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Prevalence of Methicillin-resistant *Staphylococcus aureus* in Livestock Production System of Nigeria: A Systematic Review

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Abstract

Recently, methicillin-resistant *Staphylococcus aureus* (MRSA) has been identified as a growing concern in livestock. Animals can serve as reservoirs for MRSA, and the bacteria can be transmitted to humans who are in close contact with animals colonized by MRSA. This study evaluated the prevalence, potential source, and vehicle in the emergence and transmission of livestock-associated MRSA in Nigeria's livestock production systems over the past decade. A systematic search was conducted on Web of Science, PubMed, Google Scholar, and Scopus databases to identify relevant studies published between 2012 and 2022. Standardized keywords were used. 28 eligible articles were included in the review, and our systematic review protocol was published in Prospero (Registration number: CRD42023431777). The occurrence of MRSA varied across the studies analyzed, ranging from 0% to 53.9%. Specifically, in poultry, the prevalence ranged from 7.9% to 37.5%; in cattle, from 3.21% to 29%; in pigs, from 0% to 53.9%; and in sheep and goats, from 4.4% to 25%. Among livestock farm/abattoir workers, the prevalence of MRSA ranged from 3.1% to 71.4%. The MRSA isolates from Nigeria's livestock production systems displayed pathogenic potential with various *S. aureus protein A* (*spa*) types and clonal complexes (CC) as determined by Based Upon Repeat Pattern (BURP) analysis. These isolates carried genes associated with virulence factors such as enterotoxins, exfoliative toxins, and Panton-Valentine Leukocidin (*PVL*). One reviewed study documented the identification of the characteristic livestock-associated MRSA CC398 using Multilocus Sequence Typing (MLST) analysis. The livestock production system serves as a potential source and vehicle for the emergence and transmission of MRSA in Nigeria. To effectively prevent and control these infections, continuous monitoring using the "One Health" approach is recommended.

Keywords: Methicillin-resistant *Staphylococcus aureus*, Nigeria, Preferred Reporting Items for Systematic Reviews and Meta-Analyses, systematic review

Introduction

The *Staphylococcus aureus* is a bacterium recognized as a significant global threat in terms of its antibiotic resistance potential, based on the World Health Organization's *Global Priority Pathogens List* (World Health Organization, 2017). This Gram-positive coccus can cause infections in both humans and animals, and its impact on health is substantial, leading to conditions such as toxic shock syndrome, infective endocarditis, skin and soft tissue infections, and more (Köck et al., 2010). These infections are linked to substantial illness, death rates, and considerable economic consequences. The conservation of virulence factors in *S. aureus* strains varies, including proteases, toxins, adhesins, and microbial surface components that facilitate attachment to surfaces.

The ability of *S. aureus* to adapt to antibiotics, along with the rise and dissemination of methicillin-resistant *Staphylococcus aureus* (MRSA) has heightened the medical significance of this bacterium (Ali Alghamdi et al., 2023). Methicillin resistance primarily results from the emergence of genes that encode a particular penicillin-binding protein, specifically PBP2a. This mechanism underscores the development of resistance in methicillin-resistant strains (Fergestad et al., 2020). The *MecA* gene, responsible for encoding PBP2a, is transported by a mobile genetic element known as the "*Staphylococcal* chromosomal cassette mec" (SCCmec), which exhibits numerous subtypes and variations. Presently, 13 distinct subtypes have been identified (SCCmec type I–XIII) (Singh-Moodley et al., 2019; Uehara, 2022). Furthermore, a variant form of *MecA*, referred to as *mecC*, has been identified in Europe, primarily linked to MRSA in livestock and

wild animals, notably hedgehogs (Bengtsson et al., 2017; Paterson et al., 2014; Rasmussen et al., 2019).

Methicillin-resistant *Staphylococcus aureus* was formerly recognized as one of the main causes of nosocomial infections. It has recently appeared in livestock, pets, and wildlife and is now widespread throughout the community (Cuny et al., 2015). According to reports, livestock are regularly colonized by MRSA, and they are known to be the main source of MRSA. Individuals who interact with these livestock may be at high risk of acquiring and spreading these strains (Gaddafi et al., 2020). Specifically, MRSA associated with livestock has been isolated from individuals without any animal contact, demonstrating the potential for these microorganisms to persist in the human population (Lekkerkerk et al., 2015). This zoonotic risk and treatment complications are brought on by the cross-transmission between animals and people. Diverse sequence types (STs), *spa* types (t), and CC with global distribution have been identified through DNA sequencing methods employed for characterizing *S. aureus* strains, such as Multilocus Sequence Typing (MLST) and *spa* typing (Liu et al., 2023; Park et al., 2017). There are specific sequence types that are frequently linked to MRSA in animals. In Europe, MRSA associated with livestock is commonly connected with the CC398 strain, while in Asia, the CC9 strain is more prevalent (Butaye et al., 2016; Fetsch et al., 2021). *Spa* types t011, t034, t108, t567, t2011, and t2510 are linked to clonal complex CC398 and are among those more specifically associated with MRSA found in cattle (Köck et al., 2013; Tegegne et al., 2017).

