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Full Length Research Article

DETECTION OF *MEC(*A) GENE IN CEFOXITIN AND OXACILLIN (METHICILLIN) RESISTANT STAPHYLOCOCCUS AUREUS ISOLATED FROM READY-TO-EAT FOODS IN JOS, PLATEAU STATE, NIGERIA

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ABSTRACT
Staphylococcus aureus is a significant foodborne pathogen that can cause serious infections in humans, and its resistance to commonly used antibiotics poses a major public health threat. This study determined the prevalence of the *mec*A gene in methicillin-resistant *S. aureus* isolated from ready-to-eat foods sold in Jos, Nigeria. A total of 120 food samples were evaluated for bacterial load, Antibiotic susceptibility using the disc diffusion method and detection of methicillin resistance through PCR amplification of the *mec*A gene. The results indicate substantial bacterial contamination of the foods, with TBC ranging from 1.60×10^6 to 1.04×10^7 CFU/g and TSC ranging from 1.57×10^5 to 6.15×10^5 CFU/g. Among the food types, 'suya' showed the highest mean TBC (1.04×10^7 CFU/g) and jollof rice the lowest (1.60×10^6 CFU/g). The overall detection rate of *S. aureus* was 30.83%, with the highest occurrence in jollof rice (50.00%). Antibiotic susceptibility profiles revealed high resistance to oxacillin (81.9%) and cefoxitin (70.3%), confirming the circulation of MRSA in the food chain. Gentamicin (78.4%) and vancomycin (73.0%) were the most effective antibiotics, while notable resistance was found against trimethoprim (64.9%). Of 37 isolates, 26 (70.30%) were *mec*A carriers, with a 21.67% prevalence in the RTE foods. The Jollof rice exhibited the highest *mec*A occurrence (80.00%), while other popular dishes showed 50% to 70% positivity. The polymerase chain reaction amplification revealed a distinct band of the *mec*A genes at 533 base pairs on the agarose gel, providing strong evidence for the presence of methicillin-resistant *S. aureus* (MRSA) in the tested food samples. This study underscores the need for monitoring and control measures regarding MRSA in food products to protect public health.

Keywords: Methicillin-resistant *Staphylococcus aureus* (MRSA); *mec*A gene; Ready-to-eat foods; Antibiotic resistance; Bacterial contamination; Public health risk.

INTRODUCTION

Staphylococcus aureus is a facultative anaerobic, Gram-positive coccus pathogen often associated with foodborne poisoning. Although generally harmless, some strains can produce toxins that lead to diseases ranging from minor infections to life-threatening conditions (Omoruyi and Ibegbulan, 2023). This toxicity is due to heat-stable enterotoxins including SEA (Staphylococcal Enterotoxin A), SEB (Staphylococcal Enterotoxin B), and SEC (Staphylococcal Enterotoxin C), which are known for their high potency in certain *S. aureus* variants (Johler *et al*., 2016). Typically, these enterotoxins are notorious for causing severe gastrointestinal symptoms, such as rapid-onset nausea, vomiting, and abdominal cramps (Argudín *et al.,* 2010).

The global epidemiology of staphylococcal food poisoning underscores its significance in foodborne disease outbreaks (European Food Safety Authority, 2023; CDC, 2024). Staphylococcal infections account for approximately 20% of foodborne disease outbreaks worldwide (Kadariya *et al.,* 2014). In the U.S., around 241,000 *S. aureus*-related illnesses, with 6,000 hospitalisations, are reported annually (Liang, 2023). *S. aureus* foodborne disease outbreaks are reported in different regions worldwide (Thwala *et al*., 2021).

