

Bacterial Contamination and Antimicrobial Resistance Profiles of Street-Vended Foods in Ogwa and Ebelle, Edo State, Nigeria

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ABSTRACT

Street foods provide affordable and accessible nutrition but may serve as reservoirs of pathogenic and antimicrobial-resistant (AMR) bacteria. This study investigated bacterial contaminants and antimicrobial resistance patterns among bacteria isolated from commonly consumed street foods sold in Ogwa and Ebelle communities, Edo State, Nigeria. Twenty street food samples comprising rice-based (n=8), bread/pastry-based (n=5), and yam/plantain-based foods (n=7) were analyzed using standard microbiological techniques. Bacterial isolates were identified by colony morphology, Gram staining, biochemical characterization, and polymerase chain reaction (PCR) detection of selected resistance genes. Antimicrobial susceptibility was determined using the Kirby–Bauer disk diffusion method following CLSI guidelines. Ten bacterial isolates comprising *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas* spp., and *Salmonella* spp. were recovered. Rice-based foods recorded the highest mean total viable count ($537 \pm 42 \times 10^3$ CFU/g; $P=0.018$). All 10 isolates were resistant to ceftriaxone, ampiclox, and amoxicillin. Multidrug resistance was observed in 9 of 10 isolates (90%), based on resistance to at least one antimicrobial agent in three or more antimicrobial classes. PCR detected *mecA*, *blaTEM*, *blaCTX-M*, *tetA*, and *sul1* among MDR isolates, while *blaSHV* was not detected. These findings highlight the need for improved food hygiene, microbiological surveillance, and antimicrobial stewardship.

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INTRODUCTION

Street foods constitute an important source of affordable and convenient nutrition, particularly in low- and middle-income countries where they contribute to food security, employment and livelihoods (Peimani & Kamalipour, 2022; Tacardon *et al.*, 2023). However, their preparation and sale under informal conditions, including inadequate sanitation, poor personal hygiene, unsafe water and improper storage, may increase the risk of microbial contamination and foodborne disease transmission (Ma *et al.*, 2019; Adane *et al.*, 2018). In Nigeria, Okanlawon *et al.* (2023) reported diverse bacterial and fungal contaminants in ready-to-eat Jollof rice, demonstrating the potential of commonly consumed foods to harbour microorganisms of public health importance.

The public health concern extends beyond microbial contamination to the emergence of antimicrobial-resistant bacteria (ARB) in the food chain. Antimicrobial resistance (AMR) enables bacteria to survive antimicrobial exposure through mechanisms such as enzymatic inactivation, target modification, reduced permeability, efflux and horizontal transfer of resistance determinants (Anukampa *et al.*, 2017). Multidrug-resistant *Escherichia coli*, *Salmonella*, *Staphylococcus aureus* and other bacteria have been reported in ready-to-eat foods, indicating that food can serve as an interface for exposure to antimicrobial-resistant organisms (Gulati & Chakraborty, 2017; Sandrasaigaran *et al.*, 2023). Evidence from Nigeria and Edo State further demonstrates the occurrence of resistant bacteria across human and

environmental settings. Okanlawon *et al.* (2025a) and Okanlawon *et al.* (2026) reported antibiotic-resistant bacteria associated with environmental fomites and food related sources, while Okanlawon *et al.* (2025b) and Nosa *et al.* (2024) reported resistant bacteria in other human settings. Similarly, Oladeji *et al.* (2024) identified resistant *Pseudomonas aeruginosa* in wastewater, while Avoseh *et al.* (2024) and Okanlawon *et al.* (2024a) reported bacterial contamination of water sources. These findings are relevant because food handling may intersect with contaminated surfaces and water; however, they do not establish these environments as the sources of bacteria recovered from street foods. Rather, they demonstrate the broader occurrence of bacterial contamination and antimicrobial resistance within interconnected human and environmental compartments. More directly, studies conducted in the study area have demonstrated bacterial contamination of locally consumed foods and food-associated environments. Olatunji *et al.* (2022) isolated food-associated bacteria, including *Salmonella enterica*, *Escherichia coli*, *Staphylococcus aureus*, *Pseudomonas aeruginosa* and *Klebsiella oxytoca*, from fermented foods obtained in Ogwa and Ebelle. Ogunremi *et al.* (2021) also reported bacterial contamination and multidrug-resistant isolates from fish and meat retail surfaces in Ebelle market. These findings confirm the presence of bacteria of food-safety importance within the local food environment, but they provide limited information

on the antimicrobial resistance profiles of bacteria directly isolated from commonly consumed street foods.