The Netherlands and France were the first countries to report cases of MRSA linked to livestock in the early 2000s (Armand-Lefevre et al., 2005; Voss et al., 2005). Over the years, reports of MRSA associated with animals have been documented across Asia, Africa, America, Australia, and Europe (Gaddafi et al., 2022b; Mascaro et al., 2019; Turner et al., 2019). While initial discoveries utilized isolates from separate and unrelated collections, subsequent reports indicated that MRSA could be transmitted both among patients and healthcare workers and between livestock and farmers along with their families (Gaddafi et al., 2021a; Sassmannshausen et al., 2016). A recent study conducted in Denmark utilizing genome-wide association studies (GWAS) data demonstrated host adaptation and the transmission of MRSA from livestock to healthcare facilities (Sieber et al., 2019). The importance of keeping an eye on the emergence and distribution of MRSA strains linked to livestock is highlighted by this. Research on the occurrence of MRSA strains in Nigerian animals and foods derived from animals is scarce and has only been done in a few states (second level of administration). Considering these strains' potential pathogenicity, the dearth of studies on MRSA related to livestock in Nigeria is worrisome.

In Nigeria, animal products continue to be a fundamental protein source in human diets. However, the potential for contamination during the handling process, from farm to table, poses a risk of these products serving as carriers for the transmission of microbes responsible for foodborne illnesses (Yusuf et al., 2020). *Staphylococcus aureus* is a dangerous pathogen that is thought to be one of the main global contributors to foodborne illnesses (Wu et al., 2019). *Staphylococcal* foodborne illness, a common occurrence, results from the consumption of enterotoxins produced by enterotoxigenic strains of *Staphylococcus* spp. (Lim et al., 2023). Studying the existence of these strains in livestock production systems is crucial for food safety.

Thus, the primary objective of this systematic review was to evaluate the source and emergence of MRSA associated with livestock in Nigeria's livestock production systems over the past 10years. The review encompasses the analysis of MRSA prevalence, antimicrobial resistance profiles, and genotypes originating from animals. Additionally, the review addresses the prevalence of MRSA among farm and abattoir workers within Nigeria.

Materials and Methods

Information Sources and Search Strategies
According to the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement, this systematic review was carried out and reported (Moher et al., 2015). However, a search protocol was designed and registered on the International Prospective Register of Systematic Reviews (registration number: CRD42023431777). To find relevant papers published between January 1, 2012, and September 10, 2022, systematic searches of PubMed, Web of Science, Google Scholar, and Scopus databases were conducted. Boolean operators (AND, OR) were used to find studies using the keywords: (WEB OF SCIENCE=TS= ("methicillin-resistant *Staphylococcus aureus*" OR MRSA) AND (livestock OR animal OR cattle OR poultry OR swine OR goat OR sheep) AND Nigeria AND (prevalence OR occurrence OR epidemiology OR distribution), SCOPUS=TITLE-ABS-KEY ("methicillin-resistant *Staphylococcus aureus*" OR MRSA) AND (livestock OR animal OR cattle OR poultry OR swine OR goat OR sheep) AND Nigeria AND (prevalence OR occurrence OR epidemiology OR distribution) AND PUBYEAR > 2012 AND PUBYEAR < 2022 AND (LIMIT-TO (LANGUAGE, "English")) AND (LIMIT-TO (DOCTYPE, "ar")), PUBMED=("methicillin-resistant *Staphylococcus aureus*" [MeSH Terms] OR "MRSA"[All Fields]) AND (livestock[MeSH Terms] OR animal[MeSH Terms] OR cattle[MeSH Terms] OR poultry[MeSH Terms] OR swine[MeSH Terms] OR goat[MeSH Terms] OR sheep[MeSH Terms]) AND (Nigeria[MeSH Terms] OR Nigeria[All Fields]) AND (prevalence[MeSH Terms] OR occurrence[All Fields] OR epidemiology[MeSH Terms] OR distribution[All Fields]), GOOGLE SCHOLAR="methicillin-resistant *Staphylococcus aureus*" OR MRSA AND (livestock OR animal OR cattle OR poultry OR swine OR goat OR sheep) AND Nigeria AND (prevalence OR occurrence OR epidemiology OR distribution)) in the titles and abstracts. Filters were applied for language, document type, and year range of publications. The final search took place on September 28, 2022. A total of 3680 articles were found. Additional studies were looked for in the identified papers' reference lists for possible inclusion in the review (Figure 1).

Eligibility Criteria
To determine the eligibility of identified studies, the following inclusion criteria were employed for screening and evaluating titles and abstracts: studies of any design, excluding experimental studies; written in English; full-text articles published between 2012 and 2022; and conducted in Nigeria. Studies were excluded if they did not specify the source of the sampled isolates or if MRSA was not identified among the *S. aureus* isolates.

