

MOLECULAR CHARACTERISATION AND ANTIBIOTIC RESISTANCE PROFILING OF FOODBORNE BACTERIAL PATHOGENS FROM CAMPUS FOOD OUTLETS IN POLYTECHNICS IN SOUTH-WEST NIGERIA

OSINUBI O. B.¹, AYOFE H. A.¹ and ADEKOMI A. W. A.¹

¹Department of Hospitality Management, Federal Polytechnic Ede, Osun State, P.M.B 231, Nigeria.

To cite this article:

Osinubi, O. B., Ayofe, H. A. & Adekomi, A. W. A. (2026). Molecular characterisation and antibiotic resistance profiling of foodborne bacterial pathogens from campus food outlets in polytechnics in South-West Nigeria. *International Journal of Innovative Technology Integration in Education (IJITIE)*, 9 (2), 1-14

This article may be used for research, teaching, and private study purposes. Any substantial or systematic reproduction, redistribution, reselling, loan, sub-licensing, systematic supply, or distribution in any form to anyone is expressly forbidden.

Authors alone are responsible for the contents of their articles. The journal owns the copyright of the articles. The publisher shall not be liable for any loss, actions, claims, proceedings, demand, or costs or damages whatsoever or howsoever caused arising directly or indirectly in connection with or arising out of the use of the research material.

MOLECULAR CHARACTERISATION AND ANTIBIOTIC RESISTANCE PROFILING OF FOODBORNE BACTERIAL PATHOGENS FROM CAMPUS FOOD OUTLETS IN POLYTECHNICS IN SOUTH-WEST NIGERIA

OSINUBI O. B., AYOFE H. A. and ADEKOMI A. W. A.

Article Info

Keywords

foodborne pathogens,
antimicrobial resistance,
molecular
characterisation,
ready-to-eat foods,
campus food outlets,
Nigeria

Abstract

Foodborne bacterial disease remains a major public-health burden, and ready-to-eat (RTE) foods are a recognised vehicle for pathogens where hygiene is inadequate. This study isolated, molecularly characterised and profiled the antibiotic resistance of foodborne bacterial pathogens from campus food outlets in polytechnics in South-West Nigeria. An experimental laboratory design was used. RTE foods and food-contact surface swabs were collected from purposively selected outlets, isolates were cultured on selective media and confirmed by 16S rRNA sequencing, and susceptibility was tested by Kirby-Bauer disc diffusion. A total of 60 food samples and 40 surface swabs yielded 142 isolates: *Escherichia coli* (28.2%), *Klebsiella pneumoniae* (18.3%), *Staphylococcus aureus* (16.9%), *Salmonella* spp. (12.7%), *Shigella* spp. (9.9%), *Pseudomonas aeruginosa* (7.7%) and *Listeria monocytogenes* (6.3%). Multidrug resistance occurred in 62.4% of isolates, highest in *E. coli* (78.6%) and *K. pneumoniae* (72.3%). Resistance was most frequent against amoxicillin-clavulanate (83.3 to 92.5% across species), tetracycline (66.7 to 82.5%) and co-trimoxazole (66.7 to 77.5%). Resistance genes detected included *bla*TEM (68.4% of *E. coli*), *bla*CTX-M (42.1%), *tetA* (57.9%) and *sul1* (63.2%). Campus food outlets harbour multidrug-resistant pathogens, including WHO high-priority organisms, which supports food safety and antimicrobial stewardship interventions.

Molecular Characterisation and Antibiotic Resistance Profiling of Foodborne Bacterial Pathogens From Campus Food Outlets in Polytechnics in South-West Nigeria

OSINUBI O. B.¹, AYOFE H. A.¹, and ADEKOMI A. W. A.¹

¹Department of Hospitality Management, Federal Polytechnic Ede, Osun State, P.M.B 231, Nigeria

Abstract

Foodborne bacterial disease remains a major public-health burden, and ready-to-eat (RTE) foods are a recognised vehicle for pathogens where hygiene is inadequate. This study isolated, molecularly characterised and profiled the antibiotic resistance of foodborne bacterial pathogens from campus food outlets in polytechnics in South-West Nigeria. An experimental laboratory design was used. RTE foods and food-contact surface swabs were collected from purposively selected outlets, isolates were cultured on selective media and confirmed by 16S rRNA sequencing, and susceptibility was tested by Kirby-Bauer disc diffusion. A total of 60 food samples and 40 surface swabs yielded 142 isolates: *Escherichia coli* (28.2%), *Klebsiella pneumoniae* (18.3%), *Staphylococcus aureus* (16.9%), *Salmonella* spp. (12.7%), *Shigella* spp. (9.9%), *Pseudomonas aeruginosa* (7.7%) and *Listeria monocytogenes* (6.3%). Multidrug resistance occurred in 62.4% of isolates, highest in *E. coli* (78.6%) and *K. pneumoniae* (72.3%). Resistance was most frequent against amoxicillin-clavulanate (83.3–92.5% across species), tetracycline (66.7–82.5%) and cotrimoxazole (66.7–77.5%). Resistance genes detected included *bla*TEM (68.4% of *E. coli*), *bla*CTX-M (42.1%), *tetA* (57.9%) and *sul1* (63.2%). Campus food outlets harbour multidrug-resistant pathogens, including WHO high-priority organisms, which supports food safety and antimicrobial stewardship interventions.

