



ORIGINAL ARTICLE

FIRST MOLECULAR DETECTION OF METHICILLIN-RESISTANT *STAPHYLOCOCCUS AUREUS* IN APPARENTLY HEALTHY DROMEDARY CAMELS FROM KEBBI STATE, NIGERIA

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Ethical considerations: When reporting experiments on animals Observation of the ARRIVE guidelines 2.0: Updated guidelines for reporting animal research, published on July 14, 2020 (DOI: 10.1371/journal.pbio.3000410), is applied. The authors ensure that all procedures were performed in compliance with the guidelines for animal care of their institutions or with national/international guidelines.

ABSTRACT

Methicillin-resistant *Staphylococcus aureus* (MRSA) remains a critical global health concern due to its extensive resistance to β -lactam antibiotics and zoonotic transmission potential. However, data on MRSA carriage among camels in Nigeria are scarce. This study investigated nasal colonization of *Staphylococcus aureus* and MRSA among apparently healthy dromedary camels in Kebbi State, Nigeria. A cross-sectional study was conducted in two pastoral communities, where 120 nasal swabs were collected. Conventional culture and biochemical tests were used for preliminary identification, while PCR detection targeted the *nuc* and *mecA* genes. Antimicrobial susceptibility testing was performed using the Kirby-Bauer disk diffusion method. Overall, 66.7% (80/120) of samples were positive for *S. aureus*, while 38.3% (46/120) were confirmed as MRSA. Prevalence was significantly higher ($p < 0.05$) in young (80%) and female (70%) camels compared to adults (53.3%) and males (63.3%). All MRSA isolates carried the *mecA* gene and showed multidrug resistance, with high resistance to penicillin, tetracycline, erythromycin, chloramphenicol, and gentamicin, whereas all isolates remained susceptible to vancomycin. This study provides the first molecular evidence of MRSA colonization in dromedary camels in Nigeria, highlighting the need for routine surveillance and prudent antimicrobial use within a One Health framework.

Keywords: dromedary camels; Kebbi; methicillin-resistant *Staphylococcus aureus*; Nigeria; *Staphylococcus aureus*

INTRODUCTION

Camels play a vital role in the socio-economic fabric of pastoralist communities across arid and semi-arid regions of Nigeria, serving as crucial sources of food, transport, and income [1]. Dromedary camels, often referred to as the “ships of the desert,” are uniquely adapted to harsh climatic conditions where other livestock species struggle to thrive [2]. Their increasing use for milk, meat, and even traditional medicine such as camel milk and urine for their purported therapeutic value has amplified their significance in food security and livelihoods [3]. Recognizing these contributions, the Food and Agriculture Organization (FAO) declared 2024 as the International Year of the Camel, underscoring the species’ global relevance in climate resilience and sustainable food production [4].

Despite their importance, camels can serve as asymptomatic reservoirs for zoonotic pathogens, including *Staphylococcus aureus* and its methicillin-resistant variant (MRSA) [5]. MRSA poses a major global health threat due to its resistance to β -lactam antibiotics and its capacity for cross-species transmission, complicating both human and veterinary treatments [6, 7]. In livestock systems, particularly among pastoralists, limited biosecurity measures and frequent animal-human interactions increase the risk of MRSA circulation within and between species [8]. In Nigeria, the rapid expansion of camel husbandry and the growing demand for camel-derived products necessitate stronger surveillance of zoonotic and antimicrobial-resistant pathogens [9]. However, MRSA has been documented in Nigerian livestock such as poultry, cattle and pigs [10]; data on camels are limited. Although a study of camels slaughtered at Kano abattoir reported MRSA occurrence [11], most Nigerian studies of camels have used phenotypic approaches and molecular data remain scarce; molecular detection of MRSA in camels has, however, been demonstrated in neighbouring countries like Algeria [12], highlighting an important knowledge gap for camels in Nigeria given the increasing cross-border movement and trade of camels in north-western Nigeria.

This study therefore aimed to detect and characterize *Staphylococcus aureus* isolates, including methicillin-resistant strains, among apparently healthy dromedary camels in Kebbi State, Northwestern Nigeria, using both phenotypic and molecular methods. To the best of our knowledge, it provides the first molecular evidence of

MRSA carriage in Nigerian camels and underscores the public health significance of antimicrobial resistance at the livestock-human interface. The findings are expected to inform One Health-based strategies for antimicrobial resistance surveillance, biosecurity enhancement, and prudent antimicrobial use in pastoral production systems.

