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Microbiological Quality, Biochemical Characterization, and Antimicrobial Resistance Profiles of Foodborne Bacterial Pathogens Associated with Ready-to-Eat Foods Served During Public Gatherings in Kano State, Nigeria.

Ahmad Shehu Muazu

Department of Biochemistry, Faculty of Science, Aliko Dangote University of Science and Technology (ADUSTECH), Wudil, Kano State, Nigeria

Abstract

Large-scale public gatherings in Nigeria, particularly in Kano State, frequently involve mass preparation and serving of ready-to-eat (RTE) foods. When hygiene practices are compromised, these foods can serve as vehicles for foodborne pathogens, including multidrug-resistant (MDR) strains, posing significant public health risks. This study evaluated the microbiological quality, biochemical characteristics, and antimicrobial susceptibility patterns of bacterial pathogens isolated from RTE foods served at festive and public events in Kano State, Nigeria. A cross-sectional laboratory-based study was conducted on 100 RTE food samples comprising rice-based dishes, salads, and meat products, collected aseptically using stratified random sampling. Total viable counts (TVC) and coliform counts were determined using the pour-plate method. Isolates were identified by colony morphology, Gram staining, and conventional biochemical tests. Antimicrobial susceptibility was assessed using the Kirby–Bauer disk diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guidelines. MDR was defined as non-susceptibility to at least one agent in three or more antimicrobial categories. Mean TVC ranged from 4.82 ± 0.41 to 6.15 ± 0.53 log CFU/g, with salads having the highest microbial loads. Pathogen detection rates were *Escherichia coli* (34%), *Staphylococcus aureus* (29%), *Salmonella* spp. (19%), *Klebsiella pneumoniae* (12%), and *Bacillus cereus* (8%). Resistance to ampicillin (78–92%) and tetracycline (61–74%) was high, while 58% of isolates were MDR. Salads and meat products were significantly more contaminated than rice-based dishes ($p < 0.05$). These findings demonstrate substantial microbial contamination and MDR pathogens, emphasizing the need for improved food-handler training, cold-chain infrastructure, and routine microbiological surveillance.

Keywords

Ready-to-Eat Food;
Foodborne Pathogens;
Biochemical Characterization;
Antimicrobial Resistance;
Multidrug Resistance;
Public Health;
Kano State;
Nigeria

Corresponding Author: Ahmad Shehu Muazu, Department of Biochemistry, Faculty of Science, Aliko Dangote University of Science and Technology (ADUSTECH), Wudil, Kano State, Nigeria. Email: ahmadshehu@kust.edu.ng

1. INTRODUCTION

The culture of large-scale feasting during weddings, naming ceremonies, religious festivals, and other social events is deeply embedded in the social fabric of Kano State, Nigeria. These gatherings typically involve the mass preparation of ready-to-eat (RTE) foods, including rice-based dishes (jollof rice, fried rice), vegetable salads, meat products (suya, roasted chicken, stews), and other local delicacies. Because these foods are consumed without further heat treatment, any contamination acquired during preparation, storage, or serving poses a direct risk to consumers (World Health Organization [WHO], 2015; Okafor-Yarwood et al., 2023).

Foodborne diseases remain a major public-health challenge in low- and middle-income countries. The World Health Organization estimates that unsafe food causes approximately 600 million illnesses and 420,000 deaths annually worldwide, with the highest burden in Africa (WHO, 2015). In Nigeria, gastroenteritis and other foodborne illnesses continue to contribute substantially to morbidity, particularly among children and immunocompromised individuals (Akinyemi et al., 2021). The emergence and spread of antimicrobial-resistant (AMR) bacteria through the food chain further compounds this threat, limiting therapeutic options and increasing the risk of treatment failure (Magiorakos et al., 2012; Beshiru & Igbinosa, 2023).

