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Original Research Article

Detections of Resistant Genes Associated with *Staphylococcus aureus* in Wound Infection among Patient Attending Selected Hospitals in Kano Central, Kano Nigeria

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Abstract: This study identified isolates of *Staphylococcus aureus*, obtained the antibiotic susceptibility pattern of MRSA isolates and also determined the prevalence of MRSA strains from various wound samples collected from patients in Kano central, Kano State. Identification of *Staphylococcus* species in the present study was based on Gram staining, cultural characteristics and biochemical characterization. The isolates were positive for catalase, coagulase and DNase test. The findings revealed that out of 217 total samples tested, *S. aureus* was detected in 77 (35.48%), while Methicillin resistance *Staphylococcus aureus* (MRSA) was present in only 4 (1.84%) of the cases. Among the hospitals, *S. aureus* prevalence was highest at Murtala Muhammad Specialist Hospital (38.89%), followed by National Orthopedic Hospital Dala (42.59%), and lowest at Dawakin Kudu General Hospital (26.03%). Further investigation into antibiotic resistance patterns showed varying levels of resistance among the tested isolates showed highest resistance was observed against Amoxicillin (50.65%), Chloramphenicol (46.75%), and Ciprofloxacin (44.16%), while Oxacillin and Cefoxitin (5.19%) had the lowest resistance, which aligns with their role in MRSA screening. Molecular analysis for methicillin resistance genes (*mecA* and *mecC*) in the present study revealed that 50% of tested isolates carried the *mecA* gene, while 25% harbored *mecC*, and no isolates contained both genes simultaneously.

Keywords: Antibiotics, Methicillin Resistance *Staphylococcus aureus,* Mec A, Wound.

INTRODUCTION

Wound infection remains a major public health concern worldwide due to its contribution to prolonged hospitalization, delayed healing, increased treatment costs, and elevated morbidity and mortality rates. Wounds, whether surgical, traumatic, diabetic, or burn-related, provide an ideal environment for microbial colonization and proliferation because of tissue disruption and exposure of underlying structures to pathogenic microorganisms. Among the various bacterial pathogens implicated in wound infections, *Staphylococcus aureus* is recognized as one of the most significant causative agents due to its high virulence, adaptability, and remarkable ability to acquire resistance to multiple antibiotics (Tong *et al*., 2015).

Staphylococcus aureus is a Gram-positive, facultative anaerobic coccus commonly found as part of the normal flora of the skin and mucous membranes, particularly in the anterior nares of healthy individuals. Although it exists as a commensal organism, it can become opportunistic when there is a breach in skin integrity, causing localized and systemic infections such as abscesses, cellulitis, septicemia, osteomyelitis, pneumonia, and wound infections (Olorode *et al*., 2021). Its pathogenicity is attributed to numerous virulence factors including adhesins, toxins, enzymes, and immune evasion mechanisms that enable successful colonization and persistence within host tissues.

The increasing prevalence of antimicrobial resistance among *Staphylococcus aureus* strains poses a major challenge to effective clinical management. Of particular concern is methicillin-resistant *Staphylococcus aureus* (MRSA), which carries the mecA or mecC resistance genes. These genes encode an altered

penicillin-binding protein known as PBP2a, which has reduced affinity for β-lactam antibiotics, thereby conferring resistance to methicillin and other β-lactam agents (Olorunfemi *et al*., 2020). Other resistance genes commonly associated with *S. aureus* include blaZ (β-lactamase production), ermA, ermB, and ermC (macrolide resistance), tetK and tetM (tetracycline resistance), and vanA (vancomycin resistance, though less common). The emergence and spread of resistant *S. aureus* strains have become a global healthcare burden. According to the World Health Organization, antimicrobial resistance is among the top ten global public health threats facing humanity, with resistant bacterial pathogens contributing significantly to treatment failure and increased mortality. In both developed and developing countries, MRSA has become a frequent cause of healthcare-associated and community-acquired wound infections (WHO, 2023).