Despite increasing recognition of antimicrobial resistance as a global and local public health priority, specific information on the antimicrobial resistance profiles of bacteria associated with commonly consumed street foods in Ogwa and Ebelle remains limited. Existing local studies have demonstrated bacterial contamination of fermented foods and food-retailing environments and have identified antimicrobial-resistant bacteria in environmental and clinical settings, but there remains a need for direct characterization of antimicrobial resistance among bacteria isolated from street foods consumed by residents of these communities. This represents an important research gap because street foods provide a direct point of contact between potentially contaminated food products and consumers.

Therefore, this study investigated the bacterial contamination antimicrobial resistance patterns of bacteria isolated from commonly consumed street foods in Ogwa and Ebelle, Edo State, Nigeria, providing baseline information for food-safety surveillance, antimicrobial stewardship and efforts to limit the dissemination of antimicrobial-resistant bacteria through the food chain.

MATERIALS AND METHODS

Study Area

This study was conducted at the Microbiology Laboratory, Department of Biological Sciences, Glorious Vision University, Ogwa, Edo State, Nigeria. Ogwa is located in Esan West Local Government Area of Edo State at approximately 6°30'23"N and 6°12'39"E.

Sample Collection

A total of twenty (20) commonly consumed street-food samples, comprising ready-to-eat meals and fried or baked snacks, were collected from selected street-food vendors within Ogwa communities between January and March 2026. The sampling frame comprised ten (10) street-food vendors selected from different communities within Ogwa. The samples were categorised into three food groups: rice-based foods (R), bread/pastry-based foods (B), and yam/plantain-based foods (Y). Approximately 25 g of each food sample was aseptically collected into sterile, labelled containers. Each sample was assigned a unique identification code based on its food category and sample number. Samples were immediately placed in insulated containers and transported to the Microbiology Laboratory, where they were processed within 2 h of collection.

Preparation of Samples and Enumeration of Bacteria

For microbiological enumeration, 25 g of each food sample was aseptically transferred into 225 mL of sterile peptone water and thoroughly homogenised to obtain the initial 10⁻¹ dilution. Serial ten-fold dilutions were subsequently prepared aseptically by transferring 1 mL of the preceding dilution into 9 mL of sterile peptone water to obtain dilutions ranging from 10⁻¹ to 10⁻⁶.

Appropriate dilutions were inoculated using the pour-plate technique. For total viable bacterial counts, aliquots were

inoculated onto Nutrient Agar (NA), while MacConkey Agar was used for coliform enumeration and Mannitol Salt Agar (MSA) was used for staphylococcal enumeration. The inoculated plates were incubated aerobically at 37°C for 24 h. Each dilution was plated in triplicate. Following incubation, plates containing 30–300 colonies were selected for enumeration. The mean colony count from the triplicate plates was used to calculate the bacterial concentration, which was expressed as colony-forming units per gram (CFU/g). The resulting microbial counts were expressed as ×10³ CFU/g. For each food category, results were presented as mean ± standard deviation (SD).

Isolation and Identification of Bacterial Isolates

Following enumeration, representative colonies with distinct morphological characteristics were selected from the culture plates and repeatedly sub-cultured to obtain pure cultures. Colony characteristics, including shape, size, colour, edge, surface, pigmentation, and elevation, were recorded. Preliminary identification was based on colony morphology, Gram staining, and cellular morphology. Further characterization was carried out using standard biochemical tests, including catalase, oxidase, methyl red, hydrogen sulfide production, indole, motility, and carbohydrate fermentation tests. The resulting biochemical profiles were compared with standard characteristics for the probable identification of the bacterial isolates, following standard microbiological procedures described by Cheesbrough (2009) and Okanlawon *et al.* (2026b).