While methicillin-resistant *S. aureus* (MRSA) is primarily recognised for its role in healthcare-associated infections, it is emerging as a significant risk factor for foodborne diseases. About 20% of staphylococcal foodborne illness outbreaks are associated with MRSA in meat and poultry products (González-Machado, 2024). Nearly 70% of U.S. pork and beef farms reported MRSA in their livestock (Khairullah *et al.,* 2023). Notably, enterotoxin-producing *S. aureus* is prevalent in dairy products, creamy dishes, and improperly stored or reheated foods (Saly *et al.,* 2019). Dairy products and processed meats account for approximately 25% and 20% of reported staphylococcal food poisoning cases, respectively (CDC, 2023; FDA, 2023). With the increasing popularity of ready-to-eat (RTE) foods such as meats, rice, salads, sandwiches, and pre-packaged meals, a notable proportion (10% to 30%) of *S. aureus* from dairy products, meats, and RTE foods tested positive for enterotoxin production in Jos, Nigeria (Mawak *et al.,* 2010). These foods are at high risk of contamination by foodborne pathogens due to poor hygiene and handling practices (Mengistu *et al.,* 2022). The minimal processing of ready-to-eat foods before consumption heightens the risk of foodborne disease outbreaks (Chajecka-Wierzchowska *et al*., 2024).

The *mec*A gene is part of the staphylococcal cassette chromosome mec (SCCmec), a mobile genetic element that confers resistance to multiple antibiotic classes (Hesari *et al.,* 2020). Consequently, treating MRSA infections can be complicated due to simultaneous antibiotic resistance. Additionally, 43.2% of *mec*A-negative *S. aureus* isolates exhibited phenotypic resistance to methicillin, highlighting the complexity of antibiotic resistance arising from various mechanisms beyond the *mec*A gene (Williams *et al.,* 2020). Methicillin-resistant *S. aureus* (MRSA) poses significant public health concerns, particularly regarding food safety. Several studies

have shown alarming prevalence rates of the *mec*A gene in S. aureus isolated from ready-to-eat (RTE) foods. For instance, Wang *et al*. (2020) reported that the *mec*A gene was detected in approximately 30% of *S. aureus* isolates from RTE food samples. Although the prevalence of the *mec*A gene varies by food type, higher rates of *mec*A positivity have been reported in dairy products compared to meat products (Papadopoulos *et al.,* 2018). Additionally, the prevalence of *mec*A in *S. aureus* from RTE foods ranged from 10% to 60%, depending on geographical regions and the types of food examined (Jia *et al.,* 2023). The presence of MRSA in the food supply increases the risk of widespread infections among consumers (Titouche *et al.,* 2022), potentially resulting in increased hospitalizations and long-term health consequences (Algammal *et al.,* 2020; Naiem *et al.,* 2023). This study aimed to determine the prevalence of the *mec*A gene in methicillin-resistant *S. aureus* isolated from ready-to-eat foods sold in Jos, Nigeria.

MATERIALS AND METHODS

Sample Collection

One hundred and twenty (120) samples of ready-to-eat food were purchased from food vendors in Terminus Market (36), Farin Gada Market (30), New Market (30), and Katako Market (24) in Jos metropolis, Plateau State. The food types collected were white rice (10), jollof rice (10), beans (10), moimoi (bean pudding) (10), tuwo (Stiff Porridge) (10), eguisi soup (10), awara (tofu) (10), danwake (bean dumpling) (10), stew (10), yam porridge, okro soup (10) and suya (10). At each sampling, 300g of food was obtained in a sterile polyethene bag and transported in an ice-cold pack to the Central Diagnostic Laboratory, National Veterinary Research Institute Vom, Jos for analysis.

Enumeration of Bacteria

Twenty-five grams of each RTE food was homogenised with 225ml of sterile distilled water in a sterile zip lock bag. The resultant stock solution was then tenfold serially diluted by transferring 1ml into test tubes each containing 9 ml of sterile distilled water. This procedure was repeated aseptically until the 5^{th} dilution was obtained. An aliquot of 1ml of the diluted samples was poured into a sterile nutrient agar and mannitol salt agar plate and then incubated aerobically at 37^0C for 24 hours. Discrete colonies formed on nutrient agar and mannitol salt agar were enumerated for total bacterial count (TBC) and total *S. aureus* count (TSC) respectively and expressed as Colony Forming Units per gram of sample (CFU/g).

Characterisation of Bacterial Isolates

Pure bacterial cultures obtained were characterised based on colonial morphology and biochemical properties following standard procedures as described by Holt *et al*. (1994).