The logistical pressures of mass catering—limited access to clean water, inadequate hand-washing facilities, improper temperature control, prolonged holding times, and cross-contamination between raw and cooked foods—create favourable conditions for microbial proliferation. Previous studies in various Nigerian cities have consistently reported high bacterial loads and the presence of pathogens such as Escherichia coli, Staphylococcus aureus, Salmonella spp., and Klebsiella spp. in street-vended and event-catered RTE foods (Bichi & Adam, 2024; Okafor-Yarwood et al., 2023; Bacterial contaminants…, 2021). Many of these isolates exhibit multidrug resistance, raising concerns that public gatherings may serve as amplification points for the community dissemination of resistant bacteria (Scoping review…, 2025; Fayemi et al., 2021). Despite the high frequency of large-scale events in Kano State, empirical data on the microbiological safety of foods served at these gatherings remain limited (Bichi & Adam, 2024).This study therefore, aimed to assess the microbiological quality, biochemical characteristics, and antimicrobial resistance profiles of bacterial pathogens associated with RTE foods served during public gatherings in Kano State, Nigeria.

2. MATERIALS AND METHODS

2.1 Study Area

The study was conducted in Kano State, northwestern Nigeria. Kano is the most populous state in northern Nigeria and is characterized by frequent large social, cultural, and religious gatherings at which mass catering is common. Samples were obtained from public events held across selected local government areas within the state in 2025. Ethical approval was obtained from the relevant institutional review board of Aliko Dangote University of Science and Technology (ADUSTECH), and permission was sought from event organizers where applicable.

2.2 Sample Collection

A stratified random sampling approach was employed. One hundred (100) RTE food samples were collected from public gatherings (weddings, naming ceremonies, and religious festivals). Samples were stratified by food category: rice-based dishes (n = 40), salads (n = 30), and meat products (n = 30). Approximately 100–150 g of each food item was aseptically collected into sterile, labelled containers using sterile utensils. Samples were immediately placed in a cool box maintained at 4–8 °C and transported to the laboratory for processing within 4–6 hours of collection. Basic observational data on food-handling practices (availability of hand-washing facilities, temperature holding, and visible cross-contamination risks) were recorded at each site using a structured checklist.

Figure 1. (A) Shredded meat / beef; (B) Pepper soup / stew; (C) Fried rice / jollof-style rice; (D) Stew with meat; (E) Moi-moi (steamed bean pudding); (F) White rice with vegetables; (G) Food wrapped in leaves (e.g., moi-moi or local delicacy); (H) Assorted meat dish; (I) Vegetable salad (cabbage, carrot, cucumber). These foods represent the three main categories analysed: rice-based dishes, meat products, and salads.

2.3 Sample Preparation

Twenty-five grams of each food sample was aseptically weighed and homogenized in 225 mL of sterile buffered peptone water using a stomacher for 2 minutes to obtain a 1:10 dilution. Serial tenfold dilutions were then prepared in sterile peptone water, ranging from 10^{-1} to 10^{-6}, for subsequent microbiological analyses.

2.4 Biochemical Analysis

Presumptive colonies selected from primary isolation plates were purified by successive streaking on nutrient agar. Pure cultures were subjected to a panel of conventional biochemical tests that included catalase, coagulase (for Gram-positive cocci), oxidase, indole production, methyl red, Voges–Proskauer, citrate utilization (IMViC series), urease, triple sugar iron (TSI) agar reactions, and selected carbohydrate fermentation tests. Results were interpreted according to standard diagnostic schemes consistent with Bergey's Manual of Systematic Bacteriology.

2.5 Microbiological Analysis

Total viable counts (TVC) were determined by the pour-plate method using Plate Count Agar. Appropriate dilutions (0.1 mL or 1 mL) were plated and incubated at 37 °C for 24–48 h. Colonies were counted and results expressed as $\log_{10}$ colony-forming units per gram (log CFU/g). Coliform counts were similarly determined using MacConkey agar or Violet Red Bile Agar under the same incubation conditions. All counts were performed in duplicate and mean values calculated.