MATERIALS AND METHODS

Study Area

The study was conducted in Argungu Local Government Area (LGA) of Kebbi State, Northwestern Nigeria (Fig. 1), located at latitude 11°26'6.79" N and longitude 5°14'5.78" E. Argungu serves as the administrative headquarters of the Argungu Emirate and shares an international border with the Republic of Niger. The area is predominantly agrarian, with extensive agricultural lands, fertile soils, and abundant rivers that support mixed farming and livestock rearing. According to the 2006 National Population Census, Argungu has a population of 24,338, mainly from the Arawa and Hausa ethnic groups, with Islam as the major religion. This LGA hosts a major camel market that attracts traders and pastoralists from both within and outside Nigeria. Its proximity to an international animal control post and seasonal transhumance activities makes it a suitable site for the epidemiological surveillance of transboundary zoonotic pathogens, including *Staphylococcus aureus* and MRSA.

Study Design and Sample Size Determination

A cross-sectional study was conducted between March and May 2024 to estimate the prevalence of *S. aureus* and MRSA in dromedary camels. The sample size was determined using the formula of Thrusfield [13]:

$$n = \frac{t^2 \times P_{\text{exp}} (1 - P_{\text{exp}})}{d^2}$$

where $t = 1.96$ (for 95% confidence), $P_{\text{exp}} = 5\%$ (estimated prevalence from Yusuf [11]), and $d = 0.05$ (desired precision). The calculated minimum sample size was 73, but this was increased to 120 to enhance statistical precision and account for potential non-responses.

Sample Collection

Nasal swabs were collected from 120 apparently healthy camels randomly selected from two pastoral com-

