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Antibiogram Profiling and Molecular Detection of Enteropathogenic *Escherichia coli* in Drinking Water Sources in Kaduna Metropolis, Nigeria

Ndibe, T. Ositadinma[1*]., Bakare, Victoria[2]., Shehu, M. Genesis[3]. and Ezulike, C. Charity[4]
[1]Department of Microbiology, University on the Niger, Umunya, Anambra State
[2]Department of Biological Sciences, Nigerian Defence Academy, Kaduna, Kaduna State
[3]Department of Biological Sciences, Kaduna State University, Kaduna, Kaduna State
[4]Department of Nursing, Millennium College of Nursing Sciences, Awka, Anambra State
***Corresponding Author:** *tgodndibe@gmail.com*

ABSTRACT

Safe drinking water is essential for human health; however, microbial contamination of water sources remains a major public health concern in developing countries. This study investigated the antibiogram profile and molecular characterization of enteropathogenic *Escherichia coli* (EPEC) in selected drinking water sources in Kaduna metropolis, Nigeria. A total of eighteen water samples were collected in triplicates from six locations: Kawo (A), Unguwan Rimi (B), Tudun Wada (C), Sabon Tasha (D), Barnawa (E), and Kakuri (F). Standard microbiological methods, including Most Probable Number (MPN), total viable count, and biochemical characterization, were employed for isolation and identification of bacterial isolates. Antibiotic susceptibility testing was carried out using the disc diffusion method, while molecular detection of EPEC was performed using polymerase chain reaction (PCR) targeting virulence genes. Results revealed significant coliform contamination, with some samples recording ≥2400 MPN/100ml. Total viable bacterial counts ranged from 9.0×10^5 to 1.61×10^7CFU/ml. *Escherichia coli*, *Salmonella* spp., and *Enterobacter* spp. were identified, with *E. coli* being the most prevalent (55.9%). Antibiotic susceptibility testing showed that ciprofloxacin and pefloxacin exhibited the highest antibacterial activity against the isolates, whereas resistance was observed against commonly used antibiotics such as amoxicillin and augmentin. Molecular analysis confirmed the presence of EPEC strains through detection of characteristic gene fragments. The findings indicate widespread microbial contamination of drinking water sources in Kaduna metropolis, rendering them unsafe for human consumption. The presence of antibiotic-resistant EPEC highlights a significant public health risk, emphasizing the need for improved water treatment strategies, routine monitoring, and strengthened antimicrobial stewardship.

Keywords: Drinking Water, Antibiotic Resistance, Contamination, Enteropathogenic *Escherichia coli* (EPEC), PCR.

Introduction

Water covers approximately 71% of the Earth's surface and is indispensable for the survival of all forms of life. Despite its abundance, access to safe and potable water remains a significant global challenge, particularly in developing countries. According to the World Health Organization, an estimated 2 billion people worldwide still rely on drinking water sources contaminated with faeces, thereby increasing their risk of waterborne diseases (WHO, 2022). Unsafe water, inadequate sanitation, and poor hygiene are major contributors to morbidity and mortality, especially in low- and middle-income countries, where infections such as diarrhoea, cholera, typhoid fever, and hepatitis A remain prevalent (Ahmed et al., 2020; Onwumere-Idolor et al., 2024).

Water used for drinking and domestic purposes is obtained from diverse sources including boreholes, wells, rivers, streams, and rainwater. However, these sources are often exposed to microbial contamination due to poor sanitation practices, improper waste disposal, and environmental pollution. The presence of indicator organisms such as coliform bacteria, particularly *Escherichia coli*, is widely used as an index of faecal contamination and poor microbiological quality of water (Khan and Gupta, 2020). While most strains of *E. coli* are harmless commensals of the intestinal tract, certain pathogenic strains possess virulence factors that enable them to cause disease (Díaz-Jiménez et al., 2020).