In sub-Saharan Africa, the burden of antibiotic-resistant *S. aureus* infections is increasing due to poor antimicrobial stewardship, self-medication, and indiscriminate use of antibiotics, limited diagnostic facilities, and inadequate infection prevention practices. Studies across African countries have reported high prevalence rates of MRSA among clinical isolates, particularly from wound specimens. This trend threatens effective patient management and increases the risk of complications such as chronic wound infections and systemic dissemination (Mustoe, 2013).

In Nigeria, wound infections constitute a significant proportion of hospital-acquired infections, and *Staphylococcus aureus* remains one of the most frequently isolated bacterial pathogens. The widespread misuse and over-the-counter accessibility of antibiotics have accelerated the emergence of multidrug-resistant strains. Several studies conducted in different parts of Nigeria have identified the presence of methicillin-resistant and multidrug-resistant *S. aureus* in clinical wound samples, with resistance genes such as mecA, blaZ, and ermC being commonly detected (IGarba *et al*., 2025). The research is aim to determine resistance genes of *Staphylococcus aureus* isolated from wound infections in patients at some selected hospital in Kano central (Dawakin Kudu, Murtala Muhammad Specialist hospital and Dala Orthopedic), Kano, Nigeria.

MATERIALS AND METHODS

Study Area

The study was conducted at three selected hospitals in Kano central senatorial district namely; Dawakin Kudu general hospital on 12°00'07.9"N 8°35'31.1"E and Murtala Muhammad Specialist Hospital on 11°59'56"N 8°31'19"E and National Orthopedics Hospital Dala on 12.0202°N, 8.5031°E. Kano State has a total area of 20,131 km2 (7,777sqm) and projected population of 17.5 million as of 2026 (WPR, 2026).

Ethical Clearance

An ethical approval was obtained from Kano state Hospital management board. After signing of an informed consent form prepared in accordance with the declaration of Helsinki (McGuinness *et al.,* 2017).

Sample Size

These are patients with burns and Wounds hospital in the study area, and the out patients that report to the dressing centers and the laboratory for wound swab microscopy culture and sensitivity (MCS). The number of the samples used in the study was calculated based on the standard epidemiological formula for the determination of minimum samples size adopted from Garba *et al*., (2025).

$$N = \frac{Z^2 pq}{D^2}$$

N = Desired sample size, S = Standard deviation at 95%, Z = 1.96 Confidence interval, D = 0.05, mean deviation, n =95%

P = estimated/expected prevalence from previous study in area, P = previous prevalence = 14% = 0.14 (Hagenimana and Fidele, 2022)

From the above formula

$$N = \frac{Z^2 pq}{D^2}$$

P = 0.14,

Q = 1 – P = 1- 0.14 = 0.86

$$N = \frac{(1.96)^2\ (0.14 \times 0.86)}{(0.5)^2}$$

$$N = \frac{3.843 \times 0.1204}{0.0025}$$

$$N = \frac{0.4627}{0.0025}$$

= 185.08

Therefore, a total of 200 samples will be used for this study.

Sample Collection

A swab samples were collected from patients with wound infection attending Dawakin Kudu General Hospital, Murtala Muhammad Specialist Hospital and National Orthopedic Hospital Dala, all in Kano. Pus samples from the wounds were collected using two sterile cotton swabs after cleaning the wound with sterile normal saline. Samples were collected preferably from depth of the wound under aseptic precaution and care was taken to avoid contamination from normal flora of skin. Samples collected were transferred immediately to the laboratory of Microbiology, Aliko Dangote University of Science and Technology for isolation and identification of *S. aureus* (Garba *et al*., 2025)

Isolation and Identification of *S. Aureus*

Isolation of *S. aureus* was conducted according to the method described by Garba *et al*., (2025). Wound samples were inoculated on to the surface of solidified nutrients agar and incubated at 37^0C for 24 hours. Colonies formed were sub-cultured on Mannitol salt agar and re-incubated at 37^OC for 24 hours until a pure colony was obtained. The isolates were identified by conventional microbiological methods: Gram staining and Biochemical tests (DNase test, Catalase test, Coagulase test and Mannitol fermentation test) and molecular characterization as described by Cheesbrough (2012) and Idris *et al*., (2018)

