

Evaluation of bacterial contamination in domestic water sources in Aluu community in Rivers State, Nigeria

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Accepted 12 July, 2024

ABSTRACT

A microbiological investigation was conducted to assess the quality of domestic water in Aluu community, Rivers State, Nigeria. Ten borehole water samples (labelled A to J) from residential houses were analyzed for total heterotrophic bacteria, coliform, faecal coliform, *Salmonella*, *Shigella*, and *Escherichia coli* (*E. coli*) using standard microbiological techniques. The results showed a range of $1.3 \pm 0.01 \times 10^2$ to $7.7 \pm 0.17 \times 10^2$ CFU/ml for total heterotrophic bacteria, $0.3 \pm 0.02 \times 10^2$ to $28.8 \pm 0.04 \times 10^2$ CFU/ml for total coliform, and 0 to $17.8 \pm 0.75 \times 10^2$ CFU/ml for faecal coliform. *Salmonella* and *Shigella* were detected in some samples, while *E. coli* was present in most samples, with a maximum occurrence of 35% in water sample H. The presence of *E. coli* and other pathogens in the groundwater indicates a significant public health concern, highlighting the need to treat domestic water before consumption to minimize adverse health effects.

Keywords: Water quality, *Escherichia coli*, microbiological analysis, public health.

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INTRