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Foodborne Pathogens and Antibiotic Resistance in School Meals: Implications for Public Health

Shamsudeen Muhammad Muhammad[1], Farida Abubakar Tomo[1], Lauratu Samaila Mungadi[1]
[1]Department of Microbiology, Kebbi State University of Science and Technology, Aliero, Nigeria
Corresponding Author: Shamsudeen Muhammad Muhammad; Email: deenshams2000@gmail.com

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ABSTRACT

Food safety is a critical public health concern, particularly in school feeding programs, where improper handling and contamination pose significant health risks. This study investigates the bacteriological quality and antibiotic susceptibility patterns of *Escherichia coli* isolates from food samples obtained from two boarding schools in Zuru, Kebbi State, Nigeria. A total of 12 food samples were analyzed for microbial contamination, with Total Plate Count (TPC), Coliform Count, and *Salmonella* Count determined using standard bacteriological methods. The antibiotic susceptibility patterns of *E. coli* isolates were assessed using the disk diffusion method. The TPC ranged from 2.6×10^3 to 5.6×10^4 cfu/g in FSTC Zuru and 2.5×10^3 to 8.0×10^3 cfu/g in GSTC Zuru. Coliform counts ranged from 2.0×10^2 to 9.3×10^2 cfu/g, while *Salmonella* counts varied between 1.0×10^1 and 4.0×10^1 cfu/g. *Escherichia coli*, *Salmonella*, *Shigella*, *Staphylococcus aureus*, and *Klebsiella pneumoniae* were identified among the isolates, with *E. coli* and *Salmonella* each accounting for 33.3% of isolates. Antibiotic susceptibility testing of *E. coli* isolates revealed high resistance to Amikacin (100%), Streptomycin (75%), and Tetracycline (62.5%), while full susceptibility was observed for Gentamicin and Cefotaxime (100%). These findings highlight the microbial risks associated with school feeding programs and the prevalence of antibiotic-resistant bacteria, emphasizing stringent food safety measures, improved hygiene practices, and routine surveillance to mitigate foodborne infections and the spread of resistant pathogens.

INTRODUCTION

Assessing the safety and security of food is a critical concern today, as it serves as the primary source of energy and nutrition for all living organisms, including humans, animals, and even plants (FAO, IFAD, UNICEF, 2022). Multiple factors, physical, chemical, and biological, play a role in the notable decline in the quality of different foods and food products. Among these, biological factors are particularly critical, as they involve pathogenic microorganisms that are directly responsible for foodborne infections and intoxications (Novais et al., 2022). Providing safe food for school-age children and adolescents is a top priority for governments and other stakeholders. This effort supports the health, growth, and development of the target population, thereby promoting consistent educational engagement, especially in developing countries (Ababio et al., 2016).

School Feeding Programs (SFPs) have been increasingly adopted in developing countries, particularly in regions severely affected by childhood hunger and malnutrition. These initiatives aim to enhance students' concentration and learning abilities by providing meals during school hours, thus addressing short-term hunger that can negatively impact academic performance (Dada et al., 2024). School feeding programs have the potential to go beyond alleviating hunger by also improving school attendance, boosting academic performance, and delivering a range of benefits related to health, nutrition, and social protection (Adelman et al., 2008; Drake et al., 2017).

Escherichia coli is a Gram-negative, non-spore-forming bacterium that is typically motile due to peritrichous flagella. It naturally inhabits the intestinal tracts of humans and other warm-blooded animals. E. coli can grow within a temperature range of 8 to 44.5°C, with optimal growth occurring between 30 and 42°C. Its preferred pH range for development lies between 5.5 and 7.5. (Basavaraju & Gunashree, 2022; Percival & Williams, 2014). Contamination by *E. coli* typically arises from direct or indirect exposure to fecal matter. Poor hygiene and sanitation practices during the processes of growing, harvesting, transporting, and serving food are common contributors to *E. coli* contamination (Ekici & Dümen, 2019).

