayed a moderately low resistance against Clindamycin and gentamycin, ranging from 41% to 75%. This is consistent with the report of Khanal *et al.,* 2015 (32) that reported 42.9% resistance to gentamycin in MRSA. Compared to the aforementioned antibiotics, clindamycin and gentamycin have comparatively lower resistance. This could be because clindamycin is not frequently prescribed, which reduces abuse, whilst gentamycin is only formulated as injectable, which can only be administered by qualified healthcare professionals. On the other hand, there was 0% resistance to ceftaroline in almost all the MRSA and this is in agreement with previous reports (33-34). This could be because ceftaroline, a fifth-generation cephalosporin, is a novel drug with little stock and distribution in our environment, if any, therefore abuse will undoubtedly be uncommon. According to our research, ceftaroline may become the preferred medication for the empirical treatment of MRSA-caused infections. The result of our study also shows that MRSA displayed a generally low resistance to mupirocin, imipenem, linezolid and vancomycin and this is consistent with other reports (35, 31). This may be because these antibiotics are typically costly and can only be administered intravenously, thus there would be very little misuse of them. This implies that in the absence of ceftaroline, these antibiotics may be used empirically to treat MRSA infections. Our result is also consistent with the report of Iroha *et al.,* 2012 (36) where MRSA was reported to be highly susceptible to vancomycin and highly resistant to ciprofloxacin and sulphamethoxazole/trimethoprim. However, some of our findings are in disagreement with other reports which stated that; sulphamethoxazole/trimethoprim, was effective against MRSA (37), MRSA were highly susceptible to ciprofloxacin and gentamycin but showed low resistance to sulphamethoxazole/trimethoprim, and clindamycin (32). This could however be due to differences in environment of the studies where different strains of organisms may show different susceptibility to antibiotics. While the *pvl* gene aids in the epidemiological classification of MRSA, the detection of the *mecA* gene is crucial for the scientific identification (38). The *mecA* and *pvl* genes were detected in five of the isolates. However, *pvl* gene was detected in one isolate without corresponding detection of *mecA* gene. It is important to point out that almost all the MRSA are also resistant to beta-lactam antibiotics. The *mecA* gene, which is found on a mobile genetic element known as staphylococcal cassette chromosome mec (SCCmec), encodes penicillin-binding protein 2 , which is linked to MRSA resistance to -lactam drugs (39).

In conclusion, there is a high frequency rate of MRSA from nasal samples of patients and healthcare workers in these tertiary hospitals. Hospitalized patients and doctors have significantly higher burdens of MRSA compared to outpatients and other health care workers respectively. This evidently points to a possible nosocomial transmission of MRSA from in-patients to doctors within the hospital environment.

Declarations

Ethical approval

Ethical approvals were obtained from the Ethical committee of the AE-FUTHA (FETHA as previously called), Abakaliki and UNTH, Enugu and the clearance reference numbers are FETHA/REC/VOL1/2016/443 and UNTH/CSA/329/VOL.5 respectively. Besides, signed informed consent of all grown up subjects and assents of the parents/guardians of the minors were obtained. All samples collected from the hospital under investigation were processed and handled according to the Helsinki principles for human and animal research

Clinical Trial Number

Not applicable

Consent for publication

Not applicable

Data Availability

The generated gene sequences have been deposited and publicly available in DDBJ/ENA/GenBank and ac-

cessible with the following accession numbers: PX281425 PX281426, PX281427, PX281428. Upon reasonable request, the corresponding author will provide any other datasets generated and examined during the current work.

Conflict of interests

Authors declare no conflict of interest

Funding

The authors are solely responsible the funding of this work, its content and the decision to submit it for publication.

Author Contributions

O.C.J and I.R.I conceptualized the study. M. A and C.E performed the investigations/methods. E.E.D prepared original draft. C. S. I and E. F. N reviewed and edited the draft. I. R. I supervised the project. All authors read and agreed to the final version of the manuscript.

Acknowledgements

Not applicable

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