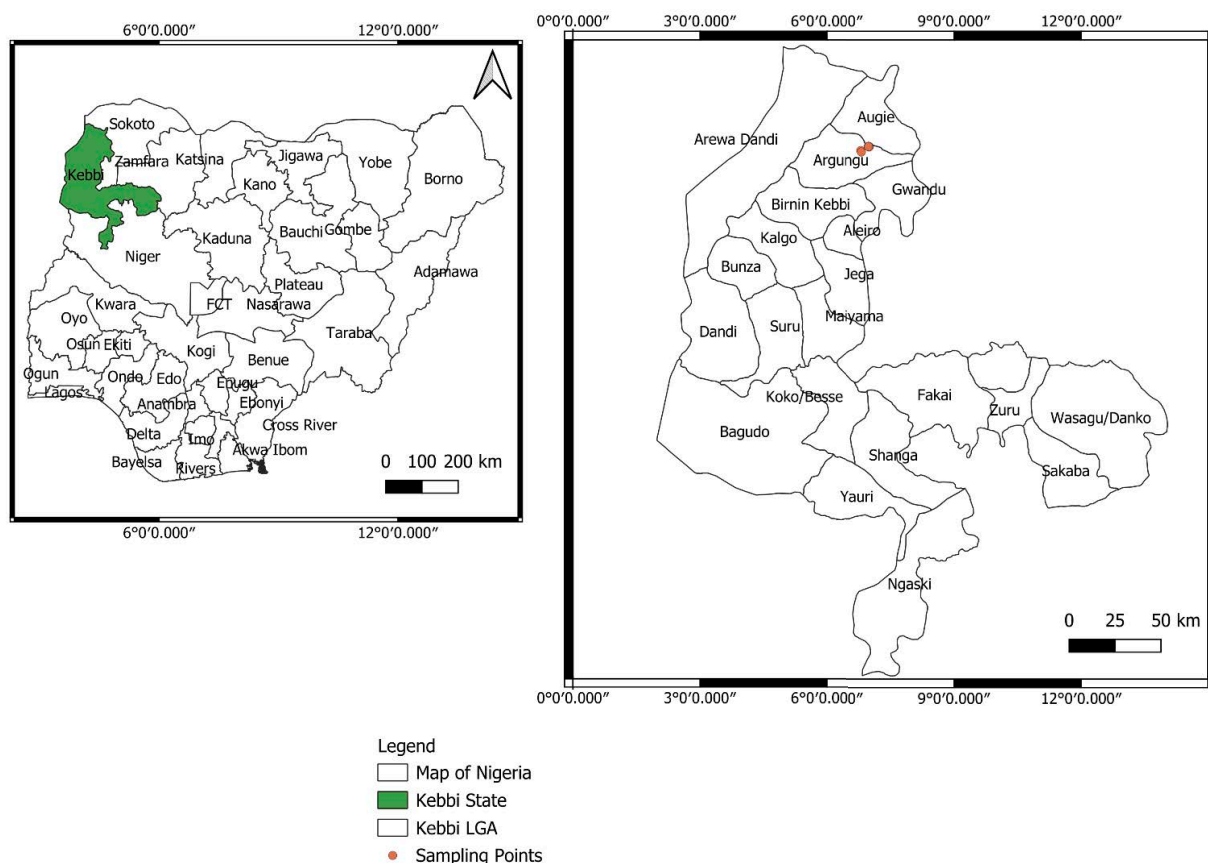


Fig. 1. A map of Nigeria showing the Kebbi states and Argungu LGA, where samples were collected (designed using QGIS, version 3.44.0)

communities (Community A and Community B). Each community contributed 60 samples, stratified equally by sex (30 males, 30 females) and age group (15 young, 15 adults per sex). Camels were humanely restrained, and sterile commercial cotton swabs were gently inserted 5–10 cm into the anterior nares and rotated along the mucosal surface for 5–10 seconds. Each swab was placed in 5 mL of tryptic soy broth supplemented with 6.5% NaCl, transported in an ice box, and processed within 6 hours at the Central Research Laboratory, Faculty of Veterinary Medicine, Usmanu Danfodiyo University, Sokoto. However, camels in the study area are managed under extensive pastoral systems with frequent informal and undocumented antimicrobial use, so reliable individual treatment histories were unavailable. Consequently, apparently healthy camels were sampled irrespective of prior antibiotic exposure.

Bacteriological Isolation and Identification

Samples were cultured on 5% horse blood agar and incubated aerobically at 37 °C for 24 hours. Colonies presumptively identified as *Staphylococcus* spp. were characterized based on morphology and Gram staining. Typical

colonies were sub-cultured on Mannitol Salt Agar (Oxoid, Basingstoke, UK) and re-incubated at 37 °C for 24 hours. Isolates showing smooth, golden-yellow colonies were further tested biochemically using catalase and coagulase tests. Confirmatory identification of *S. aureus* was achieved through PCR amplification of the thermostable nuclease (*nuc*) gene.

Phenotypic Detection of MRSA

Presumptive *S. aureus* isolates were inoculated on Oxacillin Resistance Screening Agar Base (ORSAB, Oxoid) to determine methicillin resistance phenotypically. Colonies that appeared intense blue on a colorless background were considered presumptive MRSA.

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing (AST) was performed using the Kirby-Bauer disk diffusion method on Mueller-Hinton agar (Oxoid, Manchester, UK), following Clinical and Laboratory Standards Institute (CLSI) guidelines [14]. A bacterial suspension equivalent to the 0.5 McFarland standard was spread uniformly on agar plates,

and antibiotic discs were placed aseptically on the surface. Plates were incubated at 37 °C for 18 hours, and inhibition zones were measured in millimeters. The antibiotic panel included: Aztreonam (30 µg), Cefotaxime (30 µg), Amoxicillin-clavulanic acid (30 µg), Ceftazidime (30 µg), Ceftriaxone (30 µg), Trimethoprim-sulfamethoxazole (25 µg), Chloramphenicol (30 µg), Tetracycline (30 µg), Gentamicin (10 µg), Kanamycin (30 µg), Ampicillin (10 µg), Ofloxacin (5 µg), Imipenem (10 µg), Erythromycin (15 µg), and Vancomycin (30 µg). Quality control was ensured using *Staphylococcus aureus* ATCC 25923 as a reference strain obtained from the American type culture collection (ATCC) through the Central Research Laboratory, Faculty of Veterinary Medicine, Usmanu Danfodiyo University, Sokoto. The measured inhibition zone diameters were interpreted and categorized as susceptible, intermediate, or resistant in accordance with the Clinical and Laboratory Standards Institute (CLSI) performance standards for antimicrobial susceptibility testing [14].

Multiple Antibiotic Resistance Index (MARI)

The MARI of each isolate was determined as described by Furtula [15]:

$$\text{MARI} = \frac{\text{Number of antibiotics resisted}}{\text{Total antibiotics tested}}$$

Values above 0.2 indicate isolates originating from environments with high antimicrobial use pressure.

Genomic DNA Extraction

Genomic DNA was extracted using the boiling method [16]. Briefly, a loopful of fresh overnight culture was suspended in 100 µL of sterile distilled water, heated at 96 °C for 10 min, and centrifuged at 12,000 × g for 5 min. The supernatant containing DNA was transferred to a sterile tube and stored at 4 °C until PCR analysis.