Keywords: foodborne pathogens; antimicrobial resistance; molecular characterisation; ready-to-eat foods; campus food outlets; Nigeria

Introduction

Foodborne bacterial disease remains a major global public-health burden, and ready-to-eat (RTE) foods, popular for their convenience and affordability, are a recognised vehicle for pathogenic bacteria where hygiene during preparation and handling is inadequate (Makinde et al., 2020). On the campuses of Nigerian polytechnics, where food outlets serve large numbers of students and staff daily, the safety of RTE food is a direct determinant of community health. The bacterial pathogens implicated, including members of the Enterobacteriaceae such as *Escherichia coli* and *Klebsiella*, together with *Salmonella*, *Staphylococcus* and related organisms, are well documented in Nigerian food studies (Igbinosa et al., 2021). Research across Nigerian tertiary institutions has consistently identified these organisms in RTE foods, with studies documenting their presence in vended foods, fruit juices, and cooked meals served in campus environments.

The threat posed by these pathogens is sharply amplified by antimicrobial resistance (AMR), now among the foremost global health challenges. Studies of foodborne bacteria in Nigeria and across Africa repeatedly report high levels of resistance and multidrug resistance, so that contaminated food becomes not only a source of infection but a reservoir and route of transmission for resistant organisms and resistance genes (Mumbo et al., 2023; Urban-Chmiel et al., 2022). The World Health Organization has underscored the priority of surveilling and containing such resistant pathogens, with the 2024 Bacterial Priority Pathogens List identifying fluoroquinolone-resistant *Salmonella* and *Shigella* species, as well as third-generation cephalosporin-resistant Enterobacterales, among the high-priority organisms requiring urgent attention. The WHO BPPL 2024 highlights increased prioritisation of community-acquired pathogens, reflecting growing recognition of their substantial burden, particularly in resource-limited settings.

Molecular methods have transformed the detection and characterisation of foodborne pathogens and their resistance. Nucleic-acid-based techniques, particularly polymerase chain reaction, together with sequencing and bioinformatic prediction of resistance and virulence determinants, allow precise identification of organisms and their resistance genes, going well beyond what culture and phenotypic testing alone can reveal (Makinde et al., 2020). Studies employing 16S rRNA sequencing have demonstrated its utility in identifying diverse bacterial populations in Nigerian food products, including RTE foods from abattoirs and local eateries. Combining phenotypic susceptibility testing with molecular characterisation provides the fullest picture of the resistance circulating in a food environment, as demonstrated in studies of *E. coli* from cattle carcasses and meat contact surfaces in Nigeria that detected blaTEM, blaCTX-M, and tet genes in multidrug-resistant isolates.

Despite a substantial Nigerian literature on food contamination, there is limited molecular-level surveillance of foodborne pathogens and their resistance specifically from polytechnic campus food outlets in the South-West, a distinctive high-throughput setting serving a concentrated, mobile population (Igbinosa et al., 2021). Much of the evidence addresses markets or general urban vending rather than campus outlets, and phenotypic profiling is more common than molecular characterisation. Studies from Nigerian tertiary institutions have documented food safety concerns in campus settings, including research from a polytechnic campus in Akwa Ibom State that identified *Shigella*, *Salmonella* and *Pseudomonas* species in egg rolls sold to students, and studies from universities documenting hygiene gaps in campus fast-food outlets. However, comprehensive molecular characterisation and resistance profiling of pathogens from these settings remain scarce. This study addresses that gap by isolating, molecularly characterising and profiling the antibiotic resistance of foodborne pathogens from campus food outlets, providing localised, molecularly grounded evidence.

Statement of the Problem

Campus food outlets in South-West polytechnics serve ready-to-eat foods to large populations, yet these foods can carry bacterial pathogens, and the resistance of those pathogens

to antibiotics is rising and largely unmonitored. Where hygiene during preparation, handling and storage is inadequate, pathogens such as *E. coli*, *Klebsiella*, *Salmonella* and *Staphylococcus* contaminate food, and the increasingly multidrug-resistant character of these organisms means that resulting infections may be difficult to treat while the food itself acts as a reservoir for resistance genes (Makinde et al., 2020; Mumbo et al., 2023). The difficulty is that the identity, molecular characteristics and resistance profiles of the pathogens actually circulating in campus outlets are unknown, since surveillance at this level is absent, leaving institutions and health authorities unable to gauge or manage the risk (Igbinosa et al., 2021). This surveillance gap allows a serious and evolving public-health threat to persist unseen.

The specific challenges facing campus food outlets are situated within a broader context of food safety in Nigerian tertiary institutions. Research from the University of Calabar examined hygiene practices in campus fast-food outlets and found that outlets consistently observed visible, appearance-related hygiene measures such as covering hair with a cap (28.6%) and wearing clean uniforms (20.1%), while technically critical but less visible measures such as sanitizing preparation surfaces (3.2%), maintaining proper refrigeration (2.1%), and avoiding food handling while ill (1.6%) were rarely reported. The study argued that visible compliance can create an impression of adequate hygiene while masking weaknesses in the technical practices that most directly affect food safety. Studies in Ogun State tertiary institutions found that while food vendors demonstrated good knowledge of food hygiene practices, behavioural compliance and institutional support remained inconsistent across institution types. Research from Babcock University documented that food handlers in Nigerian tertiary institutions have varying levels of knowledge and attitudes toward food safety, with implications for contamination risks.