Antibiotic Susceptibility Profile

The antibiotic susceptibility profile of *S. aureus* was evaluated using the disc diffusion method following guidelines (M100 and M 07) of Clinical Laboratory Standards Institute (CLSI) guidelines (2024). Gram-positive antibiotics single-disc (Oxoid Ltd, UK) consisting of cefoxitin (30ug), tetracycline (30ug), oxacillin (1ug), trimethoprim (5ug), ciprofloxacin (5ug), erythromycin (15ug), gentamycin (10ug), levofloxacin (5ug), azithromycin (15ug), and rifampin (5ug) were used.

A well-isolated colony of pure bacterial culture was inoculated into a sterile nutrient broth following the direct colony suspension method. The bacterial suspensions were incubated at 37°C for 18 h and then adjusted to 0.5 McFarland turbidity standard using a Nephelometer. Sterile swabs stick was dipped into the bacterial suspension and pressed on the side of the tube. It was then evenly swabbed aseptically to cover the whole surface of a sterile Mueller-Hinton agar plate. After 30 minutes, the antibiotics were placed on the inoculated plates equidistantly using an Oxoid disc dispenser. This was followed by incubation in an inverted position at 37°C for 24 hours. The zone diameter of inhibition formed around the antibiotic discs was measured to the nearest mm and classified according to CLSI guidelines (2024).

Determination of Vancomycin Susceptibility and Minimum Inhibitory Concentration (MIC) of *S. aureus*

The susceptibility of *S. aureus* to vancomycin was determined by both the agar dilution and broth microdilution methods according to CLSI guidelines (2024). For the agar dilution method, Mueller-Hinton agar plates containing vancomycin concentrations of 1, 2, 4, 8 and 16 µg/mL were prepared by dissolving vancomycin tablets (Mast Diagnostics, UK) in molten agar. Bacterial inocula equivalent to a 0.5 McFarland turbidity standard (1.5×10^6 CFU/mL) were streaked onto the plates and incubated at 35°C. Visible growth indicated vancomycin resistance. For the broth microdilution method, a bacterial suspension of *S. aureus* was prepared to match a 0.5 McFarland standard (~1.5×10^8 CFU/mL). Serial two-fold dilutions of vancomycin were made in a 96-well microtiter plate, with a starting concentration of 30 µg/mL in Mueller-Hinton broth. Each well was inoculated with 100 µL of the bacterial suspension to achieve a final bacterial load of 5×10^5 CFU/ml. The plate was incubated at 37°C for 18-24 hours, and the Minimum Inhibitory Concentration (MIC) was recorded as the lowest concentration of vancomycin that visibly inhibited bacterial growth (CLSI, 2024).

Screening for Methicillin-Resistant *Staphylococcus aureus*

S. aureus isolates were subjected to cefoxitin and oxacillin antibiotics test on Mueller Hinton agar using the disc diffusion method. The resistance to both oxacillin and cefoxitin indicated methicillin-resistant *S. aureus.*

Detection of Methicillin-Resistant Gene

The *mec*A gene was detected in *S. aureus* isolates following the genomic DNA PCR amplification method (Algammal *et al.,* 2020).

Genomic DNA Extraction

Genomic DNA from methicillin-resistant *S. aureus* (MRSA) was extracted using QIAamp DNA Mini Kit (Qiagen, Hilden, Germany), according to the manufacturer's instructions. The bacterial cells harvested were lysed with proteinase K, and the DNA was bound to a silica membrane within the spin column. The genomic DNA was subsequently washed to remove impurities and eluted in a low-salt buffer. The purity and concentration were assessed using a UV spectrophotometer with A260/A280 ratios between 1.7 and 2.0 absorbance indicating high-quality DNA. The genomic DNA was then stored at 4^oC for further analysis.