Study Quality
The assessment of reporting quality and bias selection in the eligible studies was conducted utilizing the McMaster critical evaluation methods for both quantitative and qualitative studies (Ducat & Kumar, 2015). This was done by two independent reviewers, and discrepancies were resolved through discussion.
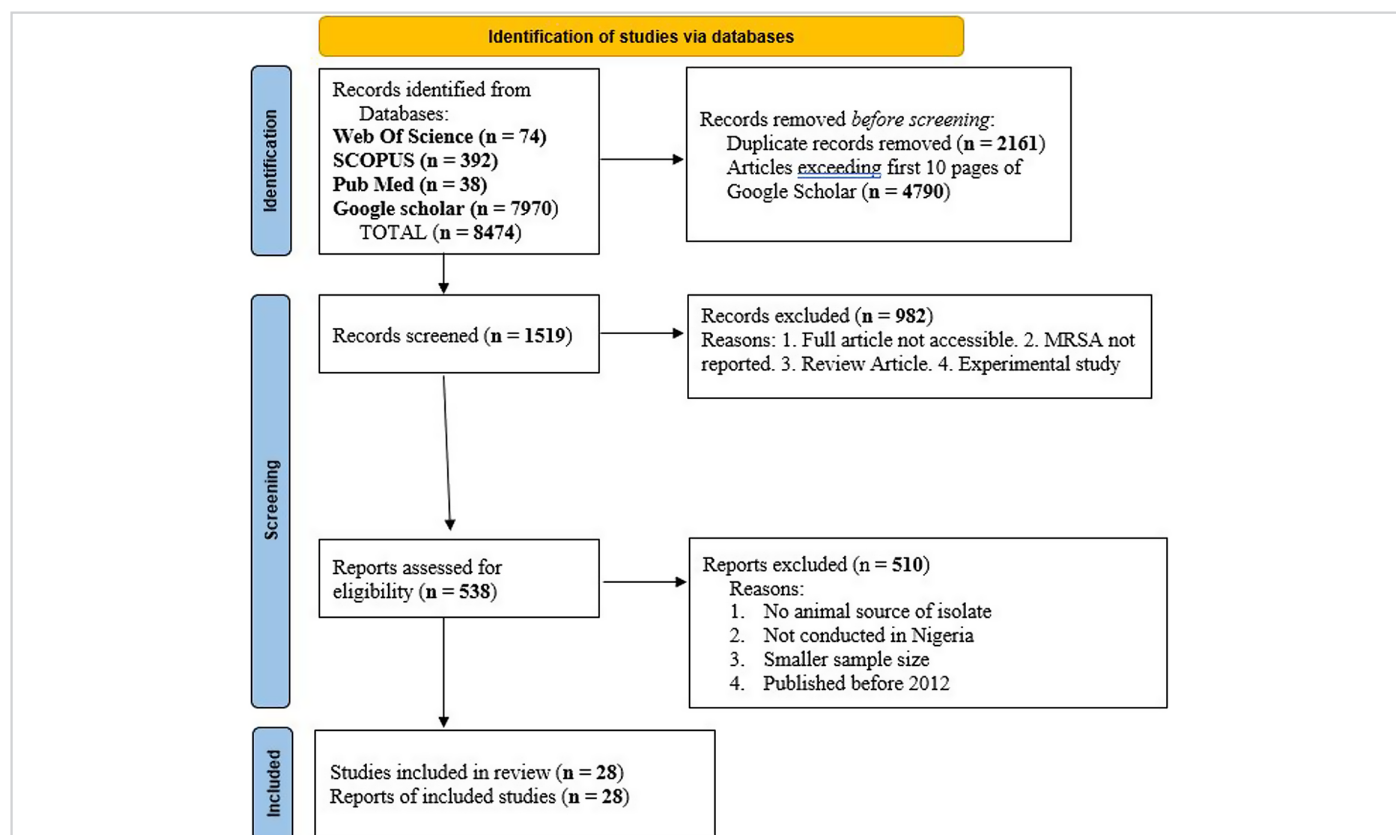
Figure 1.
Flow Diagram of the Study Selection Process for Inclusion in the Review.

Data Extraction Method
When feasible, the following details were extracted: authors' names, study design, study location, proportion of MRSA isolates, specimen type or focal infection, detection method used, antimicrobial susceptibility pattern, and molecular/genotypes of the MRSA strains. These factors were considered important for data extraction. Two independent reviewers were employed for this stage, and discrepancies were settled by the employment of a third independent reviewer through discussion.

Results

Characteristics of Reviewed Studies
For this review, a total of 28 publications (Figure 1) from 13 States in Nigeria (Figure 2) were considered based on the inclusion criteria. All 28 articles reported studies from different states, with the majority being done in north-western Nigeria.

Prevalence of Methicillin-Resistant *Staphylococcus aureus* Among Livestock, Livestock Products, and Livestock Farm and Abattoir Workers in Nigeria
Amongst the 28 studies reviewed, 12 of the studies were on pigs (live pigs = 10, Carcass = 2), 8 of those studies were on cattle (live cattle = 4, Carcass =1, product =3), 5 studies were on poultry (live birds = 3, Carcass =2), 3 studies sampled live sheep and goats (goat = 2, sheep = 2), while only 7 studies reported human–livestock contact. The prevalence of MRSA amongst live animals, carcasses,

and animal products sampled varied across different animal species. The overall prevalence of MRSA ranged from 0% to 53.9% among all the studies reviewed, with poultry ranging between 7.9% and 37.5%, cattle ranging between 3.21% and 29%, pigs ranging between 0% and 53.9%, and sheep and goats ranging between 4.4% and 25% (Table 1). The majority of studies included in the review presented prevalence rates of MRSA that varied between 3.7% and 25%, indicating a range from relatively low-to-moderately high rates (Table 1). Some studies did not provide specific prevalence rates for MRSA in their findings. Most of the conducted studies were focused on the northwestern region of Nigeria. Only 13 out of 36 states in Nigeria reported the occurrence or detection of MRSA (Figure 2). There was a noticeable variation in the prevalence of MRSA among different sources of livestock samples in the reviewed studies. Additionally, the prevalence rates of MRSA differed even among the specific livestock species considered in the studies. It is noteworthy that the majority of studies employed multiple techniques to identify and isolate methicillin resistance in *S. aureus* (Table 1).