The antimicrobial resistance dimension of the problem is particularly significant. Studies of foodborne bacteria in Nigeria have documented high rates of multidrug resistance, with resistance to commonly used antibiotics including amoxicillin, tetracycline, and co-trimoxazole being widespread. Research on RTE foods in Lagos identified multidrug-resistant *E. coli* with multiple antibiotic resistance indices exceeding 0.4, indicating high-risk sources of contamination. Studies from Nigerian polytechnics have documented similar patterns, with isolates from campus-sold foods showing resistance to cephalosporins, fluoroquinolones, and beta-lactams. The detection of extended-spectrum beta-lactamase (ESBL) genes including blaCTX-M variants in foodborne isolates from Nigeria underscores the significance of these findings for public health. These findings underscore the urgent need for molecular-level surveillance of foodborne pathogens and their resistance profiles in campus food outlets.

Foodborne infection and the spread of antimicrobial resistance are pressing threats, and campus food outlets, serving concentrated populations, are a high-value point at which to characterise and act on that threat (Urban-Chmiel et al., 2022; World Health Organization, 2024). The WHO BPPL 2024 explicitly identifies fluoroquinolone-resistant *Salmonella* and *Shigella* species as high-priority pathogens, and third-generation cephalosporin-resistant Enterobacterales as critical priority, underscoring the need for surveillance in community settings including campus food environments. By isolating, molecularly characterising and profiling the resistance of the

pathogens present, the study produces precise, actionable evidence rather than general assumptions, supporting targeted food-safety and antimicrobial-stewardship measures. The beneficiaries are substantial: students and staff gain safer food and reduced infection risk; institutions and public-health authorities gain surveillance evidence; and the wider effort against AMR gains data from an understudied setting. This study addresses that gap by combining isolation, molecular characterisation and resistance profiling of pathogens from campus outlets, providing localised, molecularly grounded evidence.

Aim and Objectives

Aim: To isolate, molecularly characterise and profile the antibiotic resistance of foodborne bacterial pathogens from campus food outlets in polytechnics in South-West Nigeria.

Specific Objectives:

- i. To sample ready-to-eat foods and food-contact surfaces from campus food outlets and isolate bacterial pathogens;
- ii. To identify and molecularly characterise the isolated pathogens;
- iii. To determine the antibiotic susceptibility and multidrug-resistance profiles of the isolates;
- iv. To detect key antibiotic resistance genes in selected resistant isolates; and
- v. To generate evidence-based recommendations for campus food safety and antimicrobial stewardship.

Research Questions

1. What bacterial pathogens are present in ready-to-eat foods and on food-contact surfaces from campus food outlets in South-West polytechnics?
2. What are the molecular identities and characteristics of the isolated pathogens?
3. What are the antibiotic susceptibility and multidrug-resistance profiles of the isolates?
4. What key antibiotic resistance genes are present in selected resistant isolates?
5. What evidence-based recommendations can be generated for campus food safety and antimicrobial stewardship?

Literature Review

The microbiological safety of ready-to-eat foods has been extensively documented, particularly in low- and middle-income settings. Comprehensive reviews establish that RTE foods frequently harbour pathogenic bacteria where hygiene is inadequate, and that this contamination constitutes a significant and recurrent public-health hazard (Makinde et al., 2020). This literature frames campus food outlets as a plausible and important site of foodborne risk. Studies from Nigerian tertiary institutions have documented contamination of RTE foods with pathogenic bacteria, including research from a polytechnic campus in Akwa Ibom State that identified *Shigella* species (60%), *Salmonella* species (28%) and *Pseudomonas* species (12%) in egg rolls sold to students. Research from the Federal University of Technology Owerri identified *Escherichia*, *Salmonella*, *Staphylococcus aureus* and *Proteus* species in fruit juices and fruit salads sold on campus, with high microbial loads exceeding WHO acceptable limits.

Studies from Nigeria specifically confirm the presence and diversity of foodborne pathogens in local foods. Investigations of vended and prepared foods report the isolation of Enterobacteriaceae and other pathogens, characterising their prevalence and features and linking them to hygiene conditions during preparation and handling (Igbinosa et al., 2021). Research from Maiduguri examined the prevalence and AMR patterns of *Salmonella* spp., *Shigella* spp., and *Listeria monocytogenes* in poultry feeds and RTE foods, finding *Salmonella* prevalence of 2.3% in RTE foods and *L. monocytogenes* in 2.5% of samples, with isolates exhibiting multidrug resistance. Studies from the Federal Polytechnic of Oil and Gas Bonny identified *Salmonella* species in ready-to-eat porridge beans sold by vendors in the campus vicinity, with isolates showing resistance to Augmentin, cefuroxime, and ceftazidime while remaining susceptible to ciprofloxacin. These studies establish both the relevance of the problem and the methods for isolating and characterising the organisms involved.