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Among the pathogenic variants, enteropathogenic *Escherichia coli* (EPEC) are a major cause of diarrhoeal illness, particularly among infants and young children in developing countries. EPEC belongs to a group of diarrhoeagenic *E. coli* pathotypes, which also include enterotoxigenic (ETEC), enterohaemorrhagic (EHEC), enteroinvasive (EIEC), enteroaggregative (EAEC), and adherent-invasive *E. coli* (AIEC) (Jang et al., 2017). EPEC is characterized by its ability to induce attaching and effacing lesions in the intestinal epithelium, mediated by virulence genes such as *eae* and *bfpA*, which are commonly targeted in molecular detection assays (Manzanas et al., 2023). Transmission of EPEC occurs primarily via the faecal–oral route through contaminated food and water, with humans serving as the principal reservoir.

The burden of EPEC-associated infections is exacerbated in environments with inadequate sanitation and limited access to clean water. Several studies have reported a higher prevalence of EPEC in contaminated water sources and in regions with poor hygiene practices (Jang et al., 2017; Bolukaoto et al., 2022; Zeki et al., 2021; WHO, 2023; Heijnen et al., 2024). In addition to its pathogenicity, the emergence and spread of antimicrobial resistance (AMR) among *E. coli* strains pose a growing global health threat. The World Health Organization has identified antimicrobial resistance as one of the top ten global public health threats, driven by factors such as misuse and overuse of antibiotics in humans and animals (WHO, 2023). Multidrug-resistant strains of EPEC have increasingly been reported, complicating treatment options and increasing the risk of severe disease outcomes (Díaz-Jiménez et al., 2020).

In Nigeria, several studies have documented the contamination of drinking water sources with enteric pathogens, including *E. coli*, *Salmonella* spp., and *Enterobacter* spp., highlighting significant public health concerns (Bolukaoto et al., 2022; Beshiru et al., 2024; Popoola et al., 2024). A previous investigation in Kaduna metropolis reported contamination of groundwater sources, particularly boreholes and shallow wells, with faecal indicator bacteria, suggesting inadequate water treatment and poor environmental sanitation (Muktar et al., 2011).

Rapid urbanization, population growth, and insufficient infrastructure further contribute to the deterioration of water quality in many Nigerian cities. Despite existing studies, there remains a need for comprehensive investigations that integrate conventional microbiological techniques with molecular approaches to accurately detect and characterize pathogenic strains such as EPEC. Furthermore, understanding the antibiotic susceptibility patterns of these organisms is essential for guiding clinical management and informing public health interventions. Therefore, this study aimed to determine the antibiogram profile and molecular characteristics of enteropathogenic *Escherichia coli* in selected water sources within Kaduna metropolis, Nigeria. The findings from this study will provide valuable insights into the microbiological safety of drinking water in the area and contribute to strategies aimed at improving water quality and reducing the burden of waterborne diseases.

Materials and Methods

Study Area

This study was conducted in Kaduna, the capital of Kaduna State, located in north-western Nigeria. Kaduna lies at latitude 10.6093°N and longitude 7.4295°E. Kaduna is characterized by rapid urbanization and increasing population density, factors that contribute to pressure on water supply systems and sanitation infrastructure. The city comprises several residential and commercial districts with diverse water sources, including boreholes, wells, and surface water bodies, which are often vulnerable to microbial contamination (Muktar et al., 2011).

Sample Collection

Kaduna metropolis was stratified into six zones: Kawo (A), Unguwan Rimi (B), Tudun Wada (C), Sabon Tasha (D), Barnawa (E), and Kakuri (F). From each zone, three water samples were collected aseptically, yielding a total of eighteen (18) samples. Sterile 200 mL screw-capped plastic bottles were used for sample collection. Prior to collection, bottles were rinsed with the sample water where applicable, except for treated sources. Samples were labeled appropriately (A1 - F3), placed in ice-packed containers (4°C), and transported within 4 hours to the Microbiology Laboratory of Kaduna State University for analysis. All analyses were initiated within 6 hours of sample collection to prevent changes in microbial load (APHA, 2017).

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Preparation of Culture Media

Nutrient agar, Eosin Methylene Blue (EMB) agar, and MacConkey broth were prepared according to manufacturer specifications. Media were sterilized by autoclaving at 121°C for 15 minutes and cooled to 45–50°C before pouring into sterile Petri dishes under aseptic conditions.

Determination of Coliform Count (Most Probable Number Method)

The Most Probable Number (MPN) technique was employed to estimate coliform density using the multiple-tube fermentation method (APHA, 2017). For each sample: five tubes containing double-strength MacConkey broth were inoculated with 10 mL of water sample, five tubes containing single-strength broth were inoculated with 1 mL, and five tubes containing single-strength broth were inoculated with 0.1 mL.

All tubes contained inverted Durham tubes for gas detection and were incubated at 37°C for 24 - 48 hours. Tubes showing acid production (color change) and gas formation were recorded as positive. MPN values were determined using standard probability Table.

Confirmation and Completed Test

Positive presumptive tubes were sub-cultured into Brilliant Green Lactose Bile broth and incubated at 37°C for 24–48 hours. Gas production confirmed the presence of coliform bacteria. Completed tests were carried out by streaking cultures onto EMB agar plates and incubating at 37°C for 24 hours. Colonies showing characteristic green metallic sheen were presumptively identified as *Escherichia coli*.

Total Viable Count (TVC)

Serial dilution (up to 10^{-3}) of water samples was performed using sterile distilled water. Aliquots (1 mL) were plated using the pour plate technique with nutrient agar. Plates were incubated at 37°C for 24–48 hours, and colonies within the range of 30 - 300 were counted. Results were expressed as colony-forming units per milliliter (CFU/mL).

$$\text{CFU/mL} = \frac{Number\ of\ Colonies \times Dilution\ Factor}{Volume\ of\ Culture\ Plated\ (mL)}$$

Gram Staining

Isolates were subjected to Gram staining using standard procedures and examined microscopically for cell morphology and Gram reaction.

Biochemical Characterization

The biochemical tests carried out to confirm *E. coli* are: Catalase test, Indole test, Citrate test, Methyl Red test, Voges-Proskauer test, Glucose test, Lactose test, Sucrose test and Triple Sugar Iron test (Cheesbrough, 2010).

Antibiotics Susceptibility Test

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton agar in accordance with Clinical and Laboratory Standards Institute (CLSI, 2023). Tested antibiotics included: Ciprofloxacin (5 µg), Pefloxacin (10 µg), Gentamicin (10 µg), Streptomycin (10 µg), Tetracycline (30 µg), Ceftazidime (30 µg), Ceftriaxone (30 µg), Amoxicillin-clavulanate (30 µg), Trimethoprim-sulfamethoxazole (25 µg). Bacterial suspensions were standardized to 0.5 McFarland turbidity.

Plates were incubated at 37°C for 18–24 hours, and zones of inhibition were measured in millimeters. Results were interpreted as susceptible, intermediate, or resistant according to CLSI breakpoints.

Molecular Detection of Enteropathogenic *E. coli* (EPEC)

DNA Extraction

Genomic DNA was extracted using a commercial extraction kit (AccuPrep Genomic DNA Extraction Kit) following the manufacturer's protocol. DNA quality and concentration were assessed spectrophotometrically and stored at 4°C prior to analysis.

Polymerase Chain Reaction (PCR)

Multiplex PCR was used for the detection of EPEC-specific virulence genes. The targeted genes included: *eae* (encoding intimin; responsible for attachment and effacement lesions) and *bfpA* (encoding bundle-forming pilus; characteristic of typical EPEC).

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Primers previously validated by Manzanas et al. (2023) and Gao et al. (2024) were used. PCR amplification was carried out in a total reaction volume of 20 µL containing: 10 µL PCR master mix, 1 µL each of forward and reverse primers, 2 µL DNA template, Nuclease-free water.

Thermal cycling conditions were: Initial denaturation: 95°C for 5 minutes, 35 cycles (Denaturation: 94°C for 30 seconds, Annealing: 52°C for 30 seconds, Extension: 72°C for 1 minute) and Final extension: 72°C for 5 minutes. Positive and negative controls were included to ensure assay reliability (Heijnen et al., 2024).

Agarose Gel Electrophoresis and Plasmid Profiling

PCR products were resolved on 1.5% agarose gel stained with ethidium bromide and visualized under UV illumination. A 100 bp DNA ladder was used as a molecular size marker. Expected amplicon sizes were: *eae*: ~790 bp and *bfpA*: ~324 bp.