If not properly handled, food prepared as part of school feeding programs can serve as a source of foodborne illnesses and poisoning. Recently, cases of foodborne diseases, including typhoid fever, diarrhea, dehydration, and other intestinal infections, have been linked to the consumption of contaminated food. It is well established that poor hygiene in food preparation and serving environments facilitates the growth and spread of pathogenic microorganisms, significantly increasing the risk of illness. (Bawah et al., 2018; Ehuwa et al., 2021). Numerous risk factors associated with the food service environment contribute to occurrences of foodborne illness. These include poor personal hygiene practices, insufficient sanitization of surfaces or equipment, cross-contamination of prepared food with contaminated ingredients, and inadequate temperature control measures (Valero et al., 2016). In its 2023 update, the World Health Organization revealed that one in ten people worldwide falls ill from contaminated food each year, affecting all countries. This contamination leads to over 200 diseases caused by consuming food contaminated with bacteria, viruses, parasites, or chemical substances like heavy metals. Children under 5 make up 9 percent of the population but carry 40 percent of the foodborne disease burden (WHO & FAO, 2023). Suspected food poisoning-related deaths have become increasingly common across Nigeria, claiming the lives of many and impacting numerous families. Although many incidents remain unreported, available data indicate dozens of fatalities associated with foodborne illnesses. Pathogens of major public health concern, such as *Escherichia coli*, *Salmonella*, *Shigella*, *Staphylococcus aureus*, and *Clostridium* species, have been identified in fresh-cut, ready-to-eat fruits, vegetables, and prepared foods sold in a wide range of settings, including street markets, schools, urban centers, and fast-food outlets throughout the country (Ajiboye & Emmanuel, 2021; Christopher MA et al., 2022; Muhammad et al., 2016; Odo et al., 2021; Onyeneho & Hedberg, 2013; Yusuf et al., 2019).

Although previous research has explored microbial contamination and antibiotic resistance in food, most studies have concentrated on street-vended foods, restaurants, or household kitchens, with limited attention given to bacterial contamination and antibiotic resistance in school meals. In particular, there is a lack of data on antibiotic-resistant *Escherichia coli* within school feeding programs, especially in the study area, despite the growing global concern over antimicrobial resistance (AMR). To address this gap, the present study aims to evaluate the microbial contamination and antibiotic resistance profile of *Escherichia coli* isolates from food samples collected in two boarding schools located in Zuru, Kebbi State, Nigeria. The results are expected to guide food safety policies, hygiene interventions, and AMR surveillance efforts to enhance the safety and effectiveness of school feeding programs.

METHODS

Study Area

Zuru serves as the administrative centre for both the Zuru local government and the Zuru emirate. Located at coordinates 112° 18.4056 N and 5° 54.7968 E, Zuru lies in the southern region of Kebbi State. Covering approximately 9000 square kilometers, Zuru shares its northern border with Zamfara State and is bordered to the south by Niger State.

Meals

The traditional meals prepared in these schools include: Breakfast options consisting of tea and bread, pap with akara, Indomie paired with egg, waina served with vegetable soup, moi moi with pap, and pap accompanied by kuli. For lunch, the menu includes jollof rice, jollof rice combined with beans, boiled yam accompanied by stew, rice and beans served with stew, spaghetti in stew, and rice with stew. Dinner offerings encompass semovita with soup, tuwon shinkafa alongside vegetable

soup, tuwon shinkafa complemented by okoro soup, eba with vegetable soup, and tuwon masara with dried okoro soup. Each meal combination varies across the days, providing a diverse menu for the school feeding program throughout the week.

Food Sampling

A total of twelve food samples were randomly collected, with six samples originating from each of the two boarding schools in Zuru town, Kebbi State. The schools involved were the Federal Science College (FSTC) Zuru and the Government Science and Technical College (GSTC) Zuru. The sampling process occurred immediately before the food was to be distributed to the students. Each sample was carefully collected, labeled accurately, and placed in a specimen container under aseptic conditions. To maintain freshness and prevent spoilage, the containers were then placed in coolers with ice packs. The samples were subsequently transported to the microbiology laboratory at Kebbi State University of Science and Technology, Aliero, for further analysis.