PCR Amplification

The amplified target mecA gene associated with methicillin resistance was detected according to the method adopted by Algammal *et al.* (2020). Using specific primers (forward-5'-

AAAATCGATGGTAAAGGTTGGC-3' and reverse-5'-AGTTCTGCAGTACCGGATTTGC-3') the PCR reaction was performed under the following conditions. The procedure began with an initial denaturation phase, where the temperature was raised to 95°C for 2 min to separate the DNA strands. This was followed by 50 amplification cycles, each consisting of the three key steps: denaturation at 95°C for 30 s to maintain strand separation, annealing at 55°C for 30 s to allow primers to bind to the target sequence, and a final extension at 72°C for 1 min to synthesize new DNA strands. To ensure the complete extension of all DNA fragments, the process was concluded with a final elongation step at 72°C for 5 min (Naeim *et al.,* 2023).

PCR Products Analysis

The PCR products were examined was passed through 1.5% agarose gel electrophoresis, with the gel stained by ethidium bromide for visualization. Ten microliters of each PCR product, along with the loading dye were introduced into the gel wells, alongside a DNA ladder ranging from 100 to 1000 base pairs. Electrophoresis was conducted at 98 volts for 45 min and the bands were visualized with a UV transilluminator (Algammal *et al.,* 2020). The presence of the *mecA* gene, indicative of methicillin resistance, was confirmed by the appearance of a distinct band at 533 bp, which corresponds to the expected size of the amplified *mecA* gene fragment.

Data Analysis

The total bacterial count (TBC) and *S. aureus* count (TSC) are presented as mean ± standard deviation. In addition, statistically significant variation in the bacterial loads across the various food types was determined using one-way ANOVA at $p < 0.05$. A chi-square test was also conducted to correlate the relationship between the occurrence of *S. aureus* and the type of ready-to-eat food samples.

RESULTS

Table 1 presents the bacterial load of ready-to-eat food samples from various markets in Jos Metropolis, Nigeria. The result indicates significant bacterial contamination with notable variation ($p < 0.05$) in the total aerobic count (TBC) and total *S. aureus* count (TSC) across food types. Among the food types, 'suya' ($1.04 \times 10^7 \pm 1.92 \times 10^6$ CFU/g) had the highest mean TBC followed by beans ($9.69 \times 10^6 \pm 4.23 \times 10^6$ CFU/g), while jollof rice ($1.60 \times 10^6 \pm 1.41 \times 10^6$ CFU/g) was the least contaminated. The highest staphylococcal count was observed on 'awara' ($6.15 \times 10^5 \pm 3.51 \times 10^5$ CFU/g), while white rice maintained the lowest ($1.57 \times 10^5 \pm 8.10 \times 10^4$ CFU/g).

The occurrence of *S. aureus* based on ready-to-eat foods is presented in Table 2. Out of 120 food samples tested, the overall detection rate of *S. aureus* was 30.83%. A significant variation ($p > 0.05$) was not observed in the incidence of *S. aureus* among the different food types. The highest occurrence of *S. aureus* was reported on jollof rice (50.00%), followed by both 'tuwo' and 'awara' (40.00%) while yam porridge had the lowest detection rate at 10.00%. Cramer's V indicated a weak association between the food types and the number of positives.

The prevalence of *Staphylococcus aureus* in ready-to-eat foods based on market locations is presented in Table 3. Out of 120 food samples tested, the overall detection rate of *S. aureus* was 30.83%. No significant variation ($p > 0.05$) was observed in the incidence of *S. aureus* across the different markets. The highest occurrence was reported at the Terminus market (38.89%), while the Tomatoes market had the lowest detection rate at 23.33%. Cramer's V suggests a very weak association between market locations and the number of *S. aureus* positives.

The antibiotic susceptibility profile of *S. aureus* isolated from food types (Table 4) revealed notably high resistance to oxacillin (81.9%) and cefoxitin (70.3%). This result confirms the circulation of methicillin-resistant *S. aureus* (MRSA) in the food chain. Comparatively, the antibiogram revealed that gentamicin (78.4%) was the most active antibiotic, followed by vancomycin (73.0%) while oxacillin (18.1%) was the least susceptible. Moreover, *S. aureus* showed strong susceptibility to ciprofloxacin (64.9%) and gentamicin (78.4%), but there was notably high resistance to trimethoprim (64.9%). In addition, low *S. aureus* resistance to macrolide and aminoglycoside such as azithromycin (35.1%) and erythromycin (8.1%), was observed.