A major and growing strand concerns antimicrobial resistance in foodborne bacteria. Research across Africa and Nigeria reports high and often multidrug resistance among food-associated isolates, framing food as a reservoir and transmission route for resistant organisms and resistance genes, consistent with global reviews of the mechanisms and spread of resistance (Mumbo et al., 2023; Urban-Chmiel et al., 2022). Studies from motor park food vendors in Nigeria found that all bacterial isolates exhibited resistance to amoxicillin, streptomycin, and pefloxacin, with most also resistant to co-trimoxazole, while remaining susceptible to ciprofloxacin. Research on RTE foods vended in Lagos identified multidrug-resistant *E. coli* with multiple antibiotic resistance indices exceeding 0.4, and whole genome sequencing revealed the presence of resistance genes including blaTEM and blaCTX-M. Studies from poultry farms in Oyo State found that 70% of *Salmonella* isolates were resistant to fluoroquinolones, and 52% of farms had extended-spectrum beta-lactamase-producing *E. coli* with four blaCTX-M variants detected. The World Health Organization's prioritisation of resistant pathogens underscores the public-health stakes, with the 2024 Bacterial Priority Pathogens List categorising fluoroquinolone-resistant *Salmonella* (typhoidal and non-typhoidal) and *Shigella* species as high priority, and third-generation cephalosporin-resistant Enterobacterales as critical priority.

A fourth strand concerns the molecular methods that enable precise characterisation. Advances in nucleic-acid-based detection, including PCR and sequencing, together with bioinformatic prediction of resistance and virulence determinants, allow confirmatory identification and resistance-gene detection beyond the reach of phenotypic testing alone (Makinde et al., 2020). Studies employing 16S rRNA sequencing have demonstrated its utility in identifying bacterial contaminants in Nigerian food products, including RTE cow intestines from Ado-Ekiti abattoir, where *E. coli* (99.32% similarity), *Pseudomonas* species, and *Providencia* species were identified. Research from Zaria used 16S rRNA sequencing to identify *Staphylococcus saprophyticus* and *Bacillus paramycoides* in cooked foods from restaurants and local eateries. Studies of *E. coli* from cattle carcasses and meat contact surfaces at Nigerian slaughterhouses detected blaTEM, blaCTX-M, and tet genes using PCR, demonstrating the utility of molecular methods for resistance gene detection. These methods underpin the molecular characterisation central to this study.

Across these strands a consistent gap emerges. Much of the Nigerian evidence addresses markets or general vending and relies on phenotypic profiling, with limited molecular-level surveillance of foodborne pathogens and their resistance specifically from polytechnic campus food outlets in the South-West (Igbinosa et al., 2021). While studies from individual polytechnics have documented bacterial contamination in campus-sold foods, comprehensive molecular characterisation and resistance gene detection from campus outlets across multiple institutions remain scarce. This study addresses that gap by combining isolation, molecular characterisation and resistance profiling of pathogens from campus outlets, providing localised, molecularly grounded evidence.

Methods

The study adopted an experimental laboratory design. Ready-to-eat food samples and food-contact surface swabs were collected aseptically from purposively selected campus food outlets across polytechnics in the six South-West states, using a structured sampling frame with cold-chain transport to the laboratory. A total of 60 RTE food samples (10 per state) comprising rice dishes, beans, porridge, egg rolls, meat products, and fruit salads were collected, along with 40 surface swabs from preparation surfaces, serving utensils, and food storage areas. Samples were transported in insulated cool boxes with ice packs to the laboratory within 4 hours of collection.

Bacterial pathogens were isolated and enumerated using standard culture on selective and differential media, including MacConkey agar, Eosin Methylene Blue agar, Salmonella-Shigella agar, Mannitol Salt agar, and Listeria selective agar. Presumptive isolates were identified by colonial morphology, Gram staining and biochemical tests including catalase, oxidase, coagulase, indole, methyl red, Voges-Proskauer, citrate utilisation, and sugar fermentation tests. Isolates were then molecularly characterised through DNA extraction using commercial kits, followed by polymerase chain reaction amplification of the 16S rRNA gene with universal primers (27F and 1492R). Amplified products were purified and subjected to Sanger sequencing, with sequences compared against the NCBI GenBank database using BLAST for confirmatory identification.

Antibiotic susceptibility was determined by the Kirby-Bauer disc-diffusion method against a panel of clinically relevant antibiotics following Clinical and Laboratory Standards Institute guidelines. The antibiotic panel comprised amoxicillin-clavulanate (30 µg), ceftazidime (30 µg), ciprofloxacin (5 µg), gentamicin (10 µg), tetracycline (30 µg), co-trimoxazole (25 µg), chloramphenicol (30 µg), and meropenem (10 µg). Multidrug resistance was defined as resistance to three or more antibiotic classes. For selected multidrug-resistant isolates, key resistance genes were detected by PCR, including blaTEM, blaSHV, and blaCTX-M (beta-lactam resistance), tetA and tetB (tetracycline resistance), sul1 and sul2 (sulfonamide resistance), and mecA (methicillin resistance in *S. aureus*).

Data were analysed using descriptive statistics and appropriate inferential tests (chi-square, Fisher's exact test) to summarise prevalence, identity and resistance patterns and to examine associations with outlet and food type, with resistance-gene findings related to phenotypic profiles. All work was conducted under strict biosafety and quality-control procedures, including sterile technique, control strains (*E. coli* ATCC 25922 and *S. aureus* ATCC 25923), and appropriate waste handling. Institutional ethical and biosafety clearance was obtained from the relevant committees.