Antibiotic Susceptibility Testing

The identified isolates were subjected to antibiotic susceptibility testing using the agar diffusion method as described by Bauer *et al*. (1996). Mueller Hinton agar (MHA) plates were inoculated with overnight culture of each isolate by streak plating. The antibiotic sensitivity discs containing ciprofloxacin, norfloxacin, gentamicin, amoxicillin, streptomycin, rifampicin, erythromycin, chloramphenicol, ampiclox and levofloxacin were aseptically placed at equidistance on the plates and allowed to stand for 1 hour.

MRSA Screening

The *S. aureus* suspension adjusted to 0.5 McFarland was subjected to antibiotic susceptibility testing using oxacillin and cefoxitin disc using agar disc diffusion method as described by Bauer *et al.*, (1996) and demonstrated by Olowo-Okere *et al.,* (2017).

Molecular Identification of MRSA

Detection of Resistance Gene was conducted using molecular method as described by Arunachalam and Sasidharan, (2021) through DNA extraction, Polymerase Chain Reaction (PCR) using specific mecA Gene and mecC primers, and Agarose gel electrophoresis.

Statistical Analysis

Statistical analysis was performed using Epi-Info version 7. A chi-square and ANOVA tests at a 0.5 probability level were conducted to detect differences for *S. aureus* isolated from different wound types and between different age groups.

RESULTS

Prevalence of *S. aureus* in Relation to Hospitals

The study investigated the prevalence of *Staphylococcus aureus* and Methicillin-Resistant *Staphylococcus aureus* (MRSA) across three hospitals: Dawakin Kudu General Hospital (DKDG), Murtala Muhammad Specialist Hospital (MMSH), and National Orthopedic Hospital Dala (NOHD). The findings revealed that out of 217 total samples tested, *S. aureus* was detected in 77 (35.48%) (Table 1).

Table 1: Prevalence of *Staphylococcus aureus* in relation to Hospitals

Hospitals	Sample Tested (%)	Positive of *S. aureus* (%)	Negative for S. aureus (%)
DKDG	73(33.64)	19(8.76)	19(8.76)
MMSH	90(41.47)	35(16.13)	32(14.75)
NOHD	54(24.88)	23(10.59)	22(10.13)
Total	**217(100)**	**77(35.48)**	**73(33.64)**
P-value			**0.290**

Key; DKDG – Dawakin Kudu General Hospital, MMSH – Murtala Muhammad Specialist Hospital, NOHD – National Orthopedic Hospital Dala, There is no significant difference in the prevalence of both *S. aureus* in the selected hospital at p-value < 0.05.

Biochemical Characteristics of *Staphylococcus aureus*

Table 2 showed the result of morphological and biochemical characterization of *Staphylococcus* species. *S. aureus* are positive to Gram reaction, catalase, haemolytic, coagulase, and DNase tests.

Table 2: Biochemical Characteristics of *Staphylococcus aureus*

Code	GR	CAT	COA	MFT	HAE	DNase	Identified isolate
Isolate 1	+	+	+	+	+	+	*Staphylococcus aureus*
Isolate 2	+	+	-	-	-	-	Other *Staphylococcus* spp

Key: + = positive, - = negative, GR= Gram staining, CAT = Catalase, HAE = Haemolysis, COA= Coagulase, MFT= Mannitol Fermentation, S.A = *Staphylococcus aureus*

Screening for Methicillin Resistant *Staphylococcus Aureus* (MRSA)

The screening for Methicillin Resistance *Staphylococcus aureus* (MRSA) is presented in Table 3. The result showed that out of total of 217 tested, 77 representing 35.48% were positive for *S. aureus* and only 4 out of 77 *S. aureus* were Methicillin Resistant *Staphylococcus aureus* (MRSA) representing 1.84%.