Sample Processing

The procedure began by homogenizing 10 grams of each food sample with 90 milliliters of buffered peptone water to obtain a uniform mixture suitable for microbiological analysis. Serial dilutions of the homogenate were then prepared, extending up to a 10^{-3} dilution. From the 10^{-2} dilution, 0.1 milliliters were plated onto nutrient agar to enumerate total viable bacteria. MacConkey agar was employed as a selective medium for the enumeration of coliforms, while Salmonella Shigella agar was used to detect and quantify Salmonella species.

Bacteriological Analysis

Total Plate Count

The Total Plate Count was determined by employing the pour plate technique on nutrient agar. After incubation, colonies were counted, and the results were expressed as Colony Forming Units (CFU) per gram of sample (Collee, 1996).

Coliform Count

For the enumeration of coliform bacteria, MacConkey agar plates were utilized. A loopful of the sample was transferred onto the MacConkey agar plate and spread evenly using a sterile wire loop. Following an incubation period of 24 hours at 37°C, typical pinkish colonies indicative of lactose-fermenting bacteria were counted. Non-lactose fermenting bacteria appeared colorless. The results were reported as CFU per gram of food (Hawkey, 2006).

Salmonella Count

The enumeration of Salmonella was conducted through the Direct Plating Method. Colonies of Salmonella spp., characterized by a colorless appearance with a black center, were counted. The counts were presented as colony-forming units per gram (CFU/g) of the sample (Andrews *et al*., 2023).

Characterization and Identification of Isolates

The identification of the isolates was conducted according to Cheesbrough (2003). The observation and documentation of colony appearance were performed, while the assessment of the morphology and gram reaction of the bacterial isolates was carried out through Gram's reaction. Furthermore, biochemical tests, including indole, citrate utilization, catalase, and coagulase tests, were conducted (Cheesbrough, 2003).

Antibiotic Sensitivity Test

The antibiotic susceptibility pattern of the *E. coli* isolates (n=8) was examined using the disc diffusion assay on Mueller-Hinton agar. To ensure complete contact with the agar surface, the antibiotic discs were evenly distributed onto the surface of the inoculated agar plates using a disc dispenser and gently pressed down. The antibiotics tested included: Amoxicillin/clavulanic acid (10/20g), Erythromycin (15g), Gentamicin (10g), Ampicillin (10g), Streptomycin (25g), Tetracycline (30g), Cefotaxime (30g), Trimethoprim (20g), and Amikacin (30g). The plates were inverted and incubated at 37oC for 18 to 24 hours. Subsequently, the zone of inhibition of growth around each disk was measured in millimeters, and the zone diameters were interpreted according to established standards (CLIS, 2020).

Data Analysis

Data analysis was performed using SPSS Statistics (version 24). Descriptive statistics, including mean and standard deviation, were used to summarize the microbial counts. An independent t-test was conducted to compare the mean bacterial counts between the two schools, with statistical significance set at $p < 0.05$. Microsoft Excel was used for data visualization.

RESULTS AND DISCUSSION

School feeding programs have emerged as a key response to recent food and economic crises and are implemented in various forms worldwide. These programs serve as a multi-sectoral strategy, influencing education, health, and nutrition while also offering potential long-term benefits (Rabiu et al., 2023; Wang & Fawzi, 2020; Watkins et al., 2024). Foodborne illnesses caused by pathogens are a significant global public health concern, prompting countries to invest substantial resources in their prevention and control (Walls et al., 2019). Bacterial food infections remain a major challenge for both developed and developing nations (Grace, 2023).