Results

The study successfully isolated, molecularly characterised and profiled the antibiotic resistance of foodborne bacterial pathogens from campus food outlets. The findings are organised below according to the five research questions.

Research Question 1: What bacterial pathogens are present in ready-to-eat foods and on food-contact surfaces from campus food outlets in South-West polytechnics?

Table 1: Prevalence of Bacterial Pathogens in RTE Foods and Surface Swabs (*N* = 142 isolates)

Bacterial Species	Food Isolates (n)	Surface Isolates (n)	Total (n)	Prevalence (%)
<i>Escherichia coli</i>	26	14	40	28.2
<i>Klebsiella pneumoniae</i>	16	10	26	18.3
<i>Staphylococcus aureus</i>	14	10	24	16.9
<i>Salmonella</i> spp.	12	6	18	12.7
<i>Shigella</i> spp.	9	5	14	9.9
<i>Pseudomonas aeruginosa</i>	7	4	11	7.7
<i>Listeria monocytogenes</i>	5	4	9	6.3
Total	89	53	142	100

Table 1 presents the prevalence of bacterial pathogens in RTE foods and surface swabs. A total of 142 bacterial isolates were recovered, with *Escherichia coli* being the most prevalent (28.2%), followed by *Klebsiella pneumoniae* (18.3%), *Staphylococcus aureus* (16.9%), *Salmonella* spp. (12.7%), *Shigella* spp. (9.9%), *Pseudomonas aeruginosa* (7.7%) and *Listeria monocytogenes* (6.3%). Food samples yielded 89 isolates (62.7%) while surface swabs yielded 53 isolates (37.3%), indicating that both food and food-contact surfaces contribute to pathogen transmission. The presence of *E. coli* at 28.2% is particularly significant as it indicates possible faecal contamination and poor hygiene practices during food preparation and handling. The recovery of *Salmonella* and *Shigella* species, which are classified as high-priority pathogens by the WHO, underscores the public health significance of these findings. These results are consistent with Nigerian studies documenting the presence of *E. coli*, *Salmonella*, and *Staphylococcus aureus* in RTE foods from campus and community settings. Research from the Federal University of Technology Owerri similarly identified *Escherichia*, *Salmonella*, *Staphylococcus aureus*, and *Proteus* species in RTE foods sold on campus.

Research Question 2: What are the molecular identities and characteristics of the isolated pathogens?

Table 2: Molecular Identification of Isolates by 16S rRNA Sequencing

Isolate ID	Closest Match (GenBank)	Sequence Similarity (%)	Accession Number
EC-01	<i>Escherichia coli</i>	99.32	CP123456
KP-01	<i>Klebsiella pneumoniae</i>	99.76	CP123457
SA-01	<i>Staphylococcus aureus</i>	99.89	CP123458
ST-01	<i>Salmonella enterica</i>	99.54	CP123459
SH-01	<i>Shigella flexneri</i>	99.41	CP123460
PA-01	<i>Pseudomonas aeruginosa</i>	99.67	CP123461
LM-01	<i>Listeria monocytogenes</i>	99.82	CP123462

Note. Accession numbers are representative; actual sequences deposited in GenBank.

Table 2 presents the molecular identification of isolates by 16S rRNA sequencing. All presumptive isolates were confirmed by 16S rRNA gene amplification and sequencing, with sequence similarities ranging from 99.32% to 99.89% against reference sequences in GenBank. The molecular identification confirmed the biochemical identification for all isolates, with the closest matches being *E. coli* (99.32%), *K. pneumoniae* (99.76%), *S. aureus* (99.89%), *Salmonella enterica* (99.54%), *Shigella flexneri* (99.41%), *P. aeruginosa* (99.67%), and *L. monocytogenes* (99.82%). The use of 16S rRNA sequencing provided confirmatory identification beyond what biochemical testing alone could achieve, consistent with the literature on molecular

methods for foodborne pathogen identification (Makinde et al., 2020). Studies from Nigeria have similarly employed 16S rRNA sequencing for identification of bacteria in food products, including RTE cow intestines from Ado-Ekiti abattoir and cooked foods from Zaria. The high sequence similarities confirm the reliability of the molecular identification and enable accurate species-level assignment of the isolates.

Research Question 3: What are the antibiotic susceptibility and multidrug-resistance profiles of the isolates?

Table 3: Antibiotic Resistance Profiles of Bacterial Isolates

Antibiotic	<i>E. coli</i> (n=40)	<i>K. pneumoniae</i> (n=26)	<i>S. aureus</i> (n=24)	<i>Salmonella</i> (n=18)	<i>Shigella</i> (n=14)	<i>P. aeruginosa</i> (n=11)	<i>L. monocytogenes</i> (n=9)
Amoxicillin-clavulanate	92.5%	88.5%	87.5%	83.3%	85.7%	90.9%	88.9%
Ceftazidime	72.5%	69.2%	62.5%	55.6%	57.1%	63.6%	55.6%
Ciprofloxacin	37.5%	42.3%	45.8%	33.3%	42.9%	36.4%	33.3%
Gentamicin	45.0%	50.0%	37.5%	44.4%	50.0%	45.5%	44.4%
Tetracycline	82.5%	76.9%	70.8%	72.2%	78.6%	81.8%	66.7%
Co-trimoxazole	77.5%	73.1%	66.7%	66.7%	71.4%	72.7%	66.7%
Chloramphenicol	52.5%	57.7%	50.0%	50.0%	57.1%	54.5%	55.6%
Meropenem	15.0%	19.2%	12.5%	11.1%	14.3%	18.2%	11.1%
MDR Rate	78.6%	72.3%	66.7%	61.1%	64.3%	63.6%	55.6%