Statistical Analysis

Microbial counts were expressed as mean ± standard deviation (SD). Differences in mean total viable, total coliform, and staphylococcal counts among rice-based, bread/pastry-based, and yam/plantain-based street foods were assessed using one-way analysis of variance (ANOVA). Where significant differences were observed, Tukey's honestly significant difference (HSD) post-hoc test was used for pairwise comparisons. Statistical significance was set at *P* < 0.05.

Molecular Characterization of Antibiotic Resistance Genes

DNA Extraction

Genomic DNA was extracted from multidrug-resistant (MDR) bacterial isolates using the boiling method. A loopful of each pure bacterial culture was suspended in 200 µL of sterile nuclease-free water and heated at 100°C for 10 min. The suspension was immediately chilled on ice for 5 min and centrifuged at 12,000 rpm for 5 min. The supernatant containing the extracted DNA was transferred into sterile microcentrifuge tubes and stored at -20°C until PCR analysis.

PCR Amplification of Antibiotic Resistance Genes

PCR was performed to detect selected antimicrobial resistance genes among the MDR isolates. The target genes were *mecA*, *blaTEM*, *blaSHV*, *blaCTX-M*, *tetA* and *sul1*. The primer sequences and expected amplicon sizes are presented in Table 1.

Table 1: Primers used for Amplification of Antibiotic Resistance Genes

Target gene	Forward primer (5'-3')	Reverse primer (5'-3')	Expected amplicon (bp)
<i>mecA</i>	AAAATCGATGGTAAAGGTTGGC	AGTTCTGCAGTACCGGATTTGC	533
<i>blaTEM</i>	CCGTTTCATCCATAGTTGCCTGAC	TTTCCGTGTGCGCCCTTATTC	800
<i>blaSHV</i>	AGCCGCTTGAGCAAATTAAC	ATCCCGCAGATAAATCACCAC	713
<i>blaCTX-M</i>	TTTGCGATGTGCAGTACCAGTAA	CGATATCGTTGGTGGTGCCATA	544

Target gene	Forward primer (5'–3')	Reverse primer (5'–3')	Expected amplicon (bp)
tetA	GCTACATCCTGCTTGCCTTC	CATAGATCGCCGTGAAGAGG	210
sul1	CGGCGTGGGCTACCTGAACG	GCCGATCGCGTGAAGTTCCG	433

Each PCR reaction was performed in a final volume of 25 μ L containing 12.5 μ L of 2 $\times$ PCR Master Mix, 1 μ L each of forward and reverse primers (10 pmol/ μ L), 2 μ L of template DNA and nuclease-free water to make up the final volume. Amplification was performed in a thermal cycler using an initial denaturation at 95°C for 5 min, followed by 35 cycles of denaturation at 95°C for 30 s, primer-specific annealing at 55–60°C for 30 s and extension at 72°C for 45 s, followed by a final extension at 72°C for 7 min. Because the target genes had different primer-specific annealing requirements, the appropriate annealing temperature was applied to each PCR assay.

A positive control containing DNA known to carry the respective target gene and a no-template negative control containing all PCR reagents except template DNA were included in each PCR run. Where available, an extraction negative control was also included to monitor contamination during DNA extraction. No isolate was classified as gene-positive solely on the basis of its phenotypic resistance; amplification of a band at the expected molecular size was required.

Molecular analysis was performed on all seven isolates classified as MDR on the basis of resistance to antimicrobial agents belonging to at least three antimicrobial classes: R1, R2, B1, B2, B3, B4 and Y1.