PCR Detection of the *nuc* and *mecA* Genes

PCR amplification was performed in 25 µL reaction mixtures containing 12.5 µL of 2× Master Mix (Qiagen), 1 µL (0.2 µM) each of forward and reverse primers (Table 1), 5 µL of DNA template, and 5.5 µL of nuclease-free water. The amplification program consisted of an initial denaturation at 94 °C for 5 min, followed by 35 cycles of denaturation at 94 °C for 1 min, annealing (*nuc*: 55 °C; *mecA*: 57 °C) for 1 min, extension at 72 °C for 1 min, and final extension at 72 °C for 7 min. PCR products were

electrophoresed in 1.5% agarose gel stained with ethidium bromide and visualized under UV illumination. Positive controls (*S. aureus* ATCC 43300 for *mecA* and *S. aureus* ATCC 25923 for *nuc*, obtained from the American Type Culture Collection (ATCC) through the Central Research Laboratory, Faculty of Veterinary Medicine, Usmanu Danfodiyo University, Sokoto) and a negative control (PCR-grade water) were included in each run.

Table 1. Primers used for the study

Gene name	Primer Sequence	Band Size (bp)	Reference
Nuc- F	5'- GCGATT GAT GGT GAT ACG GTT-3'	270	[24]
Nuc- R	5'-AGCCAAGCCTTGACGAATAAGC-3'		
Mec- F	5'- AAAATCGATGGTAAAGTTGGC-3'	533	[24]
Mec- R	5'-AGTTCTGCAGTACCGGATTGTC-3'		

Data Analysis

Data were entered and analyzed using Microsoft Excel (version 2016) and InVivoStat (version 4.1). Descriptive statistics were used to compute prevalence and proportions. Associations between MRSA carriage and host factors (age, sex, and community) were tested using the Chi-square test at $p < 0.05$. Measures of association were expressed as odds ratios (ORs) with 95% confidence intervals (CIs).

RESULTS

Nasal Carriage of *Staphylococcus aureus* and MRSA in Dromedary Camels

Out of 120 nasal swabs examined, 66.7% (80/120) yielded *Staphylococcus aureus* based on culture, biochemical, and PCR confirmation of the *nuc* gene (Table 2). The overall prevalence of MRSA, confirmed by phenotypic growth on ORS-AB and detection of the *mecA* gene, was 38.3% (46/120). The prevalence of *S. aureus* and MRSA varied across the two pastoral communities sampled. Community A recorded *S. aureus* in 60% (36/60) of camels and MRSA in 33.3% (20/60), whereas Community B recorded *S. aureus* in 73.3% (44/60) and MRSA in 43.3% (26/60) (Table 2). The difference in *S. aureus* carriage between communities was statistically significant ($\chi^2 = 6.79$, $p = 0.01$), while MRSA occurrence did not differ significantly ($\chi^2 = 3.15$, $p = 0.08$). Age- and sex-related differences were observed (Table 2). Younger camels showed

significantly higher colonization rates for both *S. aureus* (80%) and MRSA (53.3%) compared to adults (53.3% and 23.3%, respectively; $p < 0.001$). Similarly, females had higher prevalence rates for *S. aureus* (70%) and MRSA (46.7%) than males (63.3% and 30%; $p < 0.05$) (Table 2). These findings indicate that young and female camels were more likely to be colonized by *S. aureus* and MRSA.

Molecular Confirmation of *nuc* and *mecA* Genes

PCR amplification confirmed all phenotypically identified *S. aureus* isolates as *nuc*-positive, generating the expected 270 bp amplicon (Fig. 2). Similarly, all 46 MRSA isolates carried the *mecA* gene (533 bp), validating their methicillin resistance (Fig. 3). No amplification was observed in negative controls.

Antimicrobial Resistance Profiles of MRSA

All MRSA isolates exhibited resistance to at least three classes of antibiotics, confirming their multidrug-resistant (MDR) status. The highest resistance frequencies were observed against penicillin (100%), ampicillin-sulbactam (100%), tetracycline (100%), chloramphenicol (100%), gentamicin (100%), erythromycin (100%), and kanamycin (100%). Moderate resistance was observed to cefotaxime (78.3%), ceftriaxone (65.2%), and ofloxacin (56.5%), while all isolates remained susceptible to vancomycin (Fig. 4).