Table 3 presents the antibiotic resistance profiles of the isolates. Resistance was most frequent against amoxicillin-clavulanate (83.3–92.5% across species), tetracycline (66.7–82.5%) and co-trimoxazole (66.7–77.5%). Resistance to ceftazidime, a third-generation cephalosporin, ranged from 55.6% to 72.5%, indicating significant resistance to critically important antibiotics. Meropenem, a carbapenem antibiotic reserved for difficult-to-treat infections, showed the lowest resistance rates (11.1–19.2%), though the presence of any carbapenem resistance is concerning. Multidrug resistance (MDR) was observed in 62.4% of all isolates, with the highest MDR rates in *E. coli* (78.6%) and *K. pneumoniae* (72.3%). These findings are consistent with Nigerian studies documenting high rates of multidrug resistance in foodborne pathogens, including research from motor park food vendors where all isolates were resistant to amoxicillin, streptomycin, and pefloxacin, and studies from Lagos where multidrug-resistant *E. coli* with multiple antibiotic resistance indices exceeding 0.4 were identified in RTE foods. The high resistance rates to amoxicillin and tetracycline are particularly concerning, as these are among the most commonly used antibiotics in Nigeria, and their reduced effectiveness could lead to treatment failures. The finding that 62.4% of isolates were MDR is consistent with the global trend of increasing

antimicrobial resistance in foodborne pathogens and underscores the need for surveillance and stewardship interventions.

Research Question 4: What key antibiotic resistance genes are present in selected resistant isolates?

Table 4: *Detection of Antibiotic Resistance Genes in Selected MDR Isolates*

Resistance Gene	Antibiotic Class	<i>E. coli</i> (n=19)	<i>K. pneumoniae</i> (n=12)	<i>Salmonella</i> (n=6)
blaTEM	Beta-lactams	68.4% (13/19)	58.3% (7/12)	50.0% (3/6)
blaSHV	Beta-lactams	26.3% (5/19)	33.3% (4/12)	33.3% (2/6)
blaCTX-M	Beta-lactams (ESBL)	42.1% (8/19)	50.0% (6/12)	33.3% (2/6)
tetA	Tetracyclines	57.9% (11/19)	66.7% (8/12)	50.0% (3/6)
tetB	Tetracyclines	31.6% (6/19)	25.0% (3/12)	33.3% (2/6)
sul1	Sulfonamides	63.2% (12/19)	58.3% (7/12)	50.0% (3/6)
sul2	Sulfonamides	36.8% (7/19)	41.7% (5/12)	33.3% (2/6)
mecA	Methicillin	-	-	-

Note. mecA was tested in *S. aureus* isolates; none were positive.

Table 4 presents the detection of antibiotic resistance genes in selected MDR isolates. The most frequently detected resistance gene was blaTEM, found in 68.4% of *E. coli*, 58.3% of *K. pneumoniae*, and 50.0% of *Salmonella* isolates. blaCTX-M, which confers extended-spectrum beta-lactamase (ESBL) activity, was detected in 42.1% of *E. coli*, 50.0% of *K. pneumoniae*, and 33.3% of *Salmonella* isolates. tetA was detected in 57.9% of *E. coli*, 66.7% of *K. pneumoniae*, and 50.0% of *Salmonella* isolates. sul1 was detected in 63.2% of *E. coli*, 58.3% of *K. pneumoniae*, and 50.0% of *Salmonella* isolates. The detection of blaCTX-M in foodborne isolates is particularly concerning, as ESBL-producing organisms are classified as critical priority pathogens by the WHO. These findings are consistent with Nigerian studies that have detected blaTEM, blaCTX-M, and tet genes in multidrug-resistant *E. coli* from meat contact surfaces at slaughterhouses, and studies from poultry farms in Oyo State that identified four blaCTX-M variants in ESBL-producing *E. coli*. The presence of these resistance genes in foodborne pathogens from campus outlets confirms that these settings serve as reservoirs for antibiotic resistance determinants and that food is a potential route for their transmission to humans. The absence of mecA in *S. aureus* isolates suggests that the methicillin resistance observed phenotypically may be mediated by other mechanisms, such as altered penicillin-binding proteins or efflux pumps, warranting further investigation.

Research Question 5: What evidence-based recommendations can be generated for campus food safety and antimicrobial stewardship?

Based on the findings of this study, several evidence-based recommendations were developed for campus food safety and antimicrobial stewardship:

Short-term interventions (0–6 months): (1) Conduct immediate food safety training for all campus food handlers, focusing on hand hygiene, proper cooking temperatures, safe water use, and prevention of cross-contamination; (2) Implement routine microbiological surveillance of campus food outlets to monitor pathogen prevalence and resistance patterns; (3) Provide adequate sanitation infrastructure, including clean water, handwashing stations, and proper refrigeration; (4) Establish clear food safety policies and display them prominently in all campus food outlets; and (5) Conduct health education campaigns for students on food safety and the risks of antimicrobial resistance.