Gentamicin (78.4%) was the most effective antibiotic, followed by vancomycin (73.0%), while oxacillin (18.1%) was the least effective. *S. aureus* showed strong susceptibility to ciprofloxacin (64.9%) and gentamicin, but high resistance to trimethoprim (64.9%) was noted. Resistance to macrolides and aminoglycosides was low, with azithromycin resistance at 35.1% and erythromycin at 8.1%.

Out of the 37 isolates of *S. aureus* obtained from 120 food samples, 26 (70.30%) were *mec*A gene carriers as indicated in Table 5. This study reveals a 21.67% prevalence of *mec*A-carrying *S. aureus* in ready-to-eat foods sold in Jos markets. Food-specific data showed varying occurrences of *mec*A-positive *S. aureus.* Jollof rice had the highest *mec*A gene occurrence (80.00%), with 4 out of 5 positive isolates carrying the gene. Additionally, popular Nigerian dishes such as 'Tuwo' (Stiff Porridge), 'eguisi' soup, 'awara' (Tofu), and 'danwake' (Bean dumpling) showed *mec*A occurrences between 50% and 70%. A low frequency of *mec*A-positive *S. aureus* was found in Stew, yam Porridge and 'suya;' however, they exhibited a striking 100% *mec*A genes carriage. The lowest prevalence of *mec*A positivity (50%) was observed among isolates from 'awara' okro soup, and 'danwake'. The PCR amplification results in Figure 1 unequivocally confirmed the presence of the *mecA* gene, which is critically responsible for methicillin resistance, in the tested isolates of *Staphylococcus aureus*. The amplification of the *mecA* gene revealed a distinct band at 533 bp on the agarose gel, providing strong evidence for the presence of methicillin-resistant *S. aureus* (MRSA) in the tested food samples.

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Table 1: Mean Bacterial and Staphylococcal Counts of Ready-To-Eat Food Samples from Different Markets

Food Types	No. of Samples	TBC (x105)	p-value	TSC (x105)	p-value
White Rice	10	46.90 ± 19.55ab		1.57 ± 0.81b	
Jollof Rice	10	16.00 ± 14.14d		4.86 ± 2.68ab	
Beans	10	96.90 ± 42.33b		1.83 ± 0.75b	
Moimoi (Bean Pudding)	10	57.20 ± 37.58ac		5.83 ± 2.40a	
Tuwo (Stiff Porridge)	10	34.00 ± 20.34b		2.38 ± 0.95b	
Egusi Soup	10	33.10 ± 25.53c	1.3840e-13	5.70 ± 2.50a	0.143
Awara (Tofu)	10	42.60 ± 18.98a		6.15 ± 3.51a	
Danwake (Bean Dumpling)	10	88.70 ± 24.09b		5.13 ± 2.50a	
Stew	10	57.70 ± 21.70ac		5.90 ± 1.70a	
Suya	10	103.60 ± 19.23e		4.35 ± 1.48ab	
Okro Soup	10	59.60 ± 19.78ac		4.80 ± 3.82ab	
Yam Porridge	10	43.40 ± 30.54ab		1.70 ± 00b	

Keys: TBC: Total Bacterial Count, TSC: Total Staphylococcal Count.
Values are Mean and Standard Deviation (p>0.05).

Table 2: Occurrence of *Staphylococcus aureus* with the Type of Ready-To-Eat Foods

Food Types	No. of Samples	No. of Positives (%)	X^2	p-value	Cramer's V
White Rice	10	3(30.00)			
Jollof Rice	10	5(50.00)			
Beans	10	3(30.00)			
Moimoi (Bean Pudding)	10	3(30.00)			
Tuwo (Stiff Porridge)	10	4(40.00)			
Eguisi Soup	10	4(40.00)			
Awara (Tofu)	10	4(40.00)	6.99	0.8	0.241
Danwake (Bean dumpling)	10	4(40.00)			
Stew	10	2(20.00)			
Suya	10	2(20.00)			
Okro Soup	10	2(20.00)			
Yam Porridge	10	1(10.00)			
Total	**120**	**37(30.83)**			