Multiple Antibiotic Resistance Index (MARI)

Table 3 summarizes the antibiotic resistance patterns and multiple antibiotic resistance index (MARI) of MRSA

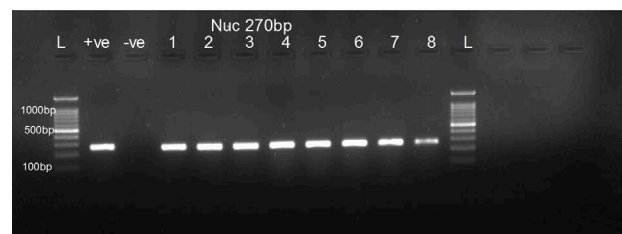


Fig. 2. Agarose gel electrophoresis showing amplification of the *nuc* gene (270 bp) from *S. aureus* isolates using a 100 bp DNA ladder. (Lane legends: L = 100 bp DNA marker; +VE = positive control; -VE = negative control)

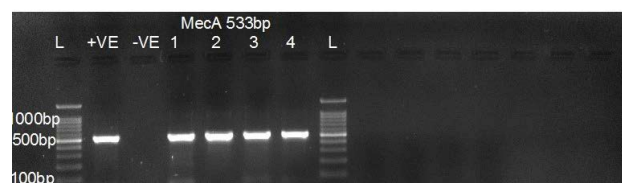


Fig. 3. Agarose gel electrophoresis showing amplification of the *mecA* gene (533 bp) from MRSA isolates using a 100 bp DNA ladder. (Lane legends: L = 100 bp DNA marker; +VE = positive control; -VE = negative control)

isolates recovered from dromedary camels. All MRSA isolates (46/46; 100%) were multidrug resistant, exhibiting resistance to three or more classes of antibiotics. Resistance consistently involved β -lactams (penicillin, ampicillin-sulbactam, amoxicillin-clavulanic acid, ceftriaxone), tetracyclines (tetracycline), aminoglycosides (gentamicin, kanamycin, amikacin, neomycin), macrolides (erythromycin), phenicols (chloramphenicol), and fluoroquinolones (ofloxacin), with some isolates also resistant to carbapenems (imipenem).

Although all isolates were classified as multidrug resistant, their resistance profiles were heterogeneous. Five distinct MDR patterns were identified, differing in both the

Table 2. Prevalence of *Staphylococcus aureus* and MRSA among dromedary camels in Argungu, Kebbi State

Variable	No. sampled	<i>S. aureus</i> positive (%)	MRSA positive (%)	χ^2	<i>p</i> -value
Community					
A	60	36 (60.0)	20 (33.3)	6.79	0.01*
B	60	44 (73.3)	26 (43.3)	3.15	0.08
Age group					
Young	60	48 (80.0)	32 (53.3)	12.22	<0.001***
Adult	60	32 (53.3)	14 (23.3)		
Sex					
Female	60	42 (70.0)	28 (46.7)	8.11	0.005**
Male	60	38 (63.3)	18 (30.0)		

Significance levels: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, χ^2 : Chi-square.

