

2
3 **Isolation and Molecular Detection of Mec-A**
4 **Gene in Methicillin Resistant Staphylococcus**
5 **aureus Colonizing Anterior Nares of School**
6 **Children in Jos South, Nigeria**
7

8
9
10
11 **ABSTRACT**
12

Aims: This study investigates and reports the carriage of MRSA in students of some Secondary Schools in Jos South Local Government

Study design: Cross sectional study

Place and Duration of Study: Molecular biology laboratory, Department of Microbiology, National Veterinary Research Institute, Vom, between February 2016 and March 2017.

Methodology: *Staphylococcus aureus* was isolated from the samples using standard cultural and microbiological methods. Antibiotic susceptibility testing was determined as described by the Clinical and Laboratory Standards Institute (CLSI). The detection of MRSA isolates was observed phenotypically using oxacillin and cefoxitin disc diffusion tests. In addition, molecular detection of MRSA *mecA* gene production was carried out using Polymerase Chain Reaction (PCR) method.

Results: All samples isolated (100%) had *Staphylococcus sp.* with 114 (29.6%) isolates being *S. aureus*. Antibiotic resistance in the isolates in decreasing order were as follows: ceftazidime (48.2%), augmentin (37.8%), cefuroxime (35.0%), ceftriaxone (23.7%), ampicillin-sulbactam (21.9%), penicillin G (14.9%), ofloxacin (12.2%), gentamycin (11.4%), erythromycin (8.8%), vancomycin (0.0%). Eighteen of the 114 coagulase positive *S. aureus* isolated (15.8%) were found to be MRSA using the oxacillin disc diffusion test, and thirteen of the MRSA detected (11.4%) identified using cefoxitin disc diffusion test to be also MRSA. The presence of methicillin-resistant gene (*mec A*) was confirmed in four (4) of the 18 MRSA isolates using the PCR technique.

Conclusion: The *S. aureus* isolates were less resistant to ampicillin-sulbactam, erythromycin, gentamycin, ofloxacin, and ceftriaxone, with vancomycin showing no resistance. In addition, *mec A* gene was detected in confirmed MRSA isolates.

13
14 **Keywords:** *Staphylococcus aureus*; MRSA; antibiotics resistance; susceptibility; gene.
15

16 **1. INTRODUCTION**

17

18 *Staphylococcus aureus* is known to be a major pathogen which causes a
19 wide spectrum of clinical manifestations, including skin and soft tissue
20 Infections, pneumonia, septicemia, endocarditis, Arthritis,
21 gastroenteritis, meningitis, urinary Tract infections, and Toxinoses (such
22 as food poisoning, scalded skin syndrome and toxic shock Syndrome) [1-
23 4]. The drugs of choice for therapy are usually the beta-lactam
24 antibiotics.

25 *Staphylococcus* was first identified in 1880 in Aberdeen Scotland by a
26 Surgeon, Sir Alexander Ogston in pus from a surgical Abscess in a knee
27 joint [5]. It is estimated that 20% of human population are long term
28 carriers of *Staphylococcus aureus* which can be found as part of the
29 normal skin flora [6] and in the anterior nares of human and different
30 animals [7,8]. Methicillin Resistant *Staphylococcus aureus* (MRSA) is a
31 strain of the bacterium *Staphylococcus aureus*. It is characterized by
32 antibiotic resistant to methicillin and many other chemotherapeutic
33 agents [9]. MRSA isolates are resistant to the β -lactam antibiotics.
34 Vancomycin is used to treat MRSA infections. Despite the efforts of
35 researchers to help improve the understanding of the pathogenesis of
36 *S. aureus*, there seems to be an increase in staphylococcal infections.

37 *Staphylococcus aureus* has a wide host range, and a diverse cellular as
38 well as environmental lifestyles. It has the ability to evolve to highly
39 drug-resistant forms that can cause diseases with epidemic potential
40 [10]. *S. aureus* exhibits its lifestyle in two ways: a commensal
41 asymptomatic state where it is harbored by 20% or more of the general
42 populations at the anterior nares; and the acute state at which it
43 attacks specific tissues and pathogenicity follows consequently.
44 Generally, *S. aureus* causes infections by self- inoculation (a process
45 whereby the organism breaches the natural barrier) or by direct or
46 indirect contact [10].