Agarose Gel Electrophoresis

PCR products were separated by electrophoresis on 1.5% agarose gel prepared in 1 $\times$ TBE buffer and stained with ethidium bromide (0.5 μ g/mL) or an appropriate nucleic-acid stain such as GelRed. Electrophoresis was performed at approximately 100 V for 45 min. A 100-bp DNA ladder was included as the molecular-size marker. The separated PCR products were visualised under ultraviolet illumination and photographed using a gel documentation system. Samples showing bands corresponding to the expected amplicon size were considered positive for the respective resistance gene.

Classification of Multidrug Resistance

MDR was defined according to antimicrobial classes rather than the absolute number of antibiotics resisted. An isolate was classified as MDR when it showed acquired non-susceptibility to at least one antimicrobial agent in three or more antimicrobial classes. The antimicrobial classes represented in the resistance profile were determined from the individual isolate-level susceptibility results. Thus, resistance

to several antibiotics belonging to the same antimicrobial class was counted as one resistant antimicrobial class.

Antimicrobial Susceptibility Testing

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disc diffusion method on Mueller–Hinton agar in accordance with the Clinical and Laboratory Standards Institute (CLSI M100, 33rd edition, 2023). The antimicrobial discs used comprised ceftriaxone (30 μ g), ciprofloxacin (5 μ g), streptomycin (10 μ g), co-trimoxazole (25 μ g; 1.25 μ g trimethoprim + 23.75 μ g sulfamethoxazole), erythromycin (15 μ g), pefloxacin (5 μ g), gentamicin (10 μ g), ampiclox (ampicillin/cloxacillin, 10/5 μ g), cefuroxime (30 μ g), and amoxicillin (10 μ g). The discs were commercially prepared and applied according to the manufacturer's specifications.

Pure colonies from 18–24 h cultures were suspended in sterile physiological saline and adjusted to the turbidity of a 0.5 McFarland standard, corresponding to approximately 1.5×10^8 CFU/mL. The standardized inoculum was evenly spread over the surface of Mueller–Hinton agar using a sterile swab. The antibiotic discs were aseptically placed on the inoculated agar surface and gently pressed to ensure complete contact. Following incubation, the diameters of the zones of inhibition were measured in millimetres and interpreted as susceptible, intermediate, or resistant using the applicable organism-specific CLSI 2023 breakpoints.

Where CLSI interpretive criteria were not available for a particular organism–antibiotic combination, the result was not assigned a CLSI susceptible, intermediate, or resistant category. Quality-control procedures were performed using appropriate reference strains where available, and the resulting inhibition zones were assessed against the recommended CLSI quality-control ranges. Multidrug resistance (MDR) was defined as acquired non-susceptibility to at least one antimicrobial agent in three or more antimicrobial classes.

RESULTS AND DISCUSSION

Table 2 shows the colony characteristics of bacterial isolates recovered from street food samples. Ten (10) bacterial isolates were obtained, coded as R1–R3, B1–B4, and Y1–Y3 to represent different food types. Colonies exhibited variations in shape, size, color, edge, surface, pigmentation, and elevation. Most isolates were circular, creamy, and smooth, with edges ranging from entire to lobate.

Table 2: Colony Morphology of Bacterial Isolates from Street Foods

Isolate Code	Shape	Size	Colour	Edge	Surface	Pigmentation	Elevation
R1	Circular	Small	Creamy	Entire	Smooth	None	Flat
R2	Circular	Small	Creamy	Lobate	Smooth	None	Raised
R3	Irregular	Big	Creamy	Crenated	Smooth	None	Flat
B1	Circular	Small	Creamy	Entire	Smooth	None	Flat
B2	Circular	Small	Creamy	Lobate	Smooth	None	Raised
B3	Circular	Big	Creamy	Entire	Smooth	None	Raised
B4	Circular	Small	Creamy	Lobate	Smooth	None	Flat
Y1	Irregular	Big	Creamy	Crenated	Smooth	None	Flat
Y2	Circular	Small	Creamy	Entire	Smooth	None	Raised
Y3	Circular	Big	Creamy	Lobate	Smooth	None	Raised

Biochemical tests were performed to determine the probable identity of the isolates (Table 3). Gram-positive cocci were identified as *Staphylococcus aureus*, while Gram-negative

rods included *Escherichia coli*, *Pseudomonas sp.*, and *Salmonella sp.* Catalase was positive in all isolates, oxidase varied, and motility tests differentiated rods from cocci.

Table 3: Biochemical Characteristics and Probable Identity of Bacterial Isolates

Test	R1	R2	R3	B1	B2	B3	B4	Y1	Y2	Y3
Gram reaction	+	+	-	-	-	-	-	+	-	-
Cell shape	Cocci	Cocci	Rod	Rod	Rod	Rod	Rod	Cocci	Rod	Rod
Catalase	+	+	+	+	+	+	+	+	+	+
Oxidase	-	-	+	-	+	+	-	-	+	-
Methyl Red	+	+	+	+	+	+	+	+	+	+
H ₂ S	-	-	+	+	+	-	+	-	+	+
Indole	-	-	+	+	-	-	-	-	+	+
Motility	Non-motile	Non-motile	Motile	Motile	Motile	Motile	Motile	Non-motile	Motile	Motile
Sucrose	+	+	+	+	+	+	+	+	+	+
Maltose	+	+	+	+	+	+	+	+	+	+
Lactose	+	+	+	+	-	-	+	+	+	+
Glucose	+	+	+	+	+	+	+	+	+	+
Probable Identity	<i>S. aureus</i>	<i>S. aureus</i>	<i>E. coli</i>	<i>E. coli</i>	<i>Pseudomonas sp.</i>	<i>Pseudomonas sp.</i>	<i>Salmonella sp.</i>	<i>S. aureus</i>	<i>E. coli</i>	<i>Salmonella sp.</i>

Table 4 presents the mean microbial counts of the street-food categories. Rice-based foods recorded the highest mean total viable count ($537 \pm 42 \times 10^3$ CFU/g), followed by yam/plantain-based foods ($428 \pm 31 \times 10^3$ CFU/g) and bread/pastry-based foods ($301 \pm 24 \times 10^3$ CFU/g). Rice-based foods also recorded the highest mean total coliform count ($3.74 \pm 0.28 \times 10^3$ CFU/g) and staphylococcal count ($2.18 \pm 0.19 \times 10^3$ CFU/g), while bread/pastry-based foods recorded the lowest values for all three microbial parameters.

Values are expressed as mean $\pm$ standard deviation (SD), based on the independent food samples within each category. The triplicate plates prepared from each sample were treated as technical replicates, and their mean count was used to obtain the microbial value for that sample. Differences among the three food categories were assessed statistically using one-way analysis of variance, subject to assessment of the relevant assumptions. Where a significant difference was detected, Tukey's HSD post-hoc test was used for pairwise comparisons, with statistical significance set at $P < 0.05$.

Table 4: Mean Microbial Counts of Street Food Categories

Food Category	n	Total Viable Count ($\times 10^3$ CFU/g)	Total Coliform Count ($\times 10^3$ CFU/g)	Staphylococcal Count ($\times 10^3$ CFU/g)
Rice-based foods (R)	8	537 ± 42	3.74 ± 0.28	2.18 ± 0.19
Bread/Pastry-based foods (B)	5	301 ± 24	2.01 ± 0.17	1.45 ± 0.12
Yam/Plantain-based foods (Y)	7	428 ± 31	3.00 ± 0.21	1.88 ± 0.15
P-value		0.018	0.011	0.024

Keys: **R** – Rice-based street foods (e.g., fried rice, jollof rice); **B** – Baked or bread-based foods (e.g., meat pies, doughnuts, pastries); **Y** – Yam or plantain-based foods (e.g., fried yam, plantain chips)

The antibiotic susceptibility profiles of the bacterial isolates are presented in Table 5. All 10 isolates (100%) were resistant to ceftriaxone, ampiclox and amoxicillin. Resistance to ciprofloxacin and streptomycin was observed in 5 (50%) isolates each, while 6 (60%) isolates were resistant to cotrimoxazole and pefloxacin. Resistance to erythromycin,

gentamicin and cefuroxime was recorded in 7 (70%) isolates each. These findings indicate substantial antibiotic resistance among the street food isolates. The susceptibility profiles were interpreted in accordance with the applicable Clinical and Laboratory Standards Institute (CLSI) guidelines.