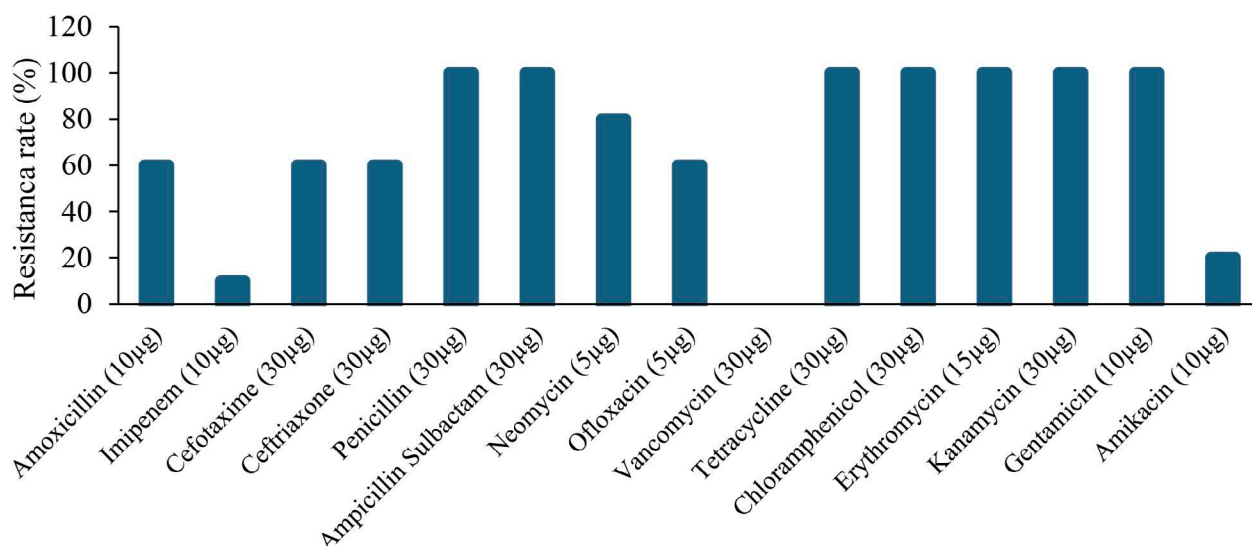


Fig. 4. Antimicrobial resistance profile of MRSA isolates from camel nasal swabs, showing percentage resistance to tested antibiotics (n = 15)

number and combination of antibiotic classes involved. The most frequent pattern, observed in 20 isolates, included resistance to β -lactams, tetracyclines, aminoglycosides, macrolides, phenicols, and fluoroquinolones, yielding a MARI value of 0.67. Other isolates exhibited narrower but still extensive resistance spectra, with MARI values ranging from 0.60 to 0.73. All resistance patterns were derived from antibiotics tested in this study, indicating that multi-drug resistance was not limited to a single antimicrobial class or fixed resistance phenotype but reflected diverse exposure histories and selective pressures within the study population. The most common resistance patterns included PEN-AMS-TET-CHL-ERY-KAN-GEN-AMC-NEO-OFL (n = 20) and PEN-AMS-TET-CHL-ERY-KAN-GEN-NEO-AMK (n = 14).

Table 3. Antibiotic Resistance Patterns and MARI of MRSA Isolates

Resistance pattern	No. of isolates	MARI
PEN-AMS-TET-CHL-ERY-KAN-GEN-AMC-NEO-OFL	20	0.67
PEN-AMS-TET-CHL-ERY-KAN-GEN-NEO-AMK	14	0.60
PEN-AMS-TET-CHL-ERY-KAN-GEN-AMC-IMP-CRO-OFL	5	0.73
PEN-AMS-TET-CHL-ERY-KAN-GEN-IMP-CRO	4	0.60
PEN-AMS-TET-CHL-ERY-KAN-GEN-IMP-OFL-AMK	3	0.67

PEN = Penicillin; AMS = Ampicillin-sulbactam; TET = Tetracycline; CHL = Chloramphenicol; ERY = Erythromycin; KAN = Kanamycin; GEN = Gentamicin; AMC = Amoxicillin-clavulanic acid; NEO = Neomycin; OFL = Ofloxacin; AMK = Amikacin; IMP = Imipenem; CRO = Ceftriaxone.

DISCUSSION

Antimicrobial resistance (AMR) continues to threaten global health, food security, and animal production systems, particularly in developing countries where antibiotic use is often unregulated [17]. The nasal cavity of camels harbors a diverse and dynamic microbial community that plays a critical role in respiratory health and microbial colonization. Previous studies in camels and other live-stock species have demonstrated that the nasal microflora is predominantly composed of commensal Gram-positive bacteria, including coagulase-negative staphylococci, *Micrococcus* spp., *Corynebacterium* spp., and *Bacillus* spp., with *Staphylococcus aureus* commonly occurring as both a commensal and opportunistic pathogen [5, 18]. In addition, Gram-negative bacteria such as *Pasteurella* and other respiratory-associated organisms have been reported in camels, particularly under conditions of environmental stress, crowding, and exposure to dust typical of arid and semi-arid pastoral systems [18, 21].

The composition of this nasal microbial ecosystem influences the ability of *S. aureus*, including methicillin-resistant strains, to establish and persist within the host. Commensal bacteria may competitively inhibit pathogenic colonization through competition for adhesion sites and nutrients; however, disruption of this balance by antimicrobial exposure or management-related stressors can facilitate MRSA carriage [5, 6]. In pastoral camel production systems, factors such as close animal-to-animal contact,

shared watering points, frequent human handling, and unregulated antimicrobial use are likely to alter the nasal microflora and create selective pressure favoring multidrug-resistant organisms [8, 22].

The detection of MRSA in apparently healthy camels in the present study therefore reflects not only antimicrobial selection pressure but also ecological shifts within the nasal microflora that permit resistant strains to persist asymptomatically. Such silent carriage is epidemiologically important, as colonized camels may serve as reservoirs for onward transmission to humans, other livestock species, and the environment, consistent with previous One Health observations of livestock-associated MRSA [6, 23].