Bacteriological Quality of Food Samples

Table 1 provides the bacteriological assessment of food samples obtained from Federal Science and Technical College (FSTC), Zuru. The table outlines the Total Plate Count (TPC), Coliform Count, and Salmonella Count, measured in colony-forming units per gram (cfu/g). The Total Plate Count (TPC) ranges from 2.6×10^3 to 5.6×10^4 cfu/g. The Coliform Count varies between 2.0×10^2 and 6.8×10^2 cfu/g, while the Salmonella Count falls within 1.0×10^1 to 3.0×10^1 cfu/g. Table 2 presents the bacteriological evaluation of food samples collected from the Government Science and Technical College (GSTC), Zuru. The Total Plate Count (TPC) varies from 2.5×10^3 to 8.0×10^3 cfu/g, while the Coliform Count ranges between 2.0×10^2 and 9.3×10^2 cfu/g. The Salmonella Count is recorded between 1.6×10^1 and 4.0×10^1 cfu/g.

Table 1. Bacteriological Quality of Food in F.S.T.C Zuru

Sample code	Total Plate Count(cfu/g)	Coliform Count (cfu/g)	*Salmonella* Count (cfu/g)
FSA	2.3×10^4	5.7×10^2	3.0×10^1
FSB	2.1×10^4	2.0×10^2	1.0×10^1
FSC	5.6×10^4	6.8×10^2	1.9×10^1
FSD	4.7×10^4	2.5×10^2	2.0×10^1
FSE	4.0×10^3	3.4×10^2	2.3×10^1
FSF	2.6×10^3	5.8×10^2	1.6×10^1

Table 2. Bacteriological Quality of Food in G.S.T.C Zuru

Sample code	Total Plate Count(cfu/g)	Coliform Count (cfu/g)	*Salmonella* Count (cfu/g)
GSA	2.8×10^3	2.0×10^2	2.7×10^1
GSB	2.5×10^3	7.2×10^2	3.4×10^1
GSC	8.0×10^3	6.3×10^2	1.9×10^1
GSD	4.9×10^3	4.9×10^2	1.6×10^1
GSE	6.5×10^3	8.6×10^2	4.0×10^1
GSF	3.8×10^3	9.3×10^2	2.1×10^1

Figure 1 below compare the bacteriological quality of food samples from F.S.T.C Zuru and G.S.T.C Zuru. The comparison includes Total Plate Count, Coliform Count, and Salmonella Count.

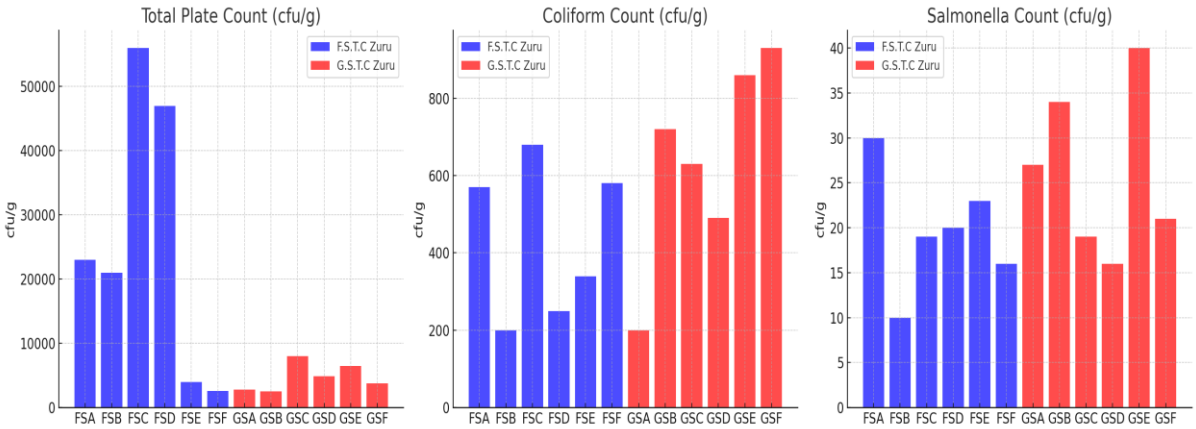

Figure 1. Bar chart comparing Total Plate Count, Coliform Count, and Salmonella Count of food samples

Descriptive Statistics and Comparison of Means (Independent t-Test)

The table below summarizes the mean, standard deviation, and t-test of Total Plate Count, Coliform Count, and Salmonella Count for food samples from both schools.