In seven studies, both humans and livestock/abattoir workers were sampled, although a few studies sampled only one of these groups (Table 1). The occurrence of MRSA among workers in livestock farms and abattoirs varied between 3.1% and 71.4%. With the exception of a single study indicating a high prevalence rate of 71.4%, the majority of studies reported relatively low MRSA prevalence rates (<25%) among the workers (Table 1).
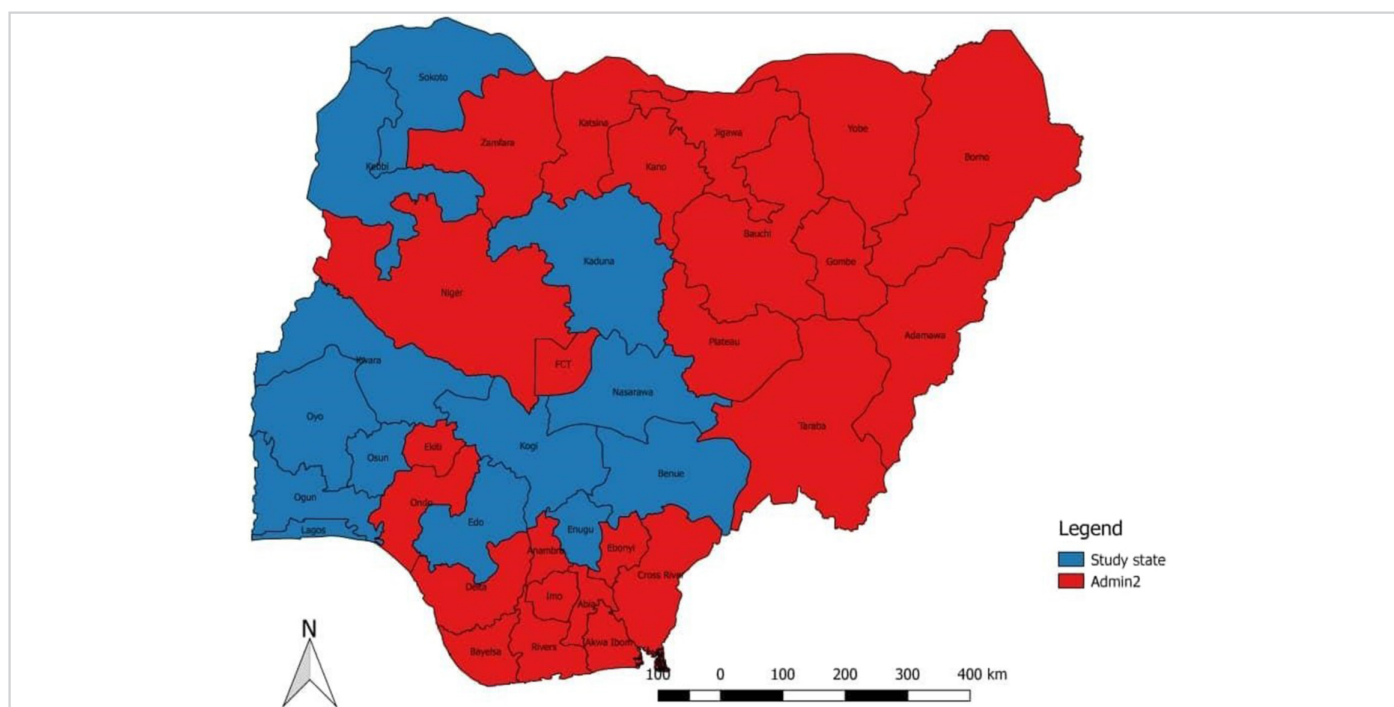
Figure 2.
Geographical Distribution of Areas Where Studies Have Been Conducted.

Antimicrobial Resistance Profiles

All studies providing information on the resistance profiles of MRSA against penicillin consistently documented a high resistance rate of 100%. Only two studies reported resistance rates for cefoxitin, which were 44% and 100%, respectively (Table 2). Most studies indicated resistance of MRSA isolates to oxacillin, with six studies reporting 100% resistance and three studies reporting varying levels of resistance (Table 2). Two out of the 13 studies demonstrated 100% resistance to tetracycline. In terms of gentamicin, three studies reported 100% susceptibility, while five studies reported 100% susceptibility to vancomycin among MRSA isolates (Table 2).

In total, ten studies reported the resistance profile to erythromycin, with two studies reporting 100% susceptibility. Four studies examined ciprofloxacin, and three of them indicated 95% to 100% susceptibility of MRSA isolates. Among the 13 studies that tested trimethoprim-sulfamethoxazole, eight reported sensitivity, with one study reporting 100% susceptibility and the remaining seven studies reporting resistance ranging from 22.5% to 55.6%. Chloramphenicol resistance profiles were reported in two studies, with one study reporting 100% sensitivity (Table 2).

Genotypic Characteristics of Livestock-associated MRSA Isolates

Eighteen (18) studies provided information on the genotypic characteristics of MRSA isolates (Table 3). Detection of *MecA* occurred in fifteen (15) out of the eighteen (18) studies, with *mecC* not being detected in any of the reviewed studies. Among the studies reviewed, four (4) mentioned the presence of SCCmec IV, SCCmec VIa, and SCCmec Vc, respectively (Table 3).