Plasmid DNA from antibiotic-resistant isolates was extracted using the alkaline lysis method and separated by agarose gel electrophoresis to determine plasmid presence and size distribution.

Data Analysis

Data obtained were analyzed using descriptive and inferential statistics. Frequencies and percentages were calculated for bacterial occurrence, Mean ± standard deviation was computed for microbial counts, and Differences between sampling locations were analyzed using one-way ANOVA. Statistical significance was set at $p < 0.05$. Analysis was performed using SPSS version 25.0 (IBM Corp., Armonk, NY, USA, 2017).

Results

The occurrence of coliform bacteria in the drinking water samples collected from six locations in Kaduna is presented in Table 1. Coliform contamination varied considerably across sampling sites. Samples A2 (Kawo) and D2 (Sabon Tasha) showed the highest level of contamination, with all fifteen tubes testing positive, corresponding to ≥2400 MPN/100 mL. Sample E2 (Barnawa) also exhibited a high coliform load of 1600 MPN/100 mL. In contrast, samples B3, C3, and E3 showed no detectable coliforms (<1.8 MPN/100 mL), indicating relatively low contamination levels. Overall, 15 out of 18 samples (83.3%) were positive for coliforms, suggesting widespread faecal contamination of water sources within the study area.

Table 1: Most probable number of coliform in 100mL (MPN/100mL) of drinking water samples

Sampling	MPN/100mL of drinking water samples in different locations					
	Kawo (A)	**Unguwan Rimi (B)**	**Tudun Wada (C)**	**Sabon Tasha (D)**	**Barnawa (E)**	**Kakuri (F)**
1	240	6.1	240	79	33	6.1
2	≥2400	2	11	≥2400	1600	9.3
3	23	<1.8	<1.8	23	<1.8	7.8
Total	2663	9.9	252.8	2502	1634.8	23.2
Mean	887.67	3.30	84.27	834.00	544.93	7.73
Mean ± SD	887.67 ± 1314.0	3.30 ± 2.43	84.27 ± 134.9	834.00 ± 1356.0	544.93 ± 914.0	7.73 ± 1.60

The total viable bacterial counts (TVBC) of the drinking water samples are presented in Table 2. Bacterial loads ranged from 9.0 × 10^5 to 1.61 × 10^7 CFU/mL, with samples D1 and D2 recorded as too numerous to count (TNTC), indicating extremely high contamination. Total bacterial counts varied across locations, with the highest recorded in Barnawa (2.70 × 10^7 CFU/mL) and the lowest in Unguwan Rimi (5.8 × 10^6 CFU/mL). Mean bacterial counts ranged from 1.93 × 10^6 to 9.00 × 10^6 CFU/mL across the sampling sites.

Variability, expressed as mean ± SD, showed notable differences among locations, with Barnawa exhibiting the highest dispersion (9.00 ± 7.48 × 10^6 CFU/mL), while Unguwan Rimi showed relatively low variability (1.93 ± 0.72 × 10^6 CFU/mL). To assess spatial variation, a one-way ANOVA was conducted (Table 3), which revealed a statistically significant difference in bacterial counts across the six sampling locations (F = 4.67, p = 0.012). This indicates that the level of microbial contamination differed significantly depending on location.

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Table 2: Total viable bacteria count (CFU/mL) of the drinking water samples

Sampling	Total bacteria count (CFU/mL) of drinking water in the Locations					
	Kawo (A)	Unguwan Rimi (B)	Tudun Wada (C)	Sabon Tasha (D)	Barnawa (E)	Kakuri (F)
1	6.9×10^6	1.1×10^6	9.0×10^5	TNTC	1.61×10^7	1.6×10^6
2	3.9×10^6	2.3×10^6	1.2×10^6	TNTC	9.7×10^6	1.1×10^6
3	1.9×10^6	2.4×10^6	4.0×10^6	7.1×10^6	1.2×10^6	5.1×10^6
Total	12.7×10^6	5.8×10^6	6.1×10^6	7.1×10^6	2.70×10^7	7.8×10^6
Mean	4.23×10^6	1.93×10^6	2.03×10^6	7.10×10^6	9.00×10^6	2.60×10^6
Mean ± SD	$4.23 \times 10^6 \pm$ 2.52	$1.93 \times 10^6 \pm$ 0.72	$2.03 \times 10^6 \pm$ 1.71	$7.10 \times 10^6 \pm$ 0.00	9.00×10^6 ± 7.48	2.60×10^6 ±2.18

Note: TNTC = Too Numerous To Count; SD = Standard Deviation

Table 3: One-Way ANOVA for Total Viable Bacteria Count across drinking water locations

Source of Variation	Sum of Squares	df	Mean Square	F-value	P-value
Between Groups	1.92×10^{14}	5	3.84×10^{13}	4.67	0.012*
Within Groups	9.85×10^{13}	12	8.21×10^{12}		
Total	2.90×10^{14}	17			

A total of 34 bacterial isolates were recovered and identified based on morphological, Gram staining, and biochemical characteristics. The distribution of isolates is summarized in Figure 1. *Escherichia coli* was the most predominant organism, accounting for 19 isolates (55.9%), followed by *Enterobacter* spp. with 10 isolates (29.4%) and *Salmonella* spp. with 5 isolates (14.7%). Characteristic green metallic sheen on EMB agar confirmed the presence of *E. coli*, while *Salmonella* spp. were identified based on hydrogen sulfide production, and *Enterobacter* spp. exhibited typical mucoid colony morphology. The spatial distribution of bacterial isolates across the sampling locations showed variation in occurrence. Kawo recorded the highest prevalence of *E. coli*, while Tudun Wada showed a higher occurrence of *Enterobacter* spp. *Salmonella* spp. were less frequently isolated and were absent in some locations. Statistical analysis using the chi-square test (Table 4) showed that the distribution of bacterial isolates across locations was statistically significant ($\chi^2 = 12.84$, $p = 0.045$). This suggests that environmental or anthropogenic factors may influence microbial distribution in the study area.

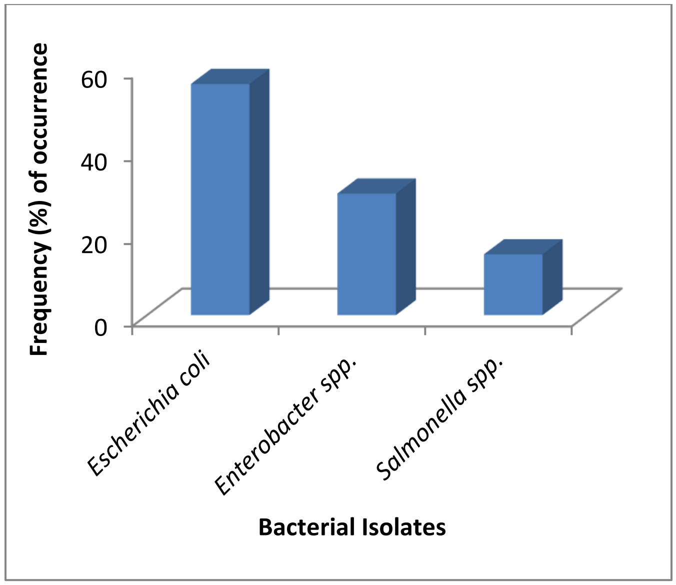

Fig. 1: Frequency of occurrence (%) of bacterial isolates in the drinking water samples

Table 4: Chi-Square Analysis of Distribution of Isolates

Variable	χ^2 Value	df	p-value
Distribution across locations	12.84	10	0.045*

The antibiotic susceptibility patterns of the bacterial isolates are presented in Table 5. With respect to *Escherichia coli*, *Ciprofloxacin* and *pefloxacin* exhibited the highest antibacterial activity, each with a mean zone of inhibition of 27 mm. Moderate susceptibility was observed for gentamicin (22 mm), ofloxacin (21 mm), and chloramphenicol (20 mm). However, complete resistance was observed against amoxicillin, augmentin, and septrin.

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For *Salmonella* spp., the highest susceptibility was recorded for ciprofloxacin and pefloxacin (28.5 mm). Resistance was observed against amoxicillin, augmentin, gentamicin, and streptomycin. While for *Enterobacter* spp., *Ciprofloxacin* showed the highest activity (25 mm), followed by ofloxacin (21.5 mm) and septrin (20.5 mm). Resistance was observed against augmentin, gentamicin, and chloramphenicol.