2.6 Isolation and Identification of Pathogens

Selective and differential media were used for the isolation of specific pathogens: MacConkey agar and Eosin Methylene Blue (EMB) agar for Escherichia coli and other Enterobacteriaceae; Mannitol Salt Agar for Staphylococcus aureus; Xylose Lysine Deoxycholate (XLD) or Salmonella-Shigella (SS) agar for Salmonella spp.; and blood agar or Bacillus cereus selective agar for Bacillus cereus. Presumptive colonies were further confirmed by Gram staining and the biochemical tests described in Section 2.4. Identification was based on colony morphology, Gram reaction, and biochemical profiles.

2.7 Antimicrobial Susceptibility Testing

Antimicrobial susceptibility was determined by the Kirby–Bauer disk diffusion method on Mueller–Hinton agar according to Clinical and Laboratory Standards Institute (CLSI) guidelines (CLSI, 2024). The antibiotics tested represented major classes and included: ampicillin (10 µg), amoxicillin–clavulanate (20/10 µg), ceftriaxone (30 µg), gentamicin (10 µg), ciprofloxacin (5 µg), tetracycline (30 µg), chloramphenicol (30 µg), and trimethoprim–sulfamethoxazole (1.25/23.75 µg). After incubation at 37 °C for 16–18 h, zones of inhibition were measured in millimetres and interpreted as susceptible (S), intermediate (I), or resistant (R) using CLSI breakpoints. Multidrug resistance (MDR) was defined as non-susceptibility to at least one agent in three or more antimicrobial categories (Magiorakos et al., 2012).

2.8 Data Analysis

Data were analysed using descriptive statistics (means, standard deviations, frequencies, and percentages). One-way analysis of variance (ANOVA) was used to compare mean microbial loads across food categories, followed by Tukey's post-hoc test where appropriate. Chi-square or Fisher's exact tests were applied to assess associations between categorical variables (e.g., hygiene practices and pathogen presence). A p-value < 0.05 was considered statistically significant. Analyses were performed using [statistical software package, e.g.

3. RESULTS

3.1 Microbial Load by Food Category

Mean total viable counts (TVC) and the proportion of samples positive for pathogenic bacteria are summarized in Table 1. Salads exhibited the highest mean TVC (6.15 ± 0.53 log CFU/g), followed by meat products (5.68 ± 0.47 log CFU/g) and rice-based dishes (4.82 ± 0.41 log CFU/g). The differences among categories were statistically significant (ANOVA, $p < 0.001$). Overall, 78% of samples exceeded the commonly referenced acceptability threshold of 10^5 CFU/g (5.0 log CFU/g).

Table 1. Prevalence and Mean Microbial Load (log CFU/g) by Food Category

Food Category	No. Samples	Mean TVC (log CFU/g) ± SD	Samples with Pathogens (%)
Rice-based dishes	40	4.82 ± 0.41	52.5
Salads	30	6.15 ± 0.53	86.7
Meat products	30	5.68 ± 0.47	73.3
Overall	**100**	**5.48 ± 0.72**	**68.0**

Note: TVC = Total Viable Count; SD = standard deviation. ANOVA $p < 0.001$ across categories.

3.2 Frequency of Bacterial Isolates

A total of 112 bacterial isolates of public-health significance were recovered from the 100 samples (Table 2). Escherichia coli was the most frequently isolated organism (34 isolates; 34% of samples), followed by Staphylococcus aureus (29%), Salmonella spp. (19%), Klebsiella pneumoniae (12%), and Bacillus cereus (8%). Co-isolation of two or more pathogens occurred in 21% of positive samples, predominantly in salads. These prevalence rates are consistent with reports from other Nigerian studies on RTE foods (Okafor-Yarwood et al., 2023; Bichi & Adam, 2024; Bacterial contaminants…, 2021).