Spa types were identified in seven out of the 18 studies that conducted genotyping (Table 3). Among these, three studies documented a single *spa* type, specifically t011, t131, and t1603. Four studies reported a diverse array of *spa* types, with t084 and t311 being commonly observed across these studies. MLST analysis was conducted in four studies, and only one of them documented the presence of CC398 among the isolates. Other CCs documented included CC5, CC152, CC15, CC97, CC80, and CC88 (Table 3).

Several virulence factors were examined, including the Panton-Valentine Leucocidin (*PVL*) gene, enterotoxins, and exfoliative toxins. The *PVL* gene was identified in five out of the18 studies, although two studies reported 0% prevalence of *PVL* among the isolates. Only two reviewed studies reported the detection of various exfoliative toxin (eta and etb) and enterotoxin (sep, sed, sea, ser, seb, sem, seh, and sec) genes (Table 3).

Discussion

Antimicrobial resistance (AMR) affects the health sector, but it is not just a health sector problem. It is fueled by many factors: poorly functioning health systems, weak regulations, substandard practices in industrial farming, and poor management of waste and wastewater (WHO, 2018). AMR disproportionately affects people in low and middle-income countries and is closely linked to poverty and a lack of access to adequate water, sanitation, and hygiene end (WHO, 2018). In 2015, the World Health Assembly adopted a global action plan on AMR. Since then, 178 countries including Nigeria have developed multi-sectoral national action plans. However, in Nigeria, these plans are not translating into actions. Only 11% of countries have dedicated financing in their national budget for implementation and monitoring. Addressing AMR and preventing its further spread requires leadership from all the member states, accountable stakeholders, and sustained financial support (WHO, 2018).

GADDAFI et al. Prevalence of Methicillin-resistant Staphylococcus aureus

Acta Veterinaria Eurasia 2025

Table 1.

Prevalence of Livestock-Related Methicillin-Resistant Staphylococcus aureus in Nigeria

S/No	Author, year	Study State	Sample Type	Method of detection	Animal Type	Animal Prevalence	H-L-C Prevalence	*S. aureus* Type (MRSA)
1	(Gaddafi et al., 2022a)	Kebbi	Cloaca	Phenotypic, Molecular	Poultry	37.5% (75/200)	71.4% (5/7)	MRSA
2	(Yakubu et al., 2022)	Sokoto	Nasal	Molecular	Dog	15% (15/100)	Not studied	MRSA
3	(Odetokun et al., 2022)	Oyo		Molecular	Cattle	Not Studied	Not studied	MRSA
4	(Gaddafi et al., 2021b)	Kebbi	Nasal	Phenotypic, Molecular	Pig	20.5% (41/200)	25% (3/12)	MRSA
5	(Mamfe et al., 2021)	Benue	Nasal	Molecular	Pig	34.2% (103/300)	33.3% (10/30)	MRSA
6	(Musawa et al., 2020)	Sokoto	Carcass Rinse	Molecular	Poultry	7.9% (15/190)	Not studied	MRSA
7	(Shittu et al., 2021)	Osun	Nasal	Phenotypic, Molecular	Goat	4.4% (4/90)	Not studied	MRSA
8	(Yusuf et al., 2020)	Sokoto	Meat, Milk	Molecular	Cattle	11% (22/200)	Not studied	MRSA
9	(Omoshaba et al., 2018)	Ogun	Milk, Nasal	Phenotypic	Sheep & Goat	25% (50/200)	Not studied	MRSA
10	(Okorie-Kanu et al., 2020)	Enugu	Carcass	Molecular	Pig, Poultry	22.8% (12/53)	Not studied	MRSA
11	(Yakubu et al., 2020)	Nasarawa	Milk	Molecular	Cattle	5% (9/180)	Not studied	MRSA
12	(Adikwu et al., 2019)	Benue	Hand, Water, Meat	Phenotypic, Serological	Pig	35% (50/200)	9.4% (3/32)	MRSA
13	(Igbinosa & Beshiru, 2019)	Edo	Nasal, Rectal	Phenotypic, Molecular	Pig	14.9% (13/27)	Not studied	MRSA
14	(Nwaogaraku et al., 2019)	Lagos	Blood	Phenotypic, Molecular	Pig	25% (25/100)	Not studied	MRSA
15	(Momoh et al., 2018)		Nasal	Phenotypic, Serological, Mass Spectrometry	Pig	5.3% (16/300)	12.9% (13/101)	MSSA
16	(Otalu et al., 2018)	Kogi	Nasal	Phenotypic, Mass Spectrometry	Pigs	4.7% (20/425)	10.9% (6/55)	MRSA
17	(Odetokun et al., 2018)	Ilorin	Nasal and surface	Phenotypic, Serological Molecular	Pigs	3.7% (3/8)	3.1%	MRSA
18	(Nworie et al., 2017)	Ebonyi		Molecular	Poultry	13.7% (247/1800)	Not studied	MRSA`
19	(Kwoji et al. 2017)	Sokoto	Cloacal Swab	Phenotypic	Poultry	8.82% (12/136)	Not studied	MRSA
20	(Usman et al., 2016)	Kaduna	Fermented Milk & Yoghurt	Phenotypic, Molecular	Cattle	3.21% (9/280)	Not studied	MRSA
21	(Okpo et al. 2016)	Kaduna	Dairy Product	Phenotypic	Cattle	Not Studied	Not studied	Not indicate
22	(Igbinosa et al., 2016)	Edo	Meat	Phenotypic, Molecular	Pig	53.9% (14/26)	Not Studied	MRSA
23	(Okunlola & Ayandele, 2015)	Oyo	Nasal	Phenotypic	Pig	43.2% (41/95)	Not Studied	MRSA
24	(Udegbunam et al. 2014)	Enugu	Ocular Swab	Phenotypic	Pig	0% (0/130)	Not Studied	MRSA
25	(Umaru et al., 2014)	Kaduna	Milk (Fresh and Fermented)	Phenotypic	Cattle	Not Studied	Not Studied	MRSA (VRSA)
26	(Ndahi et al., 2014)	Kaduna	Raw meat	Phenotypic	Cattle	37% (11/29)	Not Studied	MRSA
27	(Umaru et al., 2017)	Kaduna	Milk	Phenotypic	Cattle	Not Studied	Not Studied	MRSA
28	(Suleiman et al., 2012)	Kaduna	Milk (Subclinical mastitis)	Phenotypic	Cattle	Not Studied	Not Studied	MRSA