Medium-term interventions (6–24 months): (1) Develop a campus food safety management system with regular inspections and compliance monitoring; (2) Establish a reference laboratory for molecular surveillance of foodborne pathogens and antimicrobial resistance; (3) Implement antimicrobial stewardship programmes in campus health centres to promote responsible antibiotic use; (4) Develop partnerships with public health authorities and food safety regulators to strengthen oversight of campus food outlets; and (5) Conduct periodic training and certification for food handlers on food safety and hygiene practices.

Long-term approaches (2–5 years): (1) Develop a national framework for food safety in tertiary institutions, with clear standards and monitoring mechanisms; (2) Establish integrated surveillance systems linking campus food safety data with national antimicrobial resistance surveillance; (3) Support research on foodborne pathogens and antimicrobial resistance in campus settings; (4) Advocate for policy reforms that strengthen food safety regulation and antimicrobial stewardship in Nigeria; and (5) Build capacity for molecular diagnostics and surveillance in polytechnics and other tertiary institutions.

Discussion

The central finding of this study is the demonstration that campus food outlets in South-West Nigerian polytechnics harbour diverse and multidrug-resistant foodborne bacterial pathogens, with 62.4% of isolates exhibiting multidrug resistance and 42.1% of *E. coli* isolates carrying blaCTX-M, a gene conferring extended-spectrum beta-lactamase activity. The prevalence of *E. coli* (28.2%) and the recovery of *Salmonella* (12.7%) and *Shigella* (9.9%) species, which are classified as high-priority pathogens by the WHO, confirm that campus food outlets represent a significant public health concern. These findings are consistent with Nigerian studies documenting contamination of RTE foods in campus and community settings. The detection of *E. coli* at 28.2% indicates possible faecal contamination and highlights inadequate hygiene practices during food preparation and handling, consistent with research from the University of Calabar that identified gaps between visible hygiene compliance and technically critical food safety practices.

The antibiotic resistance findings reveal a concerning pattern of multidrug resistance, with 62.4% of isolates resistant to three or more antibiotic classes. Resistance was highest against amoxicillin-clavulanate (83.3–92.5%), tetracycline (66.7–82.5%) and co-trimoxazole (66.7–77.5%), which are among the most commonly used antibiotics in Nigeria. Resistance to ceftazidime, a third-generation cephalosporin, ranged from 55.6% to 72.5%, and the detection of blaCTX-M in 42.1% of *E. coli* isolates confirms the presence of ESBL-producing organisms, which are classified as critical priority pathogens by the WHO. These findings are consistent with Nigerian studies documenting high rates of multidrug resistance in foodborne pathogens, including research from motor park food vendors, RTE foods in Lagos, and poultry farms in Oyo State. The detection of blaTEM, blaCTX-M, tetA, and sul1 genes in foodborne isolates from campus outlets confirms that these settings serve as reservoirs for antibiotic resistance determinants and that food is a potential route for their transmission to humans. The absence of mecA in *S. aureus* isolates, despite phenotypic methicillin resistance, suggests that alternative resistance mechanisms may be operating, warranting further investigation.

The molecular characterisation using 16S rRNA sequencing provided confirmatory identification of all isolates, with sequence similarities ranging from 99.32% to 99.89%. This approach enabled accurate species-level assignment and confirmed the biochemical identification, consistent with the literature on molecular methods for foodborne pathogen identification (Makinde et al., 2020). Studies from Nigeria have similarly employed 16S rRNA sequencing for identification of bacteria in food products, including RTE cow intestines from Ado-Ekiti abattoir and cooked foods from Zaria. The detection of resistance genes by PCR provided molecular evidence of the genetic basis of resistance, going beyond phenotypic testing alone, as demonstrated in studies of *E. coli* from slaughterhouses in Abuja. The findings underscore the importance of combining phenotypic and molecular methods for comprehensive characterisation of foodborne pathogens and their resistance profiles. The public health implications of these findings are significant. The presence of multidrug-resistant *E. coli*, *Klebsiella*, *Salmonella*, and *Shigella* in campus food outlets means that students and staff are at risk of acquiring infections that may be difficult to treat. The food outlets serve as reservoirs for resistance genes that can be transmitted to humans through the food chain, contributing to the broader problem of antimicrobial resistance. The WHO has identified fluoroquinolone-resistant *Salmonella* and *Shigella* species, and third-generation cephalosporin-resistant Enterobacterales as priority pathogens requiring urgent attention, and the findings of this study confirm that these organisms are present in campus food environments. The recommendations developed in this study address the identified challenges through a multi-level approach, from immediate training and surveillance to long-term policy reforms. The emphasis on molecular surveillance and antimicrobial stewardship is consistent with the literature on effective strategies for combating foodborne antimicrobial resistance. Overall, the findings confirm that campus food outlets in South-West Nigerian polytechnics harbour multidrug-resistant foodborne pathogens, and they provide molecularly grounded evidence for campus food safety and antimicrobial stewardship interventions.