Table 5: Antibiotic Susceptibility of Bacterial Isolates from Street Foods

Antibiotic	R1	R2	R3	B1	B2	B3	B4	Y1	Y2	Y3
Rocephin (ceftriaxone)	R	R	R	R	R	R	R	R	R	R
Ciprofloxacin	S	R	S	R	R	S	R	S	S	R
Streptomycin	R	S	S	R	R	S	S	R	S	R
Seprin (co-trimoxazole)	R	S	R	R	S	S	R	R	S	R

Antibiotic	R1	R2	R3	B1	B2	B3	B4	Y1	Y2	Y3
Erythromycin	R	R	R	S	R	R	S	R	S	R
Pefloxacin	S	S	R	R	S	R	R	S	S	R
Gentamycin	S	R	R	R	R	S	R	R	S	R
Ampiclox	R	R	R	R	R	R	R	R	R	R
Zinnacef (cefuroxime)	R	S	R	R	R	R	S	R	S	R
Amoxicillin (amoxicillin)	R	R	R	R	R	R	R	R	R	R

Legend: R= Resistant; S= Susceptible; R1 = *Staphylococcus aureus*; R2 = *Staphylococcus aureus*
R3 = *Escherichia coli*; B1 = *Escherichia coli*; B2 = *Pseudomonas* sp.; B3 = *Pseudomonas* sp.; B4 = *Salmonella* sp.; Y1 = *Staphylococcus aureus*; Y2 = *Escherichia coli*; Y3 = *Salmonella* sp.

The multidrug resistance (MDR) profiles of the bacterial isolates are presented in Table 6. Based on resistance to at least one antimicrobial agent in three or more antimicrobial classes, 9 (90%) of the 10 isolates were classified as multidrug-resistant, while 1 (10%) was non-MDR. The number of antimicrobial classes resisted ranged from 2 to 6.

R3 and Y3 exhibited resistance to the highest number of antimicrobial classes (6 each), followed by R1, R2, B1, B2, B4 and Y1, which resisted 5 classes each. B3 resisted 4 antimicrobial classes, while Y2 resisted 2 classes and was therefore classified as non-MDR.

Table 6: Multidrug Resistance (MDR) Profiles of Bacterial Isolates

Isolate	Resistant antimicrobial classes	No. of classes resisted	MDR status
R1	Cephalosporin, Aminoglycoside, Folate pathway inhibitor, Macrolide, Penicillin	5	MDR
R2	Cephalosporin, Fluoroquinolone, Aminoglycoside, Macrolide, Penicillin	5	MDR
R3	Cephalosporin, Fluoroquinolone, Aminoglycoside, Folate pathway inhibitor, Macrolide, Penicillin	6	MDR
B1	Cephalosporin, Fluoroquinolone, Aminoglycoside, Folate pathway inhibitor, Penicillin	5	MDR
B2	Cephalosporin, Fluoroquinolone, Aminoglycoside, Macrolide, Penicillin	5	MDR
B3	Cephalosporin, Fluoroquinolone, Macrolide, Penicillin	4	MDR
B4	Cephalosporin, Fluoroquinolone, Aminoglycoside, Folate pathway inhibitor, Penicillin	5	MDR
Y1	Cephalosporin, Aminoglycoside, Folate pathway inhibitor, Macrolide, Penicillin	5	MDR
Y2	Cephalosporin, Penicillin	2	Non-MDR
Y3	Cephalosporin, Fluoroquinolone, Aminoglycoside, Folate pathway inhibitor, Macrolide, Penicillin	6	MDR

Legend: R1 = *Staphylococcus aureus*; R2 = *Staphylococcus aureus*; R3 = *Escherichia coli*; B1 = *Escherichia coli*; B2 = *Pseudomonas* sp.; B3 = *Pseudomonas* sp.; B4 = *Salmonella* sp.; Y1 = *Staphylococcus aureus*; Y2 = *Escherichia coli*; Y3 = *Salmonella* sp.