Beyond direct animal-to-animal and human-to-animal contact, the environment plays a critical role in the transmission and maintenance of *Staphylococcus aureus*, including methicillin-resistant strains, within pastoral production systems. *S. aureus* is well recognized for its ability to survive for prolonged periods on abiotic surfaces such as soil, dust, bedding materials, watering troughs, feeding equipment, and animal housing structures, thereby facilitating indirect transmission through environmental contamination [5, 6]. In arid and semi-arid regions such as Northwestern Nigeria, frequent exposure of camels to dust-laden environments, communal resting grounds, and shared watering points creates ideal conditions for the persistence and dissemination of environmentally derived staphylococci.

Environmental contamination is further amplified by the continuous shedding of *S. aureus* from colonized but clinically healthy animals through nasal secretions, skin contact, and faecal material. These organisms can accumulate in the surrounding environment and subsequently be reintroduced into susceptible hosts via inhalation of contaminated dust particles, direct contact with contaminated surfaces, or indirect transfer through handlers and husbandry tools [6, 8]. Such transmission pathways are particularly relevant in extensive pastoral systems, where biosecurity measures are minimal and animals from multiple herds frequently congregate at grazing fields, markets, and watering sites. The environment also acts as an important ecological interface for the selection and spread of antimicrobial-resistant *S. aureus*. Antibiotic residues introduced into soil and water through improper disposal of veterinary drugs, excreta from treated animals, and runoff from livestock holding areas can exert selective pressure

on environmental bacterial populations, promoting the survival of resistant strains and resistance genes [7, 9]. These resistant organisms may subsequently colonize camels, contributing to the high prevalence of multidrug-resistant *S. aureus* observed in the present study. This mechanism is consistent with previous One Health observations that link environmental antimicrobial contamination with increased resistance burdens in livestock and humans [6, 7].

Environmental transmission blurs the distinction between community-associated, livestock-associated, and environmentally maintained *S. aureus* strains. Camels may therefore function not only as reservoirs but also as amplifiers of environmentally acquired *S. aureus*, sustaining a cycle of contamination between animals, humans, and shared ecosystems [6, 23]. The detection of MRSA in apparently healthy camels underscores the epidemiological significance of this pathway, as asymptomatic carriers can perpetuate environmental contamination without triggering disease-based control measures.

The present study provides the first molecular evidence of methicillin-resistant *Staphylococcus aureus* (MRSA) colonization in apparently healthy dromedary camels in Nigeria, revealing a high prevalence and multidrug-resistant (MDR) phenotype. These findings underscore the growing risk of AMR dissemination at the human–livestock interface in pastoral settings. The 66.7% prevalence of *S. aureus* observed in this study is higher than previously reported among dromedary camels in Kano, Nigeria (14%; [11]) and other African and Middle Eastern studies, including Tunisia (6.6%; [18]), Egypt (17.9%; [19]), Saudi Arabia (10.7%; [20]), and Ethiopia (38.5%; [21]). Such variation may be attributed to differences in sample size, husbandry systems, hygienic practices, and antibiotic use intensity. The high prevalence recorded here likely reflects limited biosecurity and close human–animal contact typical of nomadic and transhumant camel-herding systems in Northwestern Nigeria. Similarly, the MRSA prevalence of 38.3% is markedly higher than earlier reports from Nigeria (5%; [11]), Egypt (6.8%; [19]), and Saudi Arabia (1.6%; [20]). This discrepancy could arise from differences in detection sensitivity (molecular versus phenotypic methods), the extent of antimicrobial exposure, or ecological and management factors influencing pathogen transmission. Frequent self-medication of camels with broad-spectrum antibiotics, unregulated use of veterinary drugs, and environmental contamination may contribute to the high

MRSA burden in this study area [22]. The significantly higher colonization rates among younger and female camels may reflect immunological and physiological factors. Young animals are immunologically naïve and more susceptible to bacterial colonization, while females, especially lactating ones, are more frequently handled and medicated, potentially increasing exposure to resistant strains [18, 23]. Furthermore, close animal grouping during milking or watering could facilitate nasal MRSA transmission through aerosols or fomites.