47 Antibiotic resistance is a serious public health issue. Some of the factors
48 facilitating antimicrobial resistance are irrational use of antibiotics by
49 health professionals, unskilled practitioners and the public; the ready

50 availability of antibiotics as over the counter drugs, poor quality of
51 antibiotics unhygienic conditions and inadequate surveillance [11, 12].
52 There is a rise in the prevalence of MRSA globally. It is estimated that
53 MRSA kills more than 40,000 patients every year in the United States
54 alone [13]. Data is unavailable to determine the number of patients
55 that are casualties of MRSA in Nigeria. However, from the studies
56 undertaken in Nigeria and the data from few locations [14-20], it is
57 necessary to contain antimicrobial resistance. Based on the WHO
58 antimicrobial resistance global report on surveillance, *S. Aureus* is a
59 major bacteria of international concern [21]. Some countries have
60 formulated policies and invested in surveillance methods to check this
61 public health issue, however, developing countries need do more work
62 to address antimicrobial resistance [22]. Nigeria has developed a
63 national action plan for antimicrobial resistance, 2017-2022, but its
64 implementation years later is still at the early stages with progress
65 difficult to track. In Nigeria, antibiotics are still bought over the counter,
66 thereby increasing the selective pressure of antibiotics when its
67 reduction is a strategy for containing antimicrobial resistance.
68 There is a need for urgent coordination and collaborations to contain
69 antimicrobial resistance in order to avert a major public health disaster.
70 This study focuses on the detection of *mec A* genes in MRSA isolates
71 from nares of school children in Jos South, Plateau state, Nigeria.

72

73 **2. MATERIALS AND METHODS**

74 **2.1 Materials**

75 **2.1.1 Media**

76 Bacteriological media that were used in this study included: MacConkey
77 Agar (MCA), Mueller-Hinton Agar (MHA), Nutrient agar (NA), Luria-
78 Bertani (LB) broth, Mannitol Salt Agar (MSA), Nutrient Broth (NB), Blood
79 Agar medium and Peptone water (PW). All the media were sourced
80 from Oxoid Ltd. (U.K.).

81 **2.1.2 Equipment**

82 The equipment used in this study include: Autoclave (Certoclav, Model
83 SM280E,
84 Surgifriend Medicals, England), Oven (HotboxSize One, Galenkamp,
85 U.K.), Incubator (Model12-140E, Quincy Lab Inc), Refrigerator/Freezer
86 (Model PRN 1313 HCA, BEKO, Germany), Thermocycler (Model TC-312,
87 Techne, England), Gel electrophoresis machine (Max Fill Scie-plas
88 Model HU10 serial no5237), Laminar air flow cabinet (PCR-8 re-
89 circulating laminar flow pre
90 station, Labcaire product 220/240v), Microscope (Model CME
91 1349522X, Leica, USA), Spectrophotometer (Eppendorf Biophotometer
92 8.5 mm, Lichtstrahihöhe), UV illuminator (Vilber Lourmat TFX-35-M
93 serial no NoV02 8104), Centrifuge (Model 5417R: Touch plate Super
94 Mixer, CAT No 1291, Lab-line Instrument Inc USA), Microwave oven
95 (HINARI Life Style 800watts model MX310TCSL), Electronic weighing
96 balance (Model QT 600: Touch plate Super Mixer, CAT No 1291, Lab-
97 line Instrument Inc USA), Vortex machine (Touch plate Super Mixer, CAT
98 No 1291, Lab-line Instrument Inc USA), and Gel Doc system (Biorad,
99 U.K.)

100

101 **2.1.3 Chemicals and reagents**

102 The chemicals and reagents used in this study included: Carbolfuscin,
103 Crystal violet, Ethanol, Creatinine, Potassium hydroxide and Kovac's
104 reagents, obtained from BDH chemical Ltd, England; Ethidium bromide,
105 Iodine solution, EDTA and Glycerol obtained from Sigma Chemical Ltd,
106 England; and Agarose gel from Schwarz/ Mann Biotech.