Detection of Antibiotic Resistance Genes

PCR analysis revealed the presence of antibiotic resistance genes among the multidrug-resistant bacterial isolates as seen in Table 7. The blaTEM gene was the most frequently detected β -lactam resistance determinant, followed by

blaCTX-M. The mecA gene was detected among multidrug-resistant *Staphylococcus aureus* isolates, while tetA and sul1 were detected in selected *Escherichia coli* and *Salmonella* isolates. No amplification was observed for blaSHV in the resistant isolates.

Table 7: Distribution of Antibiotic Resistance Genes among MDR Isolates

Isolate	Organism	mecA	blaTEM	blaCTX-M	blaSHV	tetA	sul1
R1	<i>S. aureus</i>	+	–	–	–	–	–
R2	<i>S. aureus</i>	+	–	–	–	–	–
R3	<i>E. coli</i>	–	+	–	–	–	–
B1	<i>E. coli</i>	–	+	+	–	+	+
B2	<i>Pseudomonas</i> sp.	–	+	–	–	–	–
B3	<i>Pseudomonas</i> sp.	–	+	–	–	–	–
B4	<i>Salmonella</i> sp.	–	+	+	–	+	+
Y1	<i>S. aureus</i>	+	–	–	–	–	–
Y3	<i>Salmonella</i> sp.	–	+	+	–	+	+

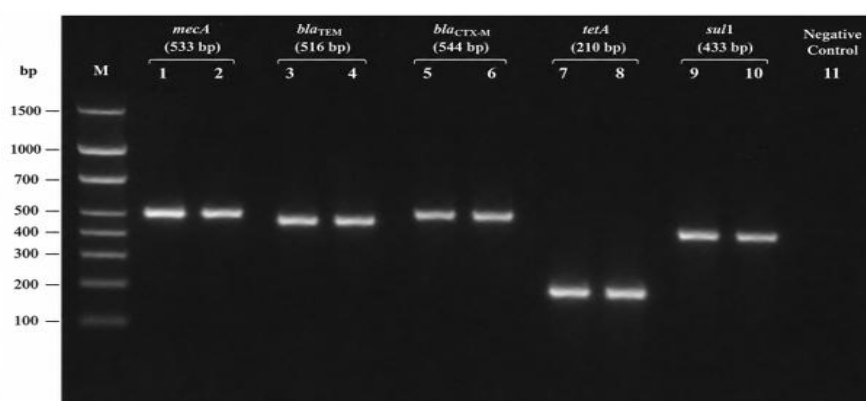


Figure 1: Agarose Gel Electrophoresis showing PCR Amplification of Antibiotic Resistance Genes in Multidrug-resistant Bacterial Isolates. M: 100 bp DNA Ladder; Lanes 1–10: Representative Bacterial Isolates; Positive Bands Correspond to the Expected Amplicon Sizes. Lane 11: Negative Control

Discussion

The present study demonstrated that commonly consumed street foods harbored diverse bacterial contaminants, including *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas* spp., and *Salmonella* spp. The occurrence of these organisms may reflect deficiencies in food preparation, handling, storage, and vending practices. The predominance of *S. aureus* and *E. coli* agrees with previous reports of bacterial contamination of ready-to-eat foods (Baloch *et al.*, 2017; Tadesse *et al.*, 2019; Ghali-Mohammed *et al.*, 2025). Okanlawon *et al.* (2023) also reported diverse bacterial contaminants in ready-to-eat Jollof rice sold within the Obafemi Awolowo University community, while Olatunji *et al.* (2022) reported spoilage and pathogenic bacteria in fermented food products from Edo State. More recent studies have similarly reported bacterial contamination and antimicrobial resistance in indigenous street-vended foods in Kaduna State (Akinyele *et al.*, 2024) and ready-to-eat foods in Lagos State (Makinde *et al.*, 2026). These findings support the microbiological significance of street-vended foods as potential vehicles for foodborne microorganisms.