Table 3: Screening for Methicillin Resistant *Staphylococcus aureus* (MRSA)

Hospital	Sample Tested (%)	Positive of *S. aureus* (%)	Prevalence of MRSA (%)
DKDG	73(33.64)	19(8.76)	0(0)
MMSH	90(41.47)	35(16.13)	3(1.38)
NOHD	54(24.88)	23(10.59)	1(0.46)
Total	**217(100)**	**77(35.48)**	**4(1.84)**

Resistance Pattern of *Staphylococcus aureus*

Further investigation into antibiotic resistance patterns showed varying levels of resistance among the tested isolates as in table 4. The highest resistance was observed against Amoxicillin (50.65%), Chloramphenicol (46.75%), and Ciprofloxacin (44.16%).

Table 4: Resistance Pattern of *Staphylococcus aureus* (n = 77)

Antibiotics	Disc potency (ug/disc)	Sensitive Isolates (%)	Resistant isolates (%)
Ciprofloxacin	30	43(55.84)	34(44.16)
Norfloxacin	30	45(58.44)	32(41.56)
Gentamicin	20	50(64.94)	27(35.06)
Amoxicillin	10	38(49.35)	39(50.65)
Streptomycin	20	58(75.32)	19(24.68)
Rifampicin	30	54(70.13)	23(29.87)
Erythromycin	30	45(58.44)	32(41.56)
Chloramphenicol	10	41(53.25)	36(46.75)
Ampiclox	30	55(71.43)	22(28.57)
Levofloxacin	30	52(67.53)	25(32.47)
Oxacillin	10	73(94.81)	04(5.19)
Cefoxitin	30	73(94.81)	04(5.19)

Note: Resistant pattern according to CLSI 2010

Screening for MRSA

The result for the screening of MRSA from S. aureus is presented in Table 5. The result showed that only 4 isolates out of 77 were resistant to both oxacillin and cefoxitin discs representing 5.19% of the species examined.

Table 5: Screening for MRSA from *Staphylococcus aureus* (n = 77)

Antibiotics	Disc potency (ug/disc)	Sensitive Isolates (%)	Resistant isolates (%)
Oxacillin	10	73(94.81)	04(5.19)
Cefoxitin	30	73(94.81)	04(5.19)

Note: Resistant pattern according to CLSI 2010

Molecular Detection of *mecA* and *mecC* Resistance Genes

Molecular analysis for methicillin resistance genes (*mecA* and *mecC*) revealed that 50% of tested isolates carried the *mecA* gene, while 25% harbored *mecC*, and no isolates contained both genes simultaneously as shown in Table 6.

Table 6: Molecular Detection of *mecA* and *mecC* resistance genes

Antibiotics	Phenotype	Genotype (%)
mecA	4	2 (50.00)
mecC	4	1 (25.00)