107 **2.1.4 Bacteria Isolates**

108 Confirmed *S. aureus* isolates from the anterior nares were obtained and
109 used for this study.

110 The antibiotic resistance profiles of the isolates are as shown in Table 2.

111 **2.2 Methods**

112 **2.2.1 Antibiotic Susceptibility Testing**

113 The antibiotic susceptibility test for *S. aureus* isolates from anterior
114 nares was carried out using the Kirby-Bauer disc diffusion method as
115 modified by the Clinical and Laboratory
116 Standards Institute - CLSI [22]. Briefly, 5 colonies of *S. aureus* isolates
117 were inoculated into 5 ml of Mueller-Hinton broth (MHB) and
118 incubated at 37°C for 24 hours after which the 24-hour
119 MHB was standardized to the turbidity equivalent to 0.5 McFarland
120 standards. The 0.5 McFarland standard was prepared as follows: 99.5
121 ml of 1% ($\frac{1\text{g}}{100\text{ml}}$) H_2SO_4 + 0.5ml of 1.172% ($\frac{1.172\text{g}}{100\text{ml}}$) $\text{BaCl}_2 \cdot 2\text{H}_2\text{O}$. A sterile cotton
122 swab stick was dipped into the standardized *S. aureus* suspension and
123 streaked on MHA plates. Antibiotics discs were gently placed on the
124 MHA plates using a pair of sterile forceps and the plates were allowed
125 to incubate at room temperature for 1 hour before re-incubating at
126 37°C for 17 hours. After incubation, the diameters of the zones of
127 inhibition were measured to the nearest millimetre (mm) using a ruler
128 and the result of the susceptibility test was interpreted using
129 susceptibility breakpoint earlier described by CLSI [22].

130 **2.2.2 Phenotypic test for MRSA**

131 All *Staphylococcus aureus* confirmed strains were screened for
132 methicillin resistance by using cefoxitin and oxacillin (oxid) 30ug and
133 1ug respectively. The discs were placed at a distance of at least 25mm
134 away from each other.

135 The isolates with inhibition zone diameter of <10mm for oxacillin and
136 <21 mm for cefoxitin were termed methicillin resistant where as those
137 showing a zone diameter of $\geq 13\text{mm}$ for oxacillin and $\geq 22\text{mm}$ for
138 cefoxitin were termed methicillin sensitive Clinical and laboratory
139 standard institute[22].

140 **2.2.3 Molecular detection of MRSA *mec A* genes**

141 Isolates that were MRSA positive were screened to detect the presence
142 of *mec A* gene.

143 **2.2.4 DNA extraction**

144 The DNA extraction was performed by the boiling method as described
145 previously [23]. Following purification on MacConkey agar, bacterial

146 DNA was isolated from a 24-h culture in Luria-Bertani broth prepared
147 according to the manufacturers' protocol. The bacterial cells were
148 harvested by centrifugation at 3200 rpm in a microcentrifuge for 2 min
149 at room temperature and the supernatant was discarded. The
150 harvested cells were re-suspended in 1 ml of sterile normal saline and
151 the micro-centrifuge tubes were placed in the vortex for 5 sec.
152 Centrifugation was carried out at 3200 rpm for 1 min and the
153 supernatant was discarded. 0.5 ml of sterile normal saline was added to
154 the pellets and the tubes were vortexed for 5 sec after which they were
155 heated in the block heater at 90°C for 10 min. immediately after
156 heating, rapid cooling was done by transferring the tubes into the
157 freezer for 10 min. Cell debris was removed after centrifugation was
158 done at 3200 rpm for 1 min and 300 µl of the supernatant was
159 transferred into a sterile 2 ml Eppendorf tube as DNA and stored at -
160 10°C until use.

161 Estimation of the concentration, purity and yield of the DNA sample
162 was accessed using the absorbance method (the measurement of
163 absorbance) with the spectrophotometer
164 (Nanodrop 1000, InqabaBiotectm, South Africa). For DNA
165 concentration, absorbance readings were performed at 260 nm (A₂₆₀)
166 and the readings were observed to be within the instrument's linear
167 range (0.1 – 1.0). DNA purity was estimated by calculating the
168 A₂₆₀/A₂₈₀ ratio and this was done by the spectrophotometer's
169 computer software (where A₂₆₀/A₂₈₀ ratio ranges from 1.7 – 1.9).