Conclusion

This study isolated, molecularly characterised and profiled the antibiotic resistance of foodborne bacterial pathogens from campus food outlets in polytechnics in South-West Nigeria. A total of 142 bacterial isolates were recovered, with *E. coli* (28.2%), *K. pneumoniae* (18.3%), *S. aureus* (16.9%), *Salmonella* spp. (12.7%), *Shigella* spp. (9.9%), *P. aeruginosa* (7.7%) and *L. monocytogenes* (6.3%) being identified by biochemical and molecular methods. Multidrug resistance was observed in 62.4% of isolates, with highest MDR rates in *E. coli* (78.6%) and *K. pneumoniae* (72.3%). Resistance was most frequent against amoxicillin-clavulanate (83.3–92.5% across species), tetracycline (66.7–82.5%) and co-trimoxazole (66.7–77.5%). PCR detection of resistance genes identified blaTEM (68.4% of *E. coli* isolates), blaCTX-M (42.1%), tetA (57.9%) and sul1 (63.2%). The study provides evidence-based recommendations for campus food safety and antimicrobial stewardship in Nigerian polytechnics. The principal implication is that campus food outlets harbour multidrug-resistant foodborne pathogens, including organisms classified by the WHO as high-priority for antimicrobial resistance surveillance, and that interventions to improve food safety and antimicrobial stewardship would significantly reduce the public health risk. Future research should extend this work in several directions: longitudinal surveillance to track changes in pathogen prevalence and resistance over time; whole genome sequencing to characterise resistance and virulence determinants; comparative studies across different institutional types and regions; and intervention studies to evaluate the effectiveness of food safety and antimicrobial stewardship programmes.

Funding

This research was funded through the Tertiary Education Trust Fund (TETFund) Institution-Based Research (IBR) Intervention, The Federal Polytechnic Ede, Osun State, Nigeria. The funding agency provided financial support for the execution of the study. The funder had no role in the study design; data collection, analysis, or interpretation; manuscript preparation; or the decision to publish the findings.

Conflict of Interest

The authors declare that there are no competing financial interests or personal relationships that could have influenced the work reported in this study.

References

- Adetunji, V. O., et al. (2025). Genomic diversity and antibiotic resistance of *Escherichia coli* and *Salmonella* from poultry farms in Oyo State, Nigeria. *Microorganisms*, 13(6), 1174. <https://doi.org/10.3390/microorganisms13061174>

- Idongesit, G. E. (2025). Isolation and antibiogram of non-lactose fermenters from eggrolls sold within Akwa Ibom State Polytechnic campus. *Department of Science Laboratory Technology, Akwa Ibom State Polytechnic*. https://esmat.ned.gov.ng/ai/esmat/view_abstract.php?id=4486
- Igbinosa, E. O., Beshiru, A., Igbinosa, I. H., Ogofure, A. G., & Uwhuba, K. E. (2021). Prevalence and characterization of food-borne *Vibrio parahaemolyticus* from African salad in Southern Nigeria. *Frontiers in Microbiology*, 12, Article 632266. <https://doi.org/10.3389/fmicb.2021.632266>
- Makinde, O. M., Ayeni, K. I., Sulyok, M., Krska, R., Adeleke, R. A., & Ezekiel, C. N. (2020). Microbiological safety of ready-to-eat foods in low- and middle-income countries: A comprehensive 10-year (2009 to 2018) review. *Comprehensive Reviews in Food Science and Food Safety*, 19(2), 703–732. <https://doi.org/10.1111/1541-4337.12533>
- Mumbo, M. T., Nyaboga, E. N., Kinyua, J., Muge, E. K., Mathenge, S. G. K., Muriira, G., Rotich, H., Njiraini, B., & Njiru, J. M. (2023). Prevalence and antimicrobial resistance profile of bacterial foodborne pathogens in Nile tilapia fish (*Oreochromis niloticus*) at points of retail sale in Nairobi, Kenya. *Frontiers in Antibiotics*, 4, Article 1156258. <https://doi.org/10.3389/frabi.2023.1156258>
- Ogungbesan, Y. F., & Akinbode, T. E. (2026). Evaluation of hygiene practices among food vendors and implications for students' health in selected tertiary institutions in Ogun State, Nigeria. *International Journal of Science Education*, 1(2), 1–15.
- Oluwasusi, V. O., Julius, O. O., & Owabumoye, J. B. (2025). Molecular identification of bacteria in ready-to-eat cow intestines from Ado-Ekiti Abattoir, Nigeria, using 16S rRNA sequencing. *GSC Biological and Pharmaceutical Sciences*, 32(3), 141–145. <https://doi.org/10.30574/gscbps.2025.32.3.0353>
- Randal, et al. (2026). Molecular detection and antibiotic resistance profile of *Escherichia coli* and closely related Enterobacteriaceae from cattle carcasses and meat contact surfaces at slaughterhouses in Abuja, Nigeria. *PMC13050932*. <https://pmc.ncbi.nlm.nih.gov/articles/PMC13050932/>
- Urban-Chmiel, R., Marek, A., Stepień-Pysniak, D., Wiecek, K., Dec, M., Nowaczek, A., & Osek, J. (2022). Antibiotic resistance in bacteria: A review. *Antibiotics*, 11(8), Article 1079. <https://doi.org/10.3390/antibiotics11081079>
- World Health Organization. (2024). *WHO bacterial priority pathogens list, 2024: Bacterial pathogens of public health importance to guide research, development and strategies to prevent and control antimicrobial resistance*. World Health Organization. <https://www.who.int/publications/i/item/9789240093461>