H-L-C, Human–livestock–contact.

GADDAFI et al. Prevalence of Methicillin-resistant Staphylococcus aureus

Acta Veterinaria Eurasia 2025

Table 2.

Antimicrobial Resistance Pattern of S. aureus and MRSA Isolated From Livestock in Nigeria

S/No	Author, year	P	Fox	Gen	Ery	Oxa	Tet	Cip	Van	Chl	Sxt
1	(Gaddafi et al., 2022a)	100%	NT	40%	43%	100%	56%	NT	0%	NT	47%
2	(Gaddafi et al., 2021b)	100%	NT	52%	52%	100%	52%	NT	0%	NT	52%
3	(Shittu et al., 2021)	100%	NT	0%	0%	100%	100%	NT	0%	NT	NT
4	(Mamfe et al., 2021)	100%	NT	7.5%	NT	NT	NT	75.8%	19.2%	NT	NT
5	(Okorie-Kanu et al., 2020)	100%	NT	NT	58.3%	NT	NT	NT	0%	NT	NT
6	(Aliyu et al., 2020)	NT	NT	0%	22.2%	NT	44.4%	0%	0%	NT	22.2%
7	(Nwaogaraku et al., 2019)	NT	44 %	NT	NT	100 %	NT	NT	NT	NT	NT
8	(Otalu et al., 2018)	100%	100%	0%	0%	0%	0%	NT	NT	0%	0%
9	(Momoh et al., 2018)	97%	NT	NT	20%	100%	62%	5%	NT	NT	52%
10	(Omoshaba et al., 2018)	NT	NT	88.2%	NT	88.2%	100%	NT	NT	NT	NT
11	(Nworie et al., 2017)	NT	NT	53%	19.1%	NT	45.7%	NT	NT	NT	40.9%
12	(Kwoji et al., 2017)	100%		88.9%	77.8%	100%	55.6%	NT	NT	88.9%	55.6%
13	(Okunlola & Ayandele, 2015)	NT	NT	70%	40%	43.9%	NT	0%	NT	NT	45%

Chl, Cchloramphenicol; Van, Vancomycin; Cip, Ciprofloxacin; Ery, Erythromycin; Fox, cefoxitin; Gen, Gentamicin; NT, not tested; Oxa, Oxacillin; P, Penicillin; R, Resistant; S, Susceptible; Sxt, Trimethoprim-sulfamethoxazole; Tet, Tetracycline.

The objective of this systematic review was to evaluate the prevalence, potential sources, and vehicle in the emergence and transmission of livestock-associated MRSA in Nigeria's livestock production systems over the past ten years. Numerous articles were collected, and out of these, 28 studies were deemed eligible for inclusion in this review. These studies were conducted in various regions across Nigeria, with a majority of them being carried out in the northwestern and southeastern parts of the country. More studies are likely conducted in certain regions of the country due to the higher number of veterinary faculties present there. For instance, the northwest region has four faculties, while the southeast region has three, surpassing the number in other regions. The existence of veterinary faculties in an area tends to contribute to increased animal research output in that specific area.

The prevalence of MRSA infection among livestock in Nigeria was found to be lower than in other countries, such as Belgium (37.8%), the Netherlands (39%), and Germany (70%), according to studies by Vanderhaeghen et al. (2010), Wulf et al. (2008), and Lienen et al. (2020) respectively. These studies reported relatively low levels of MRSA (<25%) compared to other countries (>30%). The variation in MRSA rates between Nigeria and other countries could be attributed to the absence of systematic surveillance and research on this topic in Nigeria, along with the comparatively small sample sizes employed in most studies. Nevertheless, a few of the studies in Nigeria did identify MRSA rates exceeding 40%. In contrast, in other countries, surveillance of LA-MRSA has been undertaken in human hospitals, revealing its capacity to cause severe infections in humans (Crespo-Piazuelo & Lawlor, 2021). This underscores the necessity of continuous surveillance of MRSA strains in Nigeria to preempt their emergence in hospital settings, which could exacerbate treatment challenges in already resource-limited healthcare environments. Examination of AMR patterns revealed that most strains were susceptible to antimicrobials commonly used for treatment in both human and veterinary medicine. The relatively low occurrence of MRSA and resistance to other antimicrobials among the isolates may be attributed to the fact that the majority of sampled livestock in Nigeria originate from medium to small-scale farms practicing low-intensity "backyard farming" and infrequent antibiotic use, as livestock density on a farm has been attributed. In contrast, research from other nations has concentrated on large commercial farms, where livestock density per farm has been attributed as a major factor in the emergence of antimicrobial resistance (Baudoin et al., 2021; Feingold et al., 2012; Manyi-Loh et al., 2018). Therefore, it is necessary to conduct more in-depth molecular studies on large commercial livestock farms in Nigeria, especially considering the rapid growth of the livestock industry in the country.