170 **2.2.5 DNA amplification of *mec A* genes**

171 The technique of [23] was used for the polymerase chain reaction (PCR)
172 procedure in this study. The primers (sense) *mecA1* 5'-
173 AAAATCGATGGTAAAGGTTGGC-3' and (antisense) *mecA2* 5'
174 AGTTCTGCAGTACCGGATTTGC-3' (Inqaba, South Africa) were used to
175 detect the presence of *mec A* gene in the methicillin-resistant isolates
176 by yielding a PCR product of 533 bp [23]. The master mix for PCR was
177 performed in a 50 µl reaction mixture containing 5 µl of a 10X PCR
178 buffer, 1.5µl of a 200 µM concentration of each deoxynucleoside

179 triphosphate (dNTP), 2.5 µl of a 25 mM MgCl₂, 0.25 µl of a 1.25 unit Taq
180 polymerase (Biolab, South Africa), 1 µl of a 10pM of each primer and
181 0.25 µl of a 2.5 µl of DNA template. DNA amplification was carried out
182 using GeneAmp^R PCR System9700 (Applied Biosystems, U.S.A) for 50
183 cycles in 50 µl of reaction mixture as follows: initial denaturation at
184 95°C for 2 minutes, denaturation at 95°C for 30 seconds, annealing at
185 55°C for 30 seconds and extension at 72°C for 1 minute with a final
186 extension at 72°C for 5 minutes, then kept at 4°C.

187 **2.2.6 Agarose gel electrophoresis**

188 PCR products (10 µl) was electrophorised in 1.5% agarose gel. (The gel
189 containing 5 µl of 10mg/ml ethidium bromide solution) at a 100 volts
190 for 60 minutes. 50 bp DNA marker (Fermenter^R) was used as the
191 molecular size marker. The Amplicons were visualized under automatic
192 molecular imaging transilluminator (Gel DOCTM XR+ BIORAD, U.S.A) to
193 check for the presence of the DNA PCR products at 533bp and the
194 image was stored in the computer.

195

196 **3. RESULTS AND DISCUSSION**

197 **3.1 Age and Sex Distribution of the Study Population**

198 A total of 385 students were enrolled for this study, out of which 173 were male and 212
199 were female, with male to female ratio of 1.6:2. as shown on table 1.

200

201 **Table 1. Age and Sex Distribution of the Study Population**

Schools	Age (10-15yrs)	Age (16-21yrs)	Female (%)	Male (%)
GSS Rantya	46 (11.9)	33 (8.6)	31 (8.1)	48 (12.5)
GSS Kufang	99 (25.7)	110 (28.5)	126 (32.7)	83 (21.6)
Sacred Heart	74 (19.2)	23 (5.9)	55 (14.2)	42 (10.9)
Total	219 (56.9)	166 (43.1)	212 (55.0)	173 (45.0)

202

203 **3.2 Antimicrobial Resistance Profile**

204 The antimicrobial resistance in the *S. aureus* isolates from anterior nares of school children
205 are shown in Table 1. The resistance in the isolates were as follows ceftazidime (48.2%),
206 augmentin (37.8%), cefuroxime (35.0%), ceftriaxone (23.7%), ampicillin-sulbactam (21.9%),
207 penicillin G (14.9%), ofloxacin (12.2%), gentamycin (11.4%), erythromycin (8.8%),
208 vancomycin (0.0%).

209 **Table 2. Antimicrobial Resistance and Sensitivity pattern of *Staphylococcus aureus***
 210 **isolates (n=114)**

Antibiotic	Resistance (%)	Sensitivity (%)
Augmentin	43 (37.8)	71 (62.2)
Ceftazidime	55 (48.2)	59 (51.8)
Ceftriaxone	27 (23.7)	87 (76.3)
Cefuroxime	40 (35.0)	74 (65.0)
Penicillin G	17 (14.9)	97 (85.1)
Erythromycin	10 (8.8)	104 (91.2)
Gentamycin	13 (11.4)	101 (88.6)
Ofloxacin	14 (12.2)	100 (87.8)
Ampicilin-Sulbactam	25 (21.9)	89 (78.1)
Vancomycin	0 (0)	114 (100)

211

212

213 **3.3 Biochemical Test for Isolates**

214 Out of the 385 *Staphylococci species*, 114 were confirmed by biochemical tests to be
 215 coagulase positive (*Staphylococcus aureus*) while 271 were coagulase negative giving
 216 29.6% and 70.4% respectively as represented in the pie chart as shown in Figure 1.