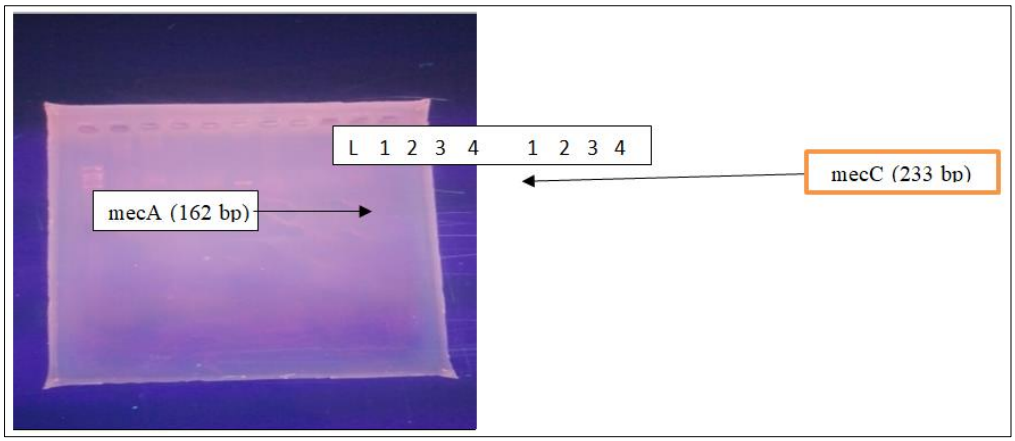

Figure 1: Gel Electrophoresis of the amplified mecA, and mecC genes

DISCUSSION

This study identified isolates of *Staphylococcus aureus*, obtained the antibiotic susceptibility pattern of MRSA isolates and also determined the prevalence of MRSA strains from various wound samples collected from patients in Kano central, Kano State. Wound infections are costly complications that increase morbidity and mortality in hospitalized patients (Chuku *et al*., 2022). It has been reported that S. *aureus*, *P. aeruginosa* and *Proteus spp.* are the most common bacteria implicated in wound infections in Nigeria. MRSA is spread throughout many hospitals and health care institutions and it is the most commonly isolated antimicrobial resistant pathogen condition (Onyang *et al*., 2008).

Identification of *Staphylococcus* species in the present study was based on Gram staining, cultural characteristics and biochemical characterization. Earlier findings by Ali *et al*., (2017); Amengialue *et al*., (2018); Yabaya *et al*., (2011); Jahan *et al*., (2005) identified and characterized *Staphylococcus aureus* on the basis of cultural characteristics, Gram staining and Biochemical characterization. From the results obtained *S. aureus* were able to ferment Mannitol producing yellow colony, they also showed β-haemolysis on blood agar medium enriched with 5% sheep blood. Gram staining of the isolates exhibited a cluster of Gram-positive cocci. The isolates were positive for catalase, coagulase and DNase test. This result was in conformity with the findings of (Ali *et al*., 2017; Ibrahim *et al*., 2019). In catalase test, hydrogen peroxide was broken down into water and oxygen by enzyme catalase. The production of oxygen was indicated by bubble formation (Jahan *et al*., 2005). The positive result of coagulase test was confirmed by the formation of curd like clotting compared to negative control. From the study, the coagulase negative *Staphylococcus* (CoNS) showed negative for both haemolysis and Mannitol fermentation. This finding was in consistent with that of Ibrahim *et al*., (2019) and that of Nwoire *et al*., (2013) who both record the presence of coagulase negative *Staphylococcus* among clinical samples of wound in Kano and Abakaliki respectively. The non-coagulase Staphylococci identified amongst these samples might have been contaminants or opportunistic pathogens. It is well known that other Staphylococci though normal commensal are opportunistic human pathogens (Baba *et al*., 2002).

The findings revealed that out of 217 total samples tested, *S. aureus* was detected in 77 (35.48%), while MRSA was present in only 4 (1.84%) of the cases. Among the hospitals, *S. aureus* prevalence was highest at MMSH (38.89%), followed by NOHD (42.59%), and lowest at DKDG (26.03%). Finding of the study correlates with that of Amenguelu *et al.,* (2015) who reported an MRSA prevalence of 43.5% in Benin, Nigeria, of which 81% was from in-patients. Similarly, Ali (2017) reported 28.6% prevalence in Kano, Nigeria with 62% from in-patients. Taiwo *et al*., (2002) had earlier reported a prevalence of 34.7% in Ilorin with 70.6% from in-patients. The findings of the present study indicate an increase in the trend of MRSA prevalence in Nigeria. Unhygienic conditions and non-adherence to or lack of relevant antibiotic policy have been suggested as possible reasons for these high carriage rates (Olowo-Okere *et al*., 2017).

Further investigation into antibiotic resistance patterns showed varying levels of resistance among the tested isolates showed highest resistance was observed against Amoxicillin (50.65%), Chloramphenicol (46.75%), and Ciprofloxacin (44.16%), while Oxacillin and Cefoxitin (5.19%) had the lowest resistance, which aligns with their role in MRSA screening. The susceptibility rate of bacterial isolates observed in this study agrees with the reports of Pondei *et al*., (2016) and Sharif *et al*., (2023). Antibiotic susceptibility of isolates to Oxacillin and Cefoxitin used antibiotics was very low; they were the most potent antimicrobial agents observed in the present study. The multiple resistance of *Staphylococcus aureus* isolates to commonly used antibiotics in the locality of this study calls for immediate action on the controlled use of antimicrobials in hospitals and the need to monitor resistance. Good antimicrobial use is necessary for effective wound management (Pondei *et al*., 2016; Sharif *et al*., 2023).