The studies reviewed in this research found that the majority of the isolates analyzed were susceptible to vancomycin, the preferred drug of choice for treating multidrug-resistant bacteria like MRSA (Che Hamzah et al., 2019). Thus, infections caused by MRSA isolates could be effectively treated with vancomycin. The studies reviewed employed multiple tests to detect methicillin resistance in the isolates, which indicates improved laboratory diagnostic capabilities in Nigeria. This improvement could be due to collaborations, which is crucial considering reports of the misidentification of MRSA (Igbinosa et al., 2023; Pillai et al., 2012). The use of multiple methods ensures a reliable, accurate identification and detection of MRSA. Also, it is worth noting from the reviewed studies that, despite recording a 100% phenotypic resistance of *S. aureus* to cefoxitin and/or oxacillin, some of the isolates lack the *mecA* gene. This complex and somewhat interesting scenario can occur possibly due to either the *S. aureus* possessing an alternative resistance mechanism that does not involve *mecA* gene but rather the *mecC* gene (a close relative of *mecA*) which can confer resistance to beta-lactam antibiotics including cefoxitin and oxacillin. Strains with *mecC* gene might not be detected in standard *mecA*-focused PCR assays (Mlynarczyk-Bonikowska et al., 2022). Similarly,

Table 3.
Genotypic Characteristics of Prevalence of Methicillin-Resistant Staphylococcus aureus Isolates

S/No	Author, year	Method	MecA	MecC	Antibioic-resistant gene	SCCmec typing	Spa typing	MLST	CC398	PvI	Entero toxins
1	(Gaddafi et al., 2022a)	PCR	100%	Not perfomed	Not pPerfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed
2	(Yakubu et al., 2022)	PCR	20%	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed
3	(Odetokun et al., 2022)	PCR	Not perfomed	Not perfomed	Not perfomed	sccmecIVa and sccmecV	t_{16571},	Not perfomed	Not perfomed	33.3%	Not perfomed
4	(Mamfe et al., 2021)	PCR	34.2	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not erfomed
5	(Gaddafi et al., 2021b)	PCR	100%	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not Perfomed
6	(Shittu et al., 2021)		4.3%	Not perfomed	Not perfomed	sccmecVII, sccmecVc	t_{127}, t_{4690}, t_{8821}	cc1, cc5, cc8, cc15, cc30, cc45, cc97, cc121, cc131, cc152, cc522	Not perfomed	Not perfomed	Not perfomed
7	(Musawa et al., 2020)	PCR	7.9%	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed
8	(Omoshaba et al., 2018)	PCR	25%	Not plerfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed
9	(Okorie-Kanu et al., 2020)	PCR	22.6%	Not perfomed	tetM	Not perfomed	T18345, t18346, t084, t311, t786, t1931, t448, t18345, t085, t2393, t304, t355, t5562, t934, t14223, t18346, t2216, t279, t346, t4690, t491	Not perfomed	Not perfomed	35.8%	Not perfomed
10	(Yusuf et al, 2020)	PCR	100%	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed
11	(Aliyu et al., 2020)	PCR	5%	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed
12	(Adikwu et al., 2019)	PCR	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	sea (7), sed (1)
13	(Nwaogaraku et al., 2019)	PCR	0%	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed	Not perfomed
14	(Momoh et al., 2018)	Multiplex PCR	100%	Not perfomed	Not perfomed	Not perfomed	t311 (1), t002(1), t442 (1), t084 (7), t5691 (1), t355 (4), t304 (1) in pigs; t311 (1), t084 (7), t2216 (3), t355 (1), t1931 (2), t127 (1), t5427 (1), t5126 (1), t5576 (1)	CC15, CC152 and CC5	Not perfomed	0%	41% (12/29), sea, seh, sei, sea and seh sed and sei

(Continued)

Table 3.
Genotypic Characteristics of Prevalence of Methicillin-Resistant Staphylococcus aureus Isolates (Continued)

S/No	Author, year	Method	MecA	MecC	Antibioic-resistant gene	SCCmec typing	Spa typing	MLST	CC398	PvL	Entero toxins
15	(Otalu et al., 2018)	Multiplex PCR	100%	Not performed	Not performed	SCCmecVIa	t1603 (100%)	CC88	CC398 Positive	Negetive	Not perfomed
16	(Odetokun et al., 2018)	PCR	Not perfomed	Not perfomed	Not performed	Not perfomed	t16571 (1/10) in pigs	Not perfomed	Not performed	Not perfomed	Not perfomed
17	(Nworie et al., 2017)	PCR	100%	Not performed	Not performed	sccmecV	T002, t084, t11469	ST15, ST5, ST121	Not performed	20%	Not performed
18	(Igbinosa et al., 2016)	Multiplex PCR	100%	Not performed	mphC, ermA, ermB, vanA	Not perfomed	Not perfomed	Not performed	Not performed	Not perfomed	Not perfomed

CC398, clonal complex 398; MLST, multi-locus sequence typing; PVL, Panton-Valantine leukocidin; SCCMEC, Staphylococcus chromosome casset mec; Spa, Staphylococcus protein A.

alterations in the native PBPs can reduce the binding affinity of beta-lactam antibiotics, leading to phenotypic resistance without harboring *mecA* (Elhassan et al., 2015).