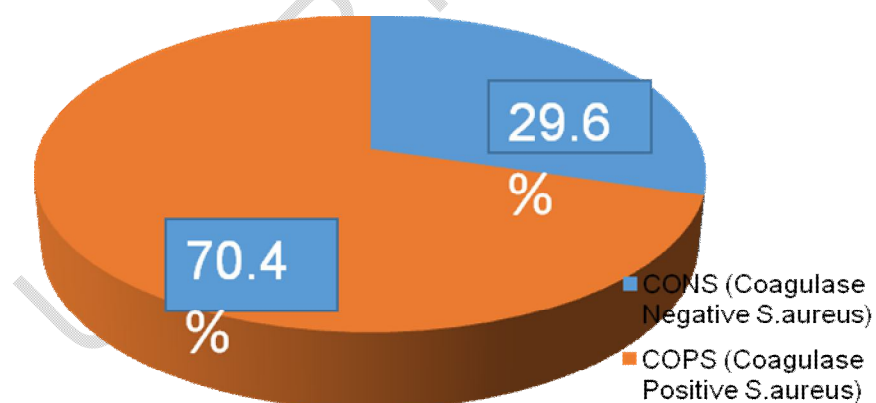


Fig. 1: Coagulase positive and negative *S. aureus* among the isolates.

217

218 **3.4 Phenotypic Confirmation of MRSA**

219 Out of the 114 coagulase positive *Staphylococcus aureus* isolated, eighteen (18) were
 220 found to be MRSA using oxacillin disc diffusion test which gave a prevalence of 15.8%

221 among *S.aureus* isolates and overall prevalence among study population of 4.7%. Only
 222 thirteen (13) of the MRSA detected were identified using cefoxitin disc diffusion test to be
 223 also MRSA, thereby giving a prevalence of MRSA among *S.aureus* isolates 11.4% and
 224 overall of 4.7% as shown in table 3.

225
 226
 227
 228

Table 3. Frequency of MRSA among the coagulase positive *staphylococcus aureus* isolates (n=114)

Confirmatory Test	Number	Frequency
	114	29.6
MRSA (oxacillin disc)	R 18	15.8
	S 96	84.2
MRSA (cefoxitin disc)	R 13	11.4
	S 101	88.6
Overall Prevalence (n= 385)	18	4.7

229 Key: **R**=Resistant **S**=Sensitive

230

231 **3.5 Molecular Detection of *mec A* Genes**

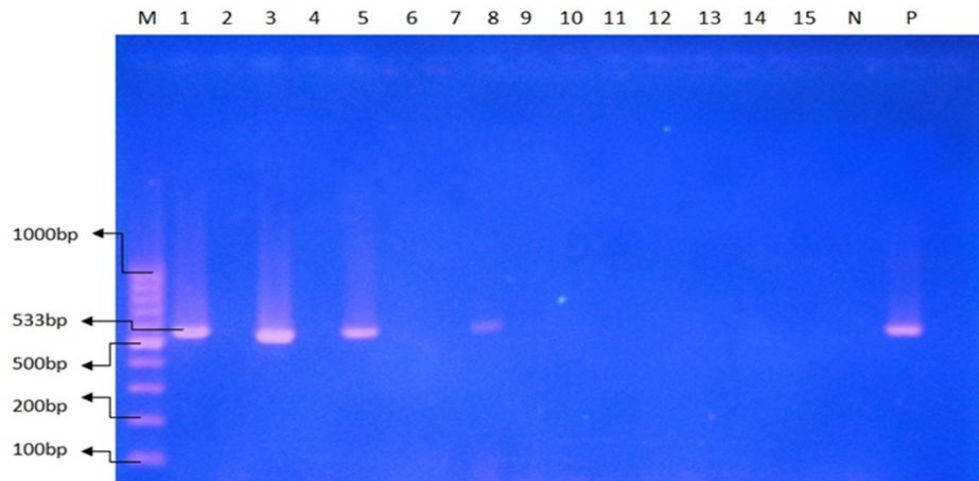
232 The presence of methicillin-resistant gene was confirmed using PCR technique. Four(4) of
 233 the 18 MRSA isolates were confirmed *mec A* positive as evidenced by the amplification of
 234 *mec A* gene at the specific amplicon of 533bp fig: 2. Hence, the *mec A* gene isolation rate
 235 among *staphylococcus aureus* isolates(n=114) was 3.51% and an overall (n=385) was
 236 1.04% as shown in Table 4.