The findings of this study revealed that *Staphylococcus aureus* isolates from wound infections exhibited varying susceptibility patterns to commonly used antibiotics. This variability reflects the organism's remarkable ability to acquire resistance mechanisms, making it a significant challenge in clinical management. In this study, a relatively high level of resistance was observed against commonly prescribed antibiotics such as penicillin and ampicillin. This is consistent with earlier reports indicating that most *Staphylococcus aureus* strains produce β-lactamase enzymes, which inactivate β-lactam antibiotics (Tong *et al*., 2015). The widespread resistance to these antibiotics limits their clinical usefulness in treating wound infections.

Molecular analysis for methicillin resistance genes (*mecA* and *mecC*) in the present study revealed that 50% of tested isolates carried the *mecA* gene, while 25% harbored *mecC*, and no isolates contained both genes simultaneously. These genes *mec*A and *mec*C gene are responsible for the resistance to methicillin which codes for penicillin-binding protein PBP 2A (Wielders *et al*., 2002). The wide spread use of antibiotic resulted in the development of resistance to antibiotics through acquisition of the mobile cassette chromosome carrying the methicillin-resistant gene mecA (Wielders *et al*., 2002) and mecC (Diekema *et al*., 2001). The resistance to methicillin was due to a penicillin-binding protein coded for by a mobile genetic element termed the methicillin-resistance gene –mecA (Diekema *et al*., 2001). In recent years, the gene has continued to evolve so that many MRSA strains are currently resistant to several different antibiotics such as penicillin, oxacillin and amoxicillin (Muller *et al*., 2003). The study also showed moderate to high susceptibility of *Staphylococcus aureus* isolates to antibiotics such as ciprofloxacin, gentamicin, and streptomycin. These findings are in agreement with previous studies that reported the continued effectiveness of these antibiotics against many *Staphylococcus aureus* strains (Khan *et al*., 2019). In particular, vancomycin remains a drug of choice for severe MRSA infections, although reduced susceptibility has been reported in some regions (WHO, 2023).

However, the emergence of multidrug-resistant (MDR) *Staphylococcus aureus* strains defined as resistance to three or more classes of antibiotics was also evident in this study. This trend is alarming and has been widely documented in both hospital and community settings (Prestinaci *et al*., 2015). The development of MDR strains is largely attributed to the misuse and overuse of antibiotics, especially in developing countries where regulation is often inadequate.

The observed susceptibility patterns emphasize the importance of antibiotic susceptibility testing in guiding treatment decisions. Empirical therapy without laboratory confirmation may lead to treatment failure and further promote resistance. Therefore, clinicians should rely on culture and sensitivity results to select the most appropriate antibiotics for managing wound infections. Additionally, the variation in susceptibility patterns observed in this study compared to other regions highlights the influence of geographic location, antibiotic usage patterns, and infection control practices on resistance trends (WHO, 2023). This underscores the need for continuous local surveillance to inform effective treatment guidelines.

CONCLUSION

Based on the finding from this study, the distribution of *Staphylococcus* species in the clinical wound samples showed that out of 217 total samples tested, *S. aureus* was detected in 77 (35.48%), while MRSA was present in only 4 (1.84%) of the cases. Finding revealed that antibiotic resistance patterns of the *S. aureus* showed varying levels of resistance among the tested isolates showed highest resistance was observed against Amoxicillin, Chloramphenicol, and Ciprofloxacin, while Oxacillin and Cefoxitin had the lowest resistance, which aligns with their role in MRSA screening. Molecular analysis for methicillin resistance genes (*mecA* and *mecC*) in the present study revealed that the tested isolates carried the *mecA* gene *mecC* gene. It is recommended that antibiotics should only be prescribed based on laboratory results to combat antimicrobial resistance.

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