Table 2. Frequency of Bacterial Isolates from RTE Foods

Organism Identified	Frequency (n)	Percentage of Samples (%)
Escherichia coli	34	34.0
Staphylococcus aureus	29	29.0
Salmonella spp.	19	19.0
Klebsiella pneumoniae	12	12.0
Bacillus cereus	8	8.0
Total isolates	**112**	—

Note: Percentages refer to the proportion of the 100 samples from which the organism was isolated. Some samples yielded more than one pathogen.

3.3 Antimicrobial Susceptibility Profiles

Antimicrobial susceptibility results for the major pathogens are presented in Table 3. Resistance to ampicillin was consistently high (78–92% across species). Tetracycline resistance ranged from 61% to 74%. Ciprofloxacin and gentamicin retained relatively better activity, although intermediate and resistant phenotypes were still observed. Overall, 65 of 112 isolates (58.0%) met the definition of multidrug resistance (MDR). These findings are in agreement with high resistance rates reported for RTE food isolates across Nigeria and West Africa (Scoping review…, 2025; Ekli et al., 2025; Antibiogram…, 2026). Representative culture plates showing zones of inhibition from the Kirby–Bauer disk diffusion assays are presented in Figure 1.

Representative Kirby–Bauer disk diffusion plates showing zones of inhibition of bacterial isolates recovered from ready-to-eat foods served at public gatherings in Kano State.