237

238 **Table 4. The isolation rate of *mec A* gene among the *S. aureus*.**

	Number	Frequency (%)
<i>mec A</i> gene prevalence among <i>S. aureus</i> isolates (n=114)	4	3.51
Overall <i>mec A</i> gene prevalence among students (n=385)	4	1.04

239



240
241
242
243

Fig 2: PCR showing four amplicons produced by four isolates at 533bp With a 100bp molecular marker.

244 **3.6 Discussion**

245 Antibiotic resistance has been described as one of the paramount microbial threats of the 21st
246 century [24]. *Staphylococcus aureus* has always been a stumbling block for antimicrobial
247 chemotherapy, and the introduction of new classes of antimicrobial agents is usually followed
248 by the emergence of resistant forms of this pathogen [25]. Methicillin-resistant *Staphylococcus*
249 *aureus* (MRSA) has been proven to be a globally- spread nosocomial pathogen of the 20th
250 century [26]. Therefore, surveillance of the antimicrobial susceptibility patterns of *S. aureus* is
251 of utmost importance in understanding new and emerging resistance trends, and in the
252 management of both hospital and community-acquired infections. In the antimicrobial resistant
253 profile, it has been shown that Ceftazidime exhibited the highest resistance pattern, while
254 Vancomycin showed no resistance. Vancomycin can therefore be used for the treatment of
255 *staphylococcus aureus* as well as other antibiotics such as Ampicillin, Gentamycin, Ofloxacin,
256 and Ceftriaxone which showed low resistance.

257 In the antibiotic susceptibility testing it was observed that Erythromycin had the highest
258 number of isolates sensitive to it i.e., 104 isolates giving a percentage of 91.2% as opposed to
259 Ceftazidime with the lowest number of isolates 59 (51.8%; n=114). Data on MRSA strains in
260 most sub-Saharan African countries, cast shadow on the public health implication and
261 awareness of the organism. Information from this study intends to provide the baseline data,
262 for eventual appreciation on the need for cautious approach and intervention measures.

263 In this study, the MRSA prevalence of 4.7% (phenotypic) and 1.04 % (genotypic) may be
264 considered to be low, especially as there isn't any previous epidemiological data on MRSA in
265 this area among school children. Although, MRSA prevalence are known to vary with
266 geographical location, type of health institutions, studied population and method of detection
267 employed. However, our MRSA prevalence may be considered very low, when compared with
268 similar study in Ibadan, Southwestern Nigeria with a prevalence level of 20.3% [27], as both
269 phenotypic and molecular methods were employed. Previous studies on MRSA in the
270 southwestern Nigeria with same detection methods, reported prevalence of less than 2% [24,
271 28]. Oxacillin disc diffusion method was the earliest method of detection for methicillin
272 resistance expression. Because of low specificity and sensitivity, cefoxitin disc diffusion was
273 introduced by CSLI, that is known as a good surrogate marker of *mec A* gene detection [29,

274 30]. Earlier MRSA prevalence reported from Nigeria were based on phenotypic methods using
275 oxacillin.

276

277 **4. CONCLUSION**

278

279 A low percentage of secondary school children in Jos are carriers of multi-drug resistant
280 *Staphylococcus aureus*. The *S. aureus* isolates were more resistant to augmentin (37.8%),
281 cefuroxime (35.0%), ceftriaxone (23.7%), ampicillin-sulbactam (21.9%), penicillin G (14.9%),
282 ofloxacin (12.2%), gentamycin (11.4%), erythromycin (8.8%), vancomycin (0.0%). This
283 implies that the antibiotics could be useful in the MRSA infections.