It is worth noting that only one of the studies reported the emergence of a highly genetically similar MRSA strain (ST88) from pigs in Nigeria using whole-genome sequencing (WGS) (O. Otalu et al., 2018). This ST88 has been isolated from both hospital and community-acquired infections in humans in several Sub-Saharan African countries, including Nigeria (Kpeli et al., 2017; Raji et al., 2013). Hence, coordinated actions and measures need to be implemented to mitigate the dissemination of these strains. Most of the clonal complexes (CCs) and *spa* types documented in the studies reviewed were linked to human lineages of MRSA (Elsayed et al., 2023; Lozano et al., 2012). One study documented the clonal lineages of MRSA linked to livestock in Nigeria, which included CC1, CC5, CC72, CC97, CC121, CC15, CC152, and CC8 (Momoh et al., 2018). Further molecular epidemiological studies are required on MRSA as it plays an important role in the emergence of diverse genetic lineages of *Staphylococcus aureus*.

The reviewed studies identified several enterotoxin genes in MRSA isolates from both livestock and humans. Particularly, the *sea* gene was the most detected Staphylococcus enterotoxin. The detection of enterotoxin genes suggests that MRSA strains from livestock and humans in Nigeria pose a potentially significant threat of causing foodborne illnesses to at-risk individuals consuming livestock and livestock products. Three studies reviewed documented the occurrence of *pvl* encoding genes (a factor that contributes to skin and soft tissue infections) with a relatively high occurrence rate. *PVL* is commonly associated with community-acquired MRSA isolates and is specific to humans (Amin et al., 2020; Bhatta et al., 2016; Darboe et al., 2019). The detection of *PVL* suggests a higher probability of MRSA originating from humans rather than livestock. Inter-species transmission is a critical concern that cannot be overlooked, posing challenges in the context of treatment, prevention, and control of infections.

Of the studies reviewed in this article, only one utilized WGS. This analysis revealed high similarity among the MRSA isolates from pigs and humans (Otalu et al., 2018). Significantly, the identification of serine-protease-like proteases (spls) in the spl operon, a rarity in Nigerian MRSA isolates, emphasizes the necessity for additional investigation in this domain. Existing research has detailed the involvement of *Staphylococcal* proteases (metalloproteinase aureolysin) in the pathogenesis of MRSA, including evasion of the complement system (Paharik et al., 2016; Reed et al., 2001). Collectively, these observations indicate that MRSA isolates associated with livestock in Nigeria possess the capability to be virulent and induce infections in human hosts.

While there is a lack of sufficient information on the potential risk factors attributed to the transmission of livestock-acquired MRSA from animals to humans in Nigeria, with only a few studies addressing this aspect, one of the studies reviewed in this research identified contact with livestock as a risk factor (Gaddafi et al., 2021a). Previous research has suggested that individuals with direct contact with livestock, especially pigs and poultry, are at a higher risk of colonization by MRSA (Kasela et al., 2023). Interestingly, the presence of human-related clonal complexes (CCs) and scn genes, combined with the potential risk factor of having a medical-related occupation within households, indicates the possibility of anthropogenic transmission.

A limitation of this study is that only four specific electronic databases were searched, and only articles written in English were included, which may have resulted in the exclusion of relevant studies or publications. However, given that the study was focused on Nigeria, whose official language is English, the likelihood of omission based on language criterion is minimized. Also, there is a dearth of available studies that reported the risk factors regarding MRSA colonization amongst livestock and their handlers. Furthermore, none of the studies reported the presence of the *mecC* gene, a typical livestock-associated MRSA strain.

Conclusion and Recommendations

This review examined 28 studies on livestock-acquired MRSA in Nigerian livestock and found potentially highly virulent MRSA strains in livestock and their products. These strains have the potential for transmission to humans, particularly those with frequent contact with animals, and these may cause food-borne illnesses or be associated with community transmissions of diseases. Also, there is a variation in the prevalence and distribution of MRSA strains amongst livestock and livestock products in Nigeria. Methicillin-resistant *Staphylococcus aureus* isolates showed high resistance to commonly used antibiotics in both human and veterinary medicine, which is a serious public health concern. This systematic review highlights the need for further systematic and structured surveillance to gain a better understanding of the epidemiology of livestock-associated MRSA. An integrated "One Health" approach is necessary to effectively prevent and control MRSA infections, as well as to address AMR in both livestock and humans. Furthermore, awareness of proper hygiene and sanitation on livestock farms and the appropriate use of antimicrobials in livestock production is needed.

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GADDAFI et al. Prevalence of Methicillin-resistant Staphylococcus aureus

Acta Veterinaria Eurasia 2025

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GADDAFI et al. Prevalence of Methicillin-resistant Staphylococcus aureus

Acta Veterinaria Eurasia 2025

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