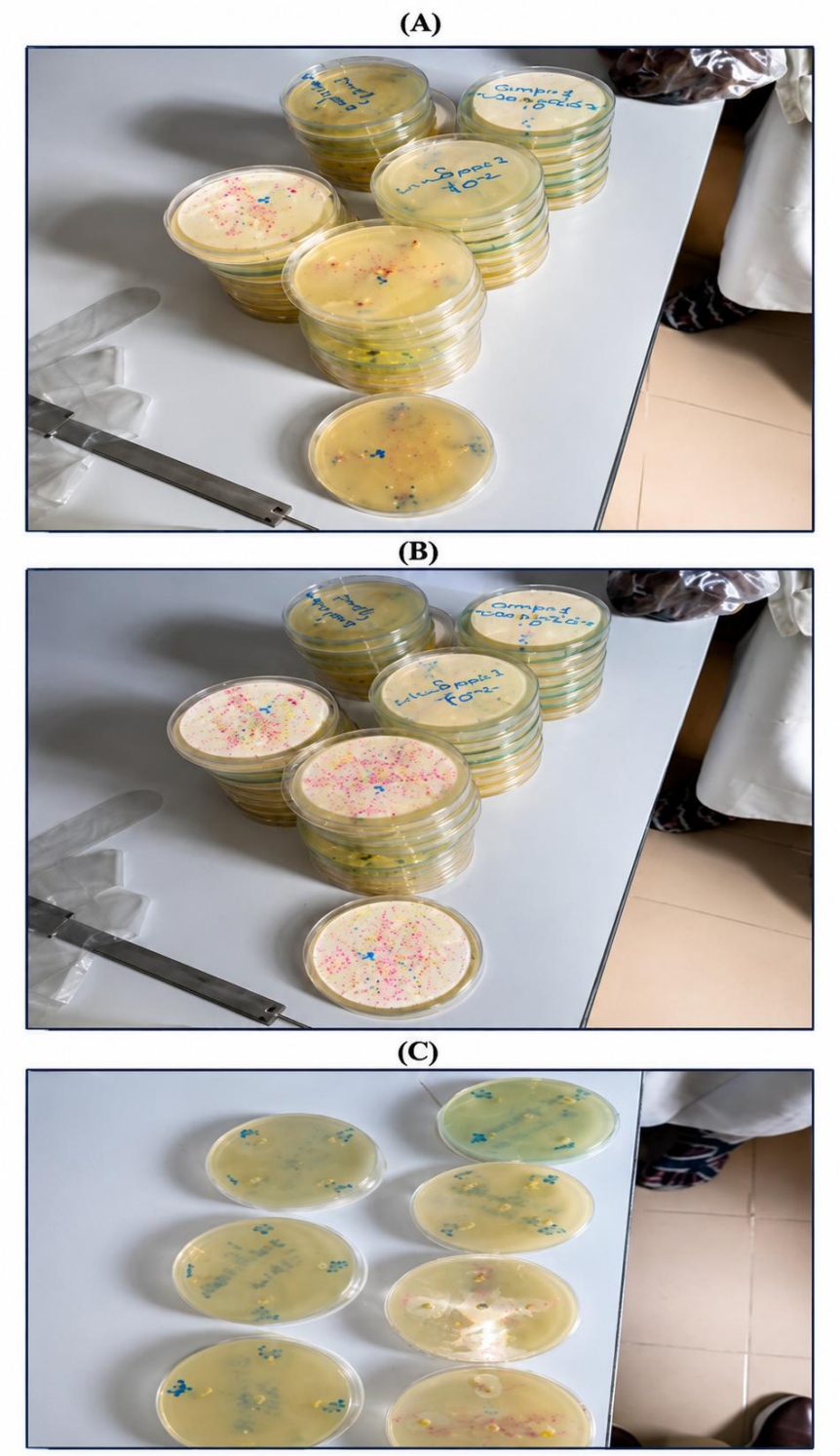

Figure 2 (A–C) Mueller–Hinton agar plates after disk diffusion testing of isolates (including Salmonella Typhi and other foodborne pathogens) recovered from RTE foods. Clear zones around antibiotic disks indicate susceptibility; reduced or absent zones indicate resistance. Plates are labelled with isolate numbers and organism identities as recorded during laboratory analysis.

Table 3. Antimicrobial Susceptibility Profiles of Major Isolates (% Resistant)

Antibiotic	E. coli (n=34)	S. aureus (n=29)	Salmonella (n=19)	K. pneumoniae (n=12)	B. cereus (n=8)
Ampicillin	88	79	84	92	75
Amox–Clav	47	41	37	58	38
Ceftriaxone	29	21	26	42	13
Gentamicin	24	17	21	33	25
Ciprofloxacin	32	28	37	25	13
Tetracycline	71	66	74	67	63
Chloramphenicol	35	31	42	33	25
SXT (Co-trimoxazole)	53	48	58	50	38

Note: Values are percentage of isolates resistant. Amox–Clav = amoxicillin–clavulanate; SXT = trimethoprim–sulfamethoxazole. Overall MDR rate = 58%.

3.4 Association with Observed Hygiene Practices

Observational data indicated that only 38% of catering setups had functional hand-washing stations with soap, and cold-holding facilities were available at fewer than 25% of sites. Samples collected from venues lacking hand-washing facilities had significantly higher mean TVC ($p = 0.012$) and higher odds of pathogen detection (odds ratio 2.4, 95% CI 1.1–5.3). Prolonged ambient holding (>4 h) was also associated with elevated microbial loads.

4. DISCUSSION

This study demonstrates that RTE foods served at public gatherings in Kano State frequently harbour high microbial loads and clinically relevant foodborne pathogens, many of which exhibit multidrug resistance. The mean TVC values, particularly for salads (6.15 log CFU/g) and meat products (5.68 log CFU/g), substantially exceed recommended microbiological criteria for RTE foods in many jurisdictions (FAO/WHO) and align with reports from other Nigerian cities (Okafor-Yarwood et al., 2023; Bichi & Adam, 2024; Meta-analysis…, 2022).

The predominance of Escherichia coli (34%) is a strong indicator of faecal contamination, most likely originating from inadequate hand hygiene of food handlers, contaminated water used for washing vegetables or utensils, or cross-contamination from raw ingredients (WHO, 2015). Staphylococcus aureus (29%) is classically associated with human skin and nasal carriage; its presence points to direct handler contamination and insufficient hand-washing or glove use (Bacterial contaminants…, 2021). Salmonella spp. (19%) raises particular concern because of its low infectious dose and potential for severe systemic infection (Akinyemi et al., 2021; Ekli et al., 2025).