284

285 **CONSENT**

286 Not applicable

287 **ETHICAL APPROVAL**

288 Not applicable

289 **REFERENCES**

- 290 1. Grisold AJ, Leitner E, Mühlbauer G, Marth E, Kessler HH,4 "Detection of
291 methicillin-resistant *Staphylococcus aureus* and simultaneous confirmation by
292 automated nucleic acid extraction and real-time PCR," *Journal of clinical*
293 *microbiology*. 2002: 40 (7), 2392-2397.
- 294 2. Ibadin EE, Enabulele IO, Muinah F. "Prevalence of *mecA* gene among
295 staphylococci from clinical samples of a tertiary hospital in Benin city, Nigeria,"
296 *African health sciences*. 2017: 17(4), 1000-1010.
- 297 3. Tong SY, Davis JS, Eichenberger E, Holland TL, Fowler VG. "*Staphylococcus*
298 *aureus* infections: Epidemiology, pathophysiology, clinical manifestations, and
299 management," *Clinical microbiology reviews*. 2015: 28 (3), 603-661.
- 300 4. Taylor TA, Unakal CG. "*Staphylococcus aureus*," In: StatPearls [Internet].
301 Treasure Island (FL): StatPearls Publishing; 2019.
- 302 5. Ogston A. "on Abscess" classic infection Disease" *Rev. Infect. Dis.* 1984: 6 (1)
303 122 – 128
- 304 6. Kluytmans, J., van Belkum, A., & Verbrugh, H. Nasal carriage of *Staphylococcus*
305 *aureus*: epidemiology, underlying mechanisms, and associated risks. *Clinical*
306 *Microbiology Reviews*. 1987: 10(3), 505-520.
- 307 7. Wertheim HFL, Voss MC, OttA, Van Belkum A, Voss A, Yolken R. H. (ASM Press
308 Washington D.C) 6th ed.; 282 – 298.
- 309 8. Weese JS, Duizkeren VE. Methicilin Resistant *Staphylococcus aureus* and
310 *Staphylococcus Pseuel Intermechius* in Veterinary Medicine, *Vet. Microbiol.*
311 2009:140: 418 – 429
- 312 9. Maurean UO, Okwu Tonye GO, Olley M, Eguagle OO. Canadian Epen biological
313 Science Journal. 2014: 1(1), 1 -12
- 314 10. Crossley KB, Jefferson KK, Archer GL, Fowler VG. *Staphylococci in human*
315 *disease*. : John Wiley & Sons, Singapore; 2009.