Key: X2: Chi-Square. Values are the number of positive occurrences of food types (p>0.05

Table 3: Prevalence of *Staphylococcus aureus* in Ready-To-Eat Foods for the Different Markets

Market	No. of Samples	No. of Positives (%)	X^2	p-value	Cramer's V
Terminus	36	14(38.89)			
New Market	30	9(30.00)			
Tomatoes	30	7(23.33)	1.93	0.59	0.13
Katako	24	7(29.17)			
Total	**120**	**37(30.83)**			

Key: X2: Chi-Square.
Values are the prevalence of Staphylococcus aureus with market areas (p>0.05)

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Table 4: Antibiotic Susceptibility Profile of *Staphylococcus aureus* Isolated from Ready-To-Eat Foods

	N=37					
Antimicrobial Agents	**Sensitive**		**Intermediate**		**Resistant**	
	No.	**%**	**No.**	**%**	**No.**	**%**
Cefoxitin (30ug)	11	29.7	0	0.0	26	70.3
Oxacillin (1ug)	7	18.1	0	0.0	30	81.9
Vancomycin (10ug)	27	73.0	0	0.0	10	27.0
Tetracycline (30ug)	19	51.4	3	8.1	15	40.5
Trimethoprim (5ug)	12	32.4	1	2.7	24	64.9
Azithromycin (15ug)	18	48.7	6	16.2	13	35.1
Ciprofloxacin (5ug)	24	64.9	6	16.2	7	18.9
Erythromycin (15ug)	20	54.1	14	37.8	3	8.1
Gentamicin (10ug)	29	78.4	3	8.1	5	13.5
Rifampin (5ug)	19	51.4	4	10.8	14	37.8
Levofloxacin (5ug)	23	62.2	7	18.9	7	18.9

Table 5. Prevalence of *mecA* gene of *S. aureus* isolated from Ready-To-Foods

Food Type	**No. of Samples**	**No. of *S. aureus* Positive Isolates**	**No. of *mecA* Positive Samples**	**% Occurrence**
White Rice	10	3	2	66.67
Jollof Rice	10	5	4	80.00
Beans	10	3	2	66.67
Moimoi (Bean Pudding)	10	3	2	66.67
Tuwo (Stiff Porridge)	10	4	3	75.00
Eguisi Soup	10	4	3	75.00
Awara (Tofu)	10	4	2	50.00
Danwake (Bean dumpling)	10	4	2	50.00
Stew	10	2	2	100.00
Suya	10	2	2	100.00
Okro Soup	10	2	1	50.00
Yam Porridge	10	1	1	100.00
Total	**120**	**37**	**26**	**70.30**

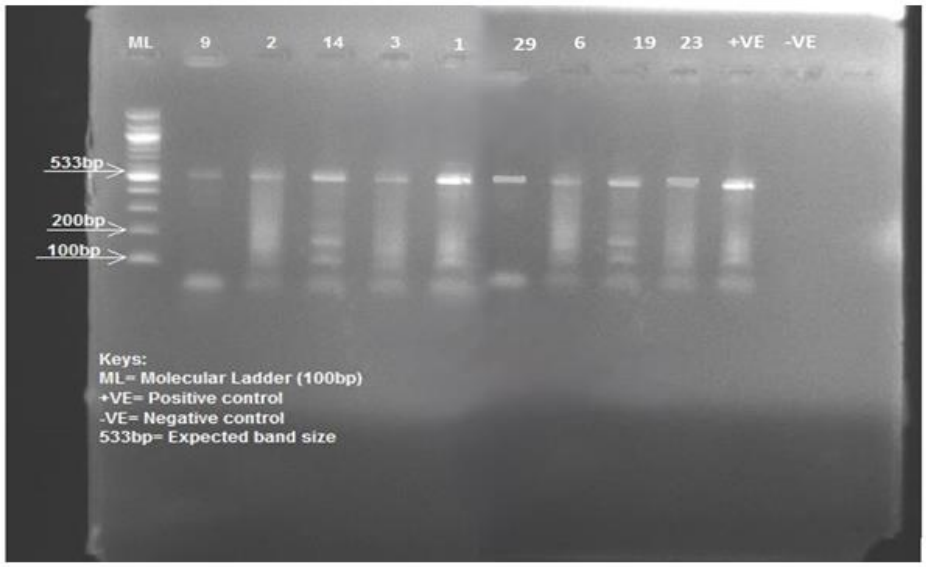

Fig 1: PCR amplification of *mecA* gene of methicillin-resistant *Staphylococcus aureus* on 1.5% agarose gel electrophoresis

DISCUSSION

This study revealed high bacterial contamination in the ready-to-eat food sampled from open markets at levels that indicate public health concerns. Like other ready-to-eat foods, these food types are susceptible to high bacterial contamination and are commonly linked to foodborne disease outbreaks (Tonjo *et al.,* 2022; Chen *et al.,* 2022). In addition, this finding indicates significant variation in the bacterial load across different food types. The variability among the food types therefore suggests potential inconsistencies in their handling and preparation practices (Yang *et al.,* 2016). Among the food types, 'suya' exhibited the highest mean TBC (1.04×10^7 CFU/g) at the levels above safe thresholds. Ready-to-eat foods like 'suya' are often prepared and sold in open environments and this could increase their risk of contamination (Osunde *et al.,* 2024). This finding aligns with the reports that meat-based dishes are often susceptible to higher levels of microbial contamination during handling and cooking (Osunde *et al.,* 2024). Furthermore, suya is a high-protein food and may be prone to bacterial proliferation due to its rich nutrient composition (Omotoso *et al.,* 2023). However, the low total bacterial count in jollof rice suggests better handling or cooking practices. Moreover, when cooked and stored properly, rice dishes are less prone to bacterial growth (Albaridi, 2022).

Currently, there is a heightened risk of staphylococcal food poisoning, especially in areas with prevalent street food consumption (Kadariya *et al.,* 2014). This risk arises from poor food handling and storage practices commonly associated with street foods (Myriam *et al.,* 2018). The situation is concerning, particularly given that the bacterial loads on these foods exceed the recommended limits of 10^3 to 10^5 CFU/g for safe ready-to-eat food consumption (WHO, 2021; FDA, 2022). Notably, significant differences exist in staphylococcal counts among different types of foods, indicating higher-risk diets. In this study, staphylococcal counts were higher in 'awara', suggesting an increased risk of staphylococcal food poisoning (Yakubu *et al.,* 2021). The lower staphylococcal counts in yam and white rice further illustrate variability based on food type (Abdullahi *et al.,* 2020). Both total bacterial count (TBC) and total staphylococcal count (TSC) levels in the foods reflect poor handling or storage practices across the markets.

A study by Afshari *et al.* (2022) reported a prevalence rate of 24.37% for *S. aureus* and 22.98% for MRSA (n=20/87) in food from Mashhad, Iran. Similarly, a prevalence of 20% for S. aureus was found in street-vended foods from Sagamu, Nigeria (Bello *et al*., 2013). Rodriguez-Lazaro *et al.* (2017) reported 15.7% for *S. aureus* and 3% for MRSA in food samples from international travelers, highlighting the global concern. Higher prevalence rates of *S. aureus* have been reported, including a 55.6% rate in street-vended foods in Calabar, Nigeria (Agbo *et al.,* 2016). Alabi *et al*. (2021) and Teniola *et al*. (2023) reported 15.8% and 41.67% prevalence rates in 'Suya' and 'Pomo', respectively. This trend in the occurrence of *S. aureus* in ready-to-eat foods is attributed to poor hygiene practices during food preparation, storage, and handling (Ho *et al.,* 2015).

In this study, the susceptibility profile of *S. aureus* isolated from ready-to-eat foods revealed a significant prevalence of resistant strains to various antimicrobial agents, particularly cefoxitin and oxacillin. This aligns with the concerning levels of methicillin-resistant *S. aureus* (MRSA) in food sources (Chajęcka-Wierzchowska *et al.,* 2021; Wang *et al.,* 2020). While this study showed a relatively high susceptibility rate to vancomycin (73.0%), earlier studies have reported vancomycin resistance in *S. aureus* isolated from foods (Hizlisoy *et al*., 2018). Other studies have suggested that antibiotic resistance is a growing concern among foodborne *S. aureus* isolates, emphasizing a worrying trend in food safety (Kim *et al.,* 2021). The presence of MRSA in ready-to-eat foods sold in Jos markets highlights a significant public health risk, affirming the circulation of antibiotic-resistant pathogens in the food cycle and facilitating the transmission of resistant bacteria to humans.