The high resistance rates of MRSA isolates to commonly used antibiotics such as tetracycline, erythromycin, chloramphenicol, gentamicin, and penicillin mirror findings in livestock from the same region [23, 24]. These antimicrobials are extensively used in both veterinary and human medicine in Northwestern Nigeria, often without prescription, promoting selection pressure and horizontal gene transfer of resistance determinants. The detection of complete susceptibility to vancomycin is reassuring, as it remains a critical “last-resort” drug for MRSA infections [7]. However, its exclusive reliance could precipitate resistance if misuse extends to veterinary applications. The Multiple Antibiotic Resistance Index (MARI) > 0.3 recorded in this study indicates substantial and sustained exposure of these bacterial populations to antimicrobial agents, consistent with reports from intensive livestock production systems [15]. The presence of multidrug resistance in *S. aureus* can be partly attributed to the acquisition of mobile genetic elements such as plasmids, transposons, and staphylococcal cassette chromosome *mec* (SCC*mec*) that carry resistance genes [25]. All MRSA isolates in this study harbored the *mecA* gene, confirming the molecular basis for their phenotypic resistance to β -lactam antibiotics and supporting earlier observations that phenotypic resistance strongly correlates with *mecA* carriage [26].

The detection of MRSA in apparently healthy camels highlights the potential for zoonotic transmission to pastoralists, herders, traders, and abattoir workers through direct contact or contaminated milk and meat. This finding is of particular concern in regions like Kebbi State, where veterinary infrastructure is limited and humans frequently share close environments with livestock. MRSA strains of livestock origin (*LA-MRSA*) have previously been reported to colonize humans, blurring the distinction between hospital, community, and animal-associated strains [6]. From a One Health perspective, this study reinforces the

interconnectedness of animal health, human health, and environmental contamination in sustaining the AMR cycle. Antibiotic residues in the environment, combined with poor hygiene and unrestricted access to antimicrobials, create selective conditions for resistant bacteria to thrive. Implementing integrated surveillance and antimicrobial stewardship programs, particularly within transboundary livestock corridors, is essential to prevent further dissemination of MRSA and other resistant pathogens.

CONCLUSION

This study provides the first molecular evidence of methicillin-resistant *Staphylococcus aureus* (MRSA) colonization among apparently healthy dromedary camels in Nigeria, revealing a high prevalence and extensive multidrug resistance pattern. The universal detection of the *mecA* gene among isolates confirms the molecular basis for methicillin resistance and suggests that camels may serve as important reservoirs and potential disseminators of resistant *S. aureus* strains within pastoral ecosystems. The high multiple antibiotic resistance index observed reflects substantial and sustained exposure of camel-associated bacterial populations to antimicrobial agents, likely resulting from unregulated antibiotic use and weak veterinary oversight. These findings have significant One Health implications, emphasizing the potential for cross-species transmission of MRSA between camels and humans, especially in pastoral communities where close animal contact and limited biosecurity are common.

The results of this study highlight the urgent need for continuous surveillance of MRSA in livestock populations, stricter antimicrobial stewardship, and strengthened collaboration between human and animal health sectors. Integrating molecular epidemiological approaches into national antimicrobial resistance monitoring frameworks will be vital for tracking transmission dynamics and informing control strategies. By establishing a molecular baseline for MRSA in camels, this study contributes valuable insights to the growing body of knowledge on zoonotic antimicrobial resistance in sub-Saharan Africa and highlights the necessity of adopting a unified One-Health approach to protect both animal and public health.

Study Limitations

The sample was restricted to two pastoral communities within a single LGA, which may not fully represent the broader camel population in Nigeria. Additionally, the absence of molecular typing methods such as *spa*-typing, SCCmec typing, or multi-locus sequence typing (MLST) limited the ability to infer genetic relatedness or potential human-animal transmission. Future studies incorporating genomic epidemiology and comparative host sampling (camels, handlers, and the environment) are warranted to elucidate MRSA transmission dynamics.

Data Availability Statement

The data sets used and/or analyzed during the current study are available within the manuscript and supplementary file.

Ethical Statement

All procedures involving animals were approved by the Animal Research Ethics Committee of the Faculty of Veterinary Medicine, Usmanu Danfodiyo University, Sokoto (Approval No.: UDUS/FAREC/03/2019). Animal handling followed institutional and international ethical standards for research involving animals.

Conflict of Interest

None to be declared.

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Generative AI Statement

No generative AI was used in writing the manuscript, however Grammarly was used to ensure grammatical consistency of the manuscript.

Authors' Contributions

Conceptualization: MSG, AHJ, MSJ, MDS. Investigation and data analysis: MSG, KOJ, MZM, SAA, AUE. Original draft preparation: MSG, KOJ. Review and editing: MSG, KOJ, MSJ, MDS, AHJ, MZM, SAA. All authors have read and agreed to the final version of the manuscript.

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