- 316 11. Okeke IN, Lamikanra A, Edelman R. "Socioeconomic and behavioral factors
317 leading to acquired bacterial resistance to antibiotics in developing countries,"
318 *Emerging infectious diseases*. 1999; 5 (1)18.
- 319 12. Chokshi A, Sifri Z, Cennimo D, Horng H. "Global contributors to antibiotic
320 resistance," *Journal of global infectious diseases*. 2019: (11)1, 36.
- 321 13. Adetayo TO, Deji-Agboola AM, Popoola MY, Atoyebi TJ, Egberongbe KJ.
322 "Prevalence of methicillin resistant *Staphylococcus aureus* from clinical specimens
323 in Ibadan, Nigeria," *International Journal of Engineering Science*. 2014: (3), 1-11.
- 324 14. Ajoke OI, Okeke IO, Odeyemi OA, Okwori A."Prevalence of methicillin-resistant
325 staphylococcus aureus from healthy community individuals volunteers in Jos south,
326 Nigeria," *Journal of Microbiology, Biotechnology and Food Sciences*. 2020: 9(5),
327 1389-1405.
- 328 15. Bunza NM, Isah AA, Hafsat MD, Asiya UI. "Antibiotic susceptibility pattern of
329 *Staphylococcus aureus* isolated from clinical samples in specialist hospital, Sokoto,"
330 *South Asian Journal of Research in Microbiology*. 2019: 1-6.
- 331 16. Ike B, Ugwu MC, Ikegbunam MN, Nwobodo D, Ejikeugwu C, Gugu T, Esimone
332 CO. "Prevalence, antibiogram and molecular characterization of community-acquired
333 methicillin-resistant *Staphylococcus aureus* in Awka, Anambra Nigeria," *The open
334 microbiology journal*. 2016:10, 211.
- 335 17. Osinupebi OA, Osiyemi JA, Deji-Agboola AM, Akinduti PA, Ejilude O,
336 Makanjuola SO, Sunmola NO, and Osiyemi EO. "Prevalence of methicillin-resistant
337 *Staphylococcus aureus* in Abeokuta, Nigeria," *South Asian Journal of Research in
338 Microbiology*. 2018: 1-8.
- 339 18. Layer F, Bakare RA, König B, König W. "Emergence of a community-associated
340 methicillin-resistant *Staphylococcus aureus* strain with a unique resistance profile in
341 southwest Nigeria," *Journal of clinical microbiology*. 2009: 47, 9. 2975-2980.
- 342 19. Udeani TK, Onyebuchi CJ, Ikpenwa MC, Ezenwaka UR. "Prevalence and
343 antibiotic susceptibility pattern of methicillin resistant *Staphylococcus aureus* in
344 burns and pressure ulcer patients," *African Journal of Clinical and Experimental
345 Microbiology*. 2016: 17, 2, 130-139.
- 346 20. World Health Organization, "Antimicrobial resistance global report on
347 surveillance: 2014 summary," *Antimicrobial resistance global report on surveillance:
348 2014 summary*, 2014.
- 349 21. Chaudhary AS. "A review of global initiatives to fight antibiotic resistance and
350 recent antibiotics' discovery," *Acta Pharmaceutica Sinica B*. 2016: 6 (6), 552-556.
- 351 22. Clinical and Laboratory Standards Institute. Performance standards for
352 antimicrobial susceptibility testing. 15th informational supplement M100–S15.
353 Clinical and Laboratory Standards Institute, 2012.
- 354 23. Porteous LA, Armstrong JL, Seidler RJ, Watrud LS. An effective method to
355 extract DNA from environmental samples for polymerase chain reaction
356 amplification and DNA fingerprint analysis. *Current microbiology*. 1994: 29(5): 301-
357 307.
- 358 24. Shittu AO, Lin J, Morrison D, Kolawole DO.(2005) The discovery of a multi-
359 resistant *Staphylococcus haemolyticus* clone in the hospital and community

360 environment in south western Nigeria. Ostomy Wound Manage. 2005:
361 51(1):67–70.

362 25. Kesah C, Ben Redjeb S, Odugbemi TO. Prevalence of methicillin-resistant
363 *Staphylococcus aureus* in eight African hospitals and Malta. Clin Microbiol Infect.
364 2003; 9 (2):153–156.

365 26. Nimmo,GR, Schooneveldt JO, O’Kane G.,Mcall B and Vickery A. Community
366 acquisition of gentamycin sensitive methicillin resistant *Staphylococcus aureus* in
367 South East Queensland, Australia. *Journal of clinical microbiology*. 2005.

368 27. Hageman JC, Morrison M. Active Bacterial Core Surveillance Program of the
369 Emerging Infections Program Network Methicillin-resistant *Staphylococcus aureus*
370 disease in three communities. N Engl J Med. 2005; 352(14):1436–1444. [[PubMed](#)]

371 28. Owolabi JB, Olorioke RC, "Prevalence and antimicrobial susceptibility of
372 methicillin resistant *Staphylococcus aureus* and coagulase-negative staphylococci
373 isolated from apparently healthy university students in Ota, Nigeria," *Prevalence*.
374 2015: 5, 24.

375 29. Diep BA, Gill SR, Chang RF, Phan TH, Chen JH, Davidson MG, Lin F, Lin J,
376 Carleton HA, Mongodin EF, "Complete genome sequence of USA300, an epidemic
377 clone of community-acquired methicillin-resistant *Staphylococcus aureus*," *The*
378 *Lancet*. 2006: 367, 731-739.

379 30. Becker K, Harmsen D, Mellmann A, Meier C, Schumann P, Peters G, & von Eiff
380 C. (2004). Development and evaluation of a quality-controlled ribosomal sequence
381 database for 16S ribosomal DNA-based identification of *Staphylococcus* species.
382 *Journal of Clinical Microbiology*. 2004: 42(11), 4988-4995.
383 doi:10.1128/JCM.42.11.4988-4995.