Table 5: Antibiotic Susceptibility Profile (Zone of Inhibition in mm)

Antibiotic	*E. coli*	*Salmonella* spp.	*Enterobacter* spp.
Ciprofloxacin	27	28.5	25
Pefloxacin	27	28.5	20
Gentamicin	22	–	–
Ofloxacin	21	20	21.5
Streptomycin	18.5	–	–
Chloramphenicol	20	20.5	–
Amoxicillin	–	–	14
Augmentin	–	–	–
Septrin	–	–	20.5

The multidrug resistance profile of the isolates is summarized in Table 6. Out of the 34 isolates tested, 14 were resistant to three or more classes of antibiotics, giving an MDR prevalence of 41.2%. This high level of resistance indicates the presence of antibiotic-resistant bacteria in the water sources, posing potential public health risks.

Table 6: Multidrug Resistance (MDR) Pattern

Parameter	Value
Total isolates tested	34
MDR isolates	14
MDR prevalence	41.2%

Molecular detection of enteropathogenic *Escherichia coli* (EPEC) was carried out using PCR targeting the *eae* and *bfpA* virulence genes. As shown in Table 8, Both *eae* and *bfpA* genes were detected in a subset of isolates, classifying them as typical EPEC, while isolates positive for *eae* but lacking *bfpA* were identified as atypical EPEC.

A considerable number of isolates showed no amplification of either gene and were classified as non-EPEC. The detection of these virulence markers indicates the presence of pathogenic *E. coli* strains in the sampled drinking water, thereby increasing the health risks associated with consumption of contaminated water.

Table 8: PCR Detection of EPEC Virulence Genes in *E. coli* Isolated from Water Samples

E. coli Isolate	eae gene (790 bp)	bfpA gene (324 bp)	Classification
1	+	+	Typical EPEC
2	+	–	Atypical EPEC
3	–	–	Non-EPEC
4	+	–	Atypical EPEC
5	–	–	Non-EPEC
6	–	–	Non-EPEC
7	+	+	Typical EPEC
8	+	–	Atypical EPEC
9	–	–	Non-EPEC
10	+	+	Typical EPEC
11	+	–	Atypical EPEC
12	–	–	Non-EPEC
13	+	+	Typical EPEC
14	+	–	Atypical EPEC
15	–	–	Non-EPEC
16	+	–	Atypical EPEC
17	–	–	Non-EPEC
18	–	–	Non-EPEC
19	+	+	Typical EPEC

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Discussion

The present study revealed widespread microbial contamination of drinking water sources in Kaduna, with a high prevalence of coliform bacteria and pathogenic *Escherichia coli*. The detection of coliforms in 83.3% of the samples indicates significant faecal contamination, rendering most of the water sources unsuitable for human consumption according to the World Health Organization guideline of zero coliforms per 100 mL of potable water (WHO, 2022).

The high MPN values (≥2400 MPN/100 mL) observed in several samples are indicative of severe contamination and are comparable to findings from similar studies in Nigeria and other developing regions. For instance, recent investigations have reported high coliform counts in untreated water sources due to poor sanitation infrastructure and environmental exposure (Rabiu et al., 2024). Globally, elevated faecal indicator bacteria in drinking water systems have been associated with increased risks of waterborne diseases, particularly in rapidly urbanizing areas (Zeki et al., 2021; Gomes et al., 2024).

The total viable bacterial counts recorded in this study (up to 1.61×10^7 CFU/mL) further confirm substantial microbial load in the sampled water sources. These values exceed permissible limits for drinking water and are consistent with reports from other Nigerian cities, where inadequate water treatment and poor hygiene practices contribute to microbial proliferation (Rabiu et al., 2023).

The statistically significant variation in bacterial counts across sampling locations ($p < 0.05$) suggests that local environmental conditions, population density, and sanitation practices play a critical role in determining water quality. The predominance of *E. coli* (55.9%) among the isolates underscores its importance as a key indicator of faecal contamination.

This finding aligns with previous studies that have identified *E. coli* as the most frequently isolated organism in contaminated water sources in Nigeria and globally (Manzanas et al., 2023). The presence of *Salmonella* spp. and *Enterobacter* spp. further highlights the potential risk of enteric infections associated with the consumption of untreated water.