Table 3. Mean, Standard deviation, and t-test results

Parameter	Mean (F.S.T.C Zuru)	Std Dev (F.S.T.C Zuru)	Mean (G.S.T.C Zuru)	Std Dev (G.S.T.C Zuru)	T-Statistic	P-Value
Total Plate Count	25600.00	21934.45	4750.00	2164.02	2.317	0.067
Coliform Count	436.67	198.86	638.33	266.49	-1.486	0.171
Salmonella Count	19.67	6.71	26.17	9.33	-1.386	0.199

Total Plate Count is higher in F.S.T.C Zuru (Mean: 25,600 cfu/g) compared to G.S.T.C Zuru (Mean: 4,750 cfu/g). The difference is not statistically significant ($p = 0.067$). Coliform Count and Salmonella Count are higher in G.S.T.C Zuru, but the differences are not statistically significant. These findings are consistent with previous studies on food contamination in institutional settings. Compared to a study in a municipal school food program (MSFP) in Jequitinhonha Valley, Brazil, this study recorded a lower coliform count (up to 1 to 5.0 log CFU/g vs. 2×10^3 cfu/g). Most notably, *Salmonella* was detected in all food samples here (10 to 40 cfu/g) but was completely absent (Trindade et al., 2014). The Total Plate Count (TPC) in this study was higher than the values reported by Oranusi et al. (2013) for ready-to-eat foods in Nigerian university cafeterias (2.5×10^3 to 9.1×10^6 cfu/g). Coliform contamination, ranging from 200 to 930 cfu/g, was consistent with findings from Al-askari & Faqeh (2024), with coliform ranging (1.0×10^3 to 1.3×10^3 cfu/g). The Total plate Count (TPC) and coliform count in this study were significantly lower than those in foods sold in private and public primary schools in Abeokuta, South-western Nigeria (1.86×10^6 to 2.95×10^7 cfu/g and 1.0×10^6 to 3.47×10^6 cfu/g) (Afolabi et al., 2013). In contrast, Oyedeji et al. (2023) reported TPC levels between 0.1×10^6 and 4.13×10^6 cfu/g in Nigerian university food samples, which were notably higher than those observed in the present study. The high Total Plate Count (TPC) observed in the present study suggests inadequate hygiene in food handling and storage. Although high TPC does not confirm the presence of pathogens, it indicates increased microbial load, accelerating food spoilage and raising contamination risks (Karanth et al., 2023). The detection of coliforms and *Salmonella* in food samples highlights serious public health concerns, as coliforms indicate possible fecal contamination (Ghougal et al., 2021), while *Salmonella* is a major cause of foodborne illnesses,

leading to diarrhoea, fever, and cramps (Lamichhane et al., 2024). Several factors could contribute to the microbial contamination observed in school meals, including school infrastructure, water quality, and food handling practices. Inadequate kitchen facilities, poor ventilation, lack of proper food storage, and unhygienic dining areas can create an environment conducive to bacterial growth and cross-contamination.

Characterization and Identification of Isolates

Table 4 presents the distribution of bacterial isolates identified in food samples, showing their frequency and percentage occurrence. *Escherichia coli* and Salmonella were the most prevalent isolates, each accounting for 33.3%. Shigella was present in 16.6%, *Staphylococcus aureus* constituted 12.5%, while *Klebsiella pneumoniae* had the lowest occurrence at 4.1%.