Rice-based street foods recorded significantly higher total viable, coliform, and staphylococcal counts than bread/pastry- and yam/plantain-based foods ($P < 0.05$). This higher contamination may be associated with prolonged holding at ambient temperature, repeated handling, and inadequate temperature control. Environmental sources may also contribute to contamination. Okanlawon *et al.* (2024a) reported considerable bacteriological contamination of water reservoirs in Ogwa and Ebelle, while Avoseh *et al.* (2024) reported high bacterial loads in River Obazagbon. Thus, contaminated water, utensils, food-contact surfaces, and the surrounding environment represent plausible contamination pathways, although the present study did not directly establish these sources. The recovery of *S. aureus*, *E. coli*, *Pseudomonas* spp., and *Salmonella* spp. is also consistent with reports from Nigerian street-vended and ready-to-eat foods (Akinyele *et al.*, 2024; Kintum *et al.*, 2025; Usman and Umar, 2025).

Antimicrobial susceptibility testing revealed considerable resistance to several β -lactam antibiotics, including amoxicillin, ampiclox, ceftriaxone, and cefuroxime. Similar resistance has been reported among Nigerian environmental, food-associated, and clinical bacteria (Oladeji *et al.*, 2024; Nosa *et al.*, 2024; Okanlawon *et al.*, 2025a; Okanlawon *et al.*, 2025b). More directly, Akinyele *et al.* (2024) and Nwajiobi *et al.* (2025) reported antimicrobial-resistant bacteria in street-

vended and ready-to-eat foods in Nigeria. In the present study, 9 of 10 isolates (90%) were classified as multidrug-resistant, while one isolate was non-MDR. This high proportion of MDR isolates is comparable with observations reported in food-associated bacteria (Adhikari *et al.*, 2023; Adeleke & Owoseni, 2022) and recent Nigerian studies of street-vended foods (Akinyele *et al.*, 2024; Nwajiobi *et al.*, 2025).

PCR analysis detected several antibiotic resistance genes. *blaTEM* was the most frequently detected β -lactam resistance gene, followed by *blaCTX-M*, while *mecA* was detected in the *S. aureus* isolates and *tetA* and *sul1* occurred in selected *E. coli* and *Salmonella* isolates. These findings demonstrate carriage of the targeted resistance determinants but should be interpreted cautiously. Detection of *blaTEM* or *blaCTX-M* alone does not definitively establish phenotypic ESBL production, while detection of *mecA* provides evidence of a methicillin-resistance determinant but does not by itself constitute complete phenotypic confirmation of MRSA. Similarly, detection of *tetA* and *sul1* indicates gene carriage but does not necessarily establish gene expression. Although horizontal transfer of resistance genes is biologically plausible, it was not demonstrated in the present study because plasmid localization, transferability, or genomic relatedness was not investigated. Therefore, the findings demonstrate bacterial contamination, phenotypic antimicrobial resistance, and carriage of selected resistance genes in the examined street foods, while the specific contamination sources and mechanisms of resistance-gene dissemination require further investigation.

CONCLUSION

This study demonstrated that the sampled street-vended foods from Ogwa and Ebelle communities harbored potentially pathogenic bacteria, including *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas* spp., and *Salmonella* spp. Rice-based foods had significantly higher microbial loads, while most of the isolates were multidrug-resistant and carried resistance-associated genes such as *mecA*, *blaTEM*, *blaCTX-M*, *tetA*, and *sul1*. However, these findings are limited to the sampled foods and isolates and should not be generalized to the wider communities or interpreted as evidence of direct transmission. Improved food hygiene, vendor education, and routine microbiological surveillance are therefore recommended to reduce the occurrence of antimicrobial-resistant bacteria in street-vended foods.

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