A major finding of this study is the high level of antimicrobial resistance observed among the isolates. The effectiveness of fluoroquinolones such as ciprofloxacin and pefloxacin is consistent with previous reports indicating their continued efficacy against Gram-negative bacteria. However, the observed resistance to commonly used antibiotics such as amoxicillin and amoxicillin-clavulanate is concerning and reflects the growing global burden of antimicrobial resistance (AMR). According to the World Health Organization, AMR is one of the top ten global public health threats, driven largely by antibiotic misuse and environmental dissemination of resistant organisms (WHO, 2023).

The detection of multidrug resistance (41.2%) among isolates in this study is comparable to recent findings from environmental and clinical settings in sub-Saharan Africa, where multi-drug resistant *E. coli* strains are increasingly reported (Bolukaoto et al., 2022).

The presence of plasmids in resistant isolates suggests the potential for horizontal gene transfer, which may facilitate the spread of resistance genes within microbial communities. This observation is supported by recent studies highlighting the role of mobile genetic elements in the dissemination of antibiotic resistance in aquatic environments (Sarker et al., 2025).

Molecular analysis confirmed the presence of enteropathogenic *E. coli* (EPEC) in the drinking water sources through the PCR detection of *eae* and *bfpA* genes. This finding is significant, as EPEC is a well-known cause of diarrhoeal disease, particularly in children in developing countries. The use of PCR for detection enhances the sensitivity and specificity of pathogen identification compared to conventional culture methods, as demonstrated in recent studies (Yoon et al., 2021; Heijnen et al., 2024). The presence of EPEC in drinking water sources represents a serious public health concern, given its ability to cause outbreaks of diarrhoeal illness (Ahmed et al., 2020). The identification of both typical and atypical EPEC strains highlights the potential public health risk associated with consumption of contaminated water. The presence of the *eae* gene, which encodes intimin, is essential for bacterial attachment and colonization, while the *bfpA* gene is characteristic of typical EPEC strains and enhances virulence (Manzanas et al., 2023).

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The statistically significant variation in bacterial distribution across locations further emphasizes the influence of environmental and anthropogenic factors on water quality.

Factors such as proximity to waste disposal sites, poor drainage systems, and inadequate water treatment infrastructure may contribute to localized contamination. Similar patterns have been reported in other urban settings, where water quality is closely linked to sanitation and environmental management practices (Gomes et al., 2024). Moreover, the findings of this study highlight the critical need for improved water quality monitoring and management strategies in Kaduna metropolis. The combination of high microbial load, presence of pathogenic EPEC strains, and widespread antimicrobial resistance underscores a significant public health risk. These results are consistent with global concerns regarding the safety of drinking water in low-resource settings and the increasing role of environmental reservoirs in the transmission of antimicrobial resistance

Conclusion

This study provides evidence of significant microbial contamination of drinking water sources in Kaduna, with the majority of samples failing to meet acceptable microbiological standards for potable water. The high prevalence of coliform bacteria, elevated total viable bacterial counts, and the predominance of *Escherichia coli* confirm widespread faecal contamination across the study area. The molecular detection of enteropathogenic *E. coli* (EPEC) through the identification of *eae* and *bfpA* genes demonstrates the presence of virulent strains with the potential to cause diarrhoeal disease, particularly among vulnerable populations such as children and immunocompromised individuals. The co-occurrence of other enteric pathogens, including *Salmonella* spp. and *Enterobacter* spp., further highlights the microbiological risk associated with these water sources. The study also revealed a concerning level of antimicrobial resistance among bacterial isolates, with a substantial proportion exhibiting multidrug resistance. The observed resistance to commonly used antibiotics, coupled with evidence of plasmid-mediated resistance, underscores the role of environmental water sources as reservoirs and transmission pathways for resistant bacteria.

Overall, these findings emphasize the urgent need for improved water quality management, routine microbiological surveillance, and strengthened public health interventions to mitigate the risks associated with contaminated water. The integration of conventional microbiological methods with molecular techniques in this study provides a robust framework for monitoring waterborne pathogens and antibiotic resistance in similar settings.

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