Moreover, gentamicin demonstrated strong sensitivity (78.4%) compared to findings from other studies indicating higher resistance rates (Parajuli *et al.,* 2024). In our study, low resistance of *S. aureus* to macrolides and aminoglycosides, such as azithromycin and erythromycin, was observed. However, this finding contrasts with trends in other regions, where macrolide resistance has become increasingly common (Smith *et al.,* 2023; Afshari *et al.,* 2022). The development of antibiotic-resistant *S. aureus* in food is further accelerated by the indiscriminate use of antibiotics in livestock farming (Omoruyi *et al.,* 2020; Omoruyi and Ajayi, 2021).

Data from this study underscore high rates of *mec*A positivity in ready-to-eat foods, particularly in popular traditional Nigerian dishes. The circulation of the *mec*A gene in these foods reflects a concerning level of methicillin-resistant bacteria strains. Although this study detected methicillin-resistant *S. aureus* (MRSA) isolates across multiple food types, jjollof rice exhibited the highest occurrence of *mec*A genes. Methicillin-resistant *S. aureus* (MRSA) in popular dishes such as jollof rice also aligns with trends observed in other regional studies (Raji *et al*., 2019). Also, stew and suya are specific food types with alarming 100% *mec*A positivity which pose a critical risk for MRSA transmission. This outcome correlates with the report of Alabi *et al.* (2021), which showed meat and meat-based dishes at high risk of MRSA spread. Furthermore, this finding affirms earlier reports that meat and dairy products are known potential reservoirs of methicillin-resistant *S. aureus* (Soltan *et al.,* 2020; Papadopoulos *et al.,* 2018). The *mecA* gene is recognized as the primary genetic determinant conferring resistance to methicillin and other β-lactam antibiotics in *Staphylococcus aureus*.

In this study, the successful amplification of the *mecA* gene revealed a distinct band at 533 base pairs on the agarose gel, providing strong evidence for the presence of methicillin-resistant *S. aureus* (MRSA) in the tested food samples. This finding is particularly significant as it indicates the potential for food products to serve as reservoirs for MRSA, which poses a risk to public health through the food chain. Previous studies, such as those by Algammal *et al.,* (2020) and Abdeen *et al.,* (2021), have reported high rates of *mecA* gene detection in MRSA strains isolated from various food sources, corroborating the results of this investigation. These studies underscore the prevalence of MRSA in food items and highlight the importance of monitoring these strains to prevent their transmission to humans. The circulation of the *mec*A gene in the food system is concerning due to the increasing risk of widespread infections and disease complications. Therefore, strategies to improve hygiene in food handling and thorough cooking can significantly mitigate these risks (Kansaen *et al.,* 2023).

Conclusion

The study revealed significant bacterial contamination in ready-to-eat foods sold in Jos, Nigeria, with methicillin-resistant *Staphylococcus aureus* (MRSA) posing a notable public health risk. High resistance to oxacillin and cefoxitin was detected, confirming the circulation of MRSA in the food supply chain. The prevalence of the *mec*A gene, particularly in popular foods like jollof rice and suya, underscores the potential for widespread transmission of MRSA to consumers. The study's detection of the *mec*A gene in cefoxitin-resistant *S. aureus* isolates confirmed their MRSA status. As the primary genetic determinant for methicillin resistance, the *mec*A gene allows MRSA strains to resist beta-lactam antibiotics, making infections with these strains challenging to treat. This discovery in foodborne MRSA isolates calls attention to the potential risk of antibiotic-resistant bacteria being transmitted to humans through contaminated food. These findings emphasize the urgent need for improved hygiene practices in food handling, preparation, and storage to mitigate the risk of antibiotic-resistant bacterial infections from food sources..

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