The recovery of Klebsiella pneumoniae and Bacillus cereus further expands the spectrum of risk—the former being an opportunistic pathogen with well-documented resistance

potential and the latter a spore-former capable of producing emetic and diarrhoeal toxins (Okafor-Yarwood et al., 2023).

Resistance patterns observed in this study mirror national and regional trends. High resistance to ampicillin and tetracycline is consistent with the widespread, often unregulated use of these inexpensive antibiotics in both human and animal health in Nigeria (Scoping review…, 2025; Systematic review…, 2023). The 58% MDR rate falls within the range reported for RTE food isolates in other West African studies (Bacterial contaminants…, 2021; Antibiogram…, 2026) and underscores the role of the food chain as a reservoir and potential dissemination route for resistant bacteria (Magiorakos et al., 2012). While ciprofloxacin and gentamicin retained better activity, the presence of resistant phenotypes to these agents is concerning and may foreshadow further erosion of treatment options.

The significant association between poor observed hygiene infrastructure (absence of hand-washing facilities and cold-chain capacity) and higher contamination levels provides actionable evidence. Temporary event catering often operates under resource constraints that compromise basic food-safety controls. Interventions targeting handler training, provision of portable hand-washing stations, and enforcement of temperature-control requirements at large gatherings could substantially reduce risk (WHO, 2015; Odigiri, 2026).

Limitations of the present work include the use of conventional biochemical identification (which may occasionally misclassify closely related species) and the absence of molecular confirmation of virulence or resistance genes. Future studies incorporating 16S rRNA sequencing, whole-genome analysis, and quantification of specific virulence factors would strengthen the evidence base (Okafor-Yarwood et al., 2023; Antibiogram…, 2026). Nevertheless, the combination of quantitative load data, pathogen prevalence, and phenotypic resistance profiles provides a robust local snapshot that can inform public-health action.

5. CONCLUSION

This study provides clear evidence that ready-to-eat foods served at public gatherings in Kano State are frequently of unsatisfactory microbiological quality. Mean total viable counts, especially in salads and meat products, routinely exceeded widely accepted safety thresholds, and pathogenic bacteria of recognized public-health importance Escherichia coli, Staphylococcus aureus, Salmonella spp., Klebsiella pneumoniae, and Bacillus cereus were recovered from a substantial proportion of samples. More than half of the isolates displayed multidrug resistance, indicating that these foods may serve not only as sources of acute foodborne illness but also as vehicles for the community dissemination of antimicrobial-resistant bacteria.

The observed associations between inadequate hand-washing facilities, prolonged ambient holding, and elevated contamination levels highlight practical, modifiable risk factors inherent in temporary mass-catering settings. Collectively, the findings underscore an urgent need for coordinated action by caterers, event organizers, and public-health authorities to safeguard the health of consumers attending social and religious gatherings in the region. Without targeted improvements in hygiene

infrastructure, handler competence, and routine surveillance, the dual threats of foodborne disease and antimicrobial resistance will continue to be amplified at these high-attendance events.

6. RECOMMENDATIONS

1. Mandatory food-hygiene certification and periodic refresher training should be required for all caterers and food handlers serving public events.
2. Event organizers and local authorities should ensure the availability of functional hand-washing stations (with soap and clean water) and adequate cold-holding or hot-holding equipment at all large gatherings.
3. Routine microbiological surveillance of foods from public events should be institutionalized by state and local public-health authorities, with timely feedback provided to caterers.
4. Public awareness campaigns on safe food practices during festivities should be intensified, targeting both consumers and vendors.
5. Further research employing molecular methods is recommended to characterize resistance genes, virulence factors, and the genetic relatedness of isolates circulating in the local food system.

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CONFLICT OF INTEREST

The author declares that there is no conflict of interest.

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