Table 4. Distribution of bacterial isolates identified in food samples

S/N	Isolate	Frequency	Percentage (%)
1	*Escherichia coli*	8	33.3
2	Salmonella spp	8	33.3
3	Shigella spp	4	16.6
4	*Staphylococcus aureus*	3	12.5
5	*Klebsiella pneumonie*	1	4.1
	Total	24	100

The present study and previous research (Afolabi et al., 2013; Muhammad et al., 2016; Oranusi et al., 2013) identified common contaminants (*Escherichia coli*, *Staphylococcus aureus*, Salmonella, and *Klebsiella pneumonia*) in ready-to-eat foods. While *E. coli* and Salmonella were most prevalent in this study (33.3% each), Muhammad et al. (2016) reported higher *Staphylococcus aureus* (42.3%) and *E. coli* (40.8%) with lower Salmonella occurrence (5.6%). Additionally, Afolabi et al. (2013) and Oranusi et al. (2013) detected Proteus spp., *Bacillus cereus, Pseudomonas aeruginosa,* and *Enterobacter aerogenes*, which were absent in this study. The presence of *Escherichia coli*, Salmonella, Shigella, *Staphylococcus aureus*, and *Klebsiella pneumoniae* in food samples indicates significant public health risks, as these bacteria are known to cause foodborne illnesses (Odo et al., 2021). *E. coli* and Salmonella contamination suggest fecal contamination and poor hygiene practices (Al et al., 2020). Shigella is associated with bacterial dysentery, leading to severe gastrointestinal distress, while *Staphylococcus aureus* can cause food poisoning through its heat-stable toxins (Hmar et al., 2024; Oliveira et al., 2018). *Klebsiella pneumonia* is less common in foodborne outbreaks but poses risks of respiratory and gastrointestinal infections, especially in vulnerable populations (Hartantyo et al., 2020).

Antibiotic susceptibility pattern of *E.coli* isolated from food samples

The antibiotic susceptibility testing of Escherichia coli isolates from food samples revealed high sensitivity to Gentamicin Cefotaxime (100%) and Trimethoprim (87.5%). Amoxicillin/clavulanic acid also showed 75% susceptibility. However, moderate resistance was observed with Erythromycin (50%), Ampicillin and Tetracycline (62.5%), and Streptomycin (75%). Amikacin exhibited 100% resistance.

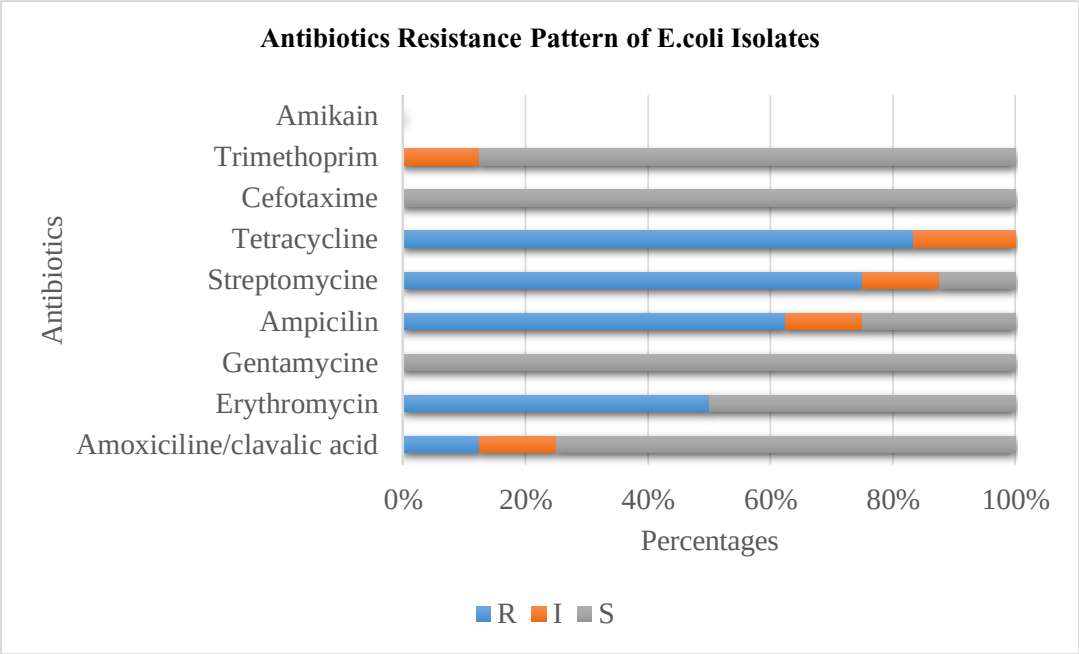

Figure 2. Antibiotic-resistant patterns of *E. coli* isolated from food samples (n = 8).

The present study found *E. coli* highly resistant to Amikacin (100%), Streptomycin (75%), Ampicillin (62.5%), and Tetracycline (62.5%) while being fully susceptible to Gentamicin and Cefotaxime (100%). Similar resistance patterns were reported in (Ema et al., 2022) and (Bako et al., 2024), with high resistance to Ampicillin, Cephalexin, and Oxytetracycline. Bako et al. (2024) also found 100% resistance to Amoxicillin, Augmentin, and Septrin, indicating a more severe trend. Jenifer & Sathiyamurthy (2020) reported 71% multidrug resistance, with 12.9% complete resistance, surpassing the present study. Likewise, *Escherichia coli* in Ready-to-eat Foods from Food Outlets at Ekiti State University recorded 100% Augmentin resistance and 80.2% to Ceftazidime, while *E. coli* in Bogor, Indonesia, showed high Gentamicin resistance, contrary to the present findings (Lukman et al., 2020). The presence of *Escherichia coli* in food samples signals fecal contamination and poor hygiene, posing a public health risk (Herawati et al., 2023). Certain strains, like Enterohemorrhagic *E. coli* (EHEC), produce toxins that cause severe diarrhea and life-threatening complications such as hemolytic uremic syndrome (HUS) (Derakhshan-Sefidi et al., 2025). Additionally, *E. coli* contamination may indicate the presence of other harmful pathogens, such as *Salmonella* and *Shigella*, increasing the risk of foodborne illnesses (Anjum et al., 2021). The presence of antibiotic-resistant *Escherichia coli* in school food samples may result from multiple sources, including poor hygiene practices, contaminated water, and environmental factors. Poor hygiene among food handlers, inadequate washing of raw ingredients, and cross-contamination from unclean utensils or surfaces can further spread resistant strains.

The study's limitations include a small sample size, as only 12 food samples from two boarding schools were analyzed, which may not fully represent food contamination across a wider population. Additionally, the study did not evaluate hygiene practices among food handlers or the sanitation conditions of kitchens, which could be key sources of contamination. Furthermore, the reliance on conventional bacteriological methods for bacterial identification and antibiotic susceptibility testing limited the precision of results, as molecular techniques like PCR or whole-genome sequencing could have provided more detailed insights into pathogen characteristics and resistance mechanisms.

CONCLUSION

This study revealed significant microbial contamination in school food samples from two boarding schools in Zuru, Kebbi State, Nigeria. The detection of *Escherichia coli*, *Salmonella*, *Shigella*, *Staphylococcus aureus*, and *Klebsiella pneumoniae*

suggests poor hygiene and possible fecal contamination. Antibiotic susceptibility tests showed alarming resistance in *E. coli* isolates, particularly to Amikacin, Streptomycin, and Tetracycline, highlighting the growing threat of antimicrobial resistance. Improving school infrastructure, ensuring access to clean water, and enforcing strict hygiene protocols for food handlers are essential steps in reducing food contamination. Regular inspection of school kitchens, water sources, and food preparation areas can help mitigate these risks and prevent foodborne illness outbreaks.

CONFLICTS OF INTEREST

The authors declare that there are no conflicts of interest regarding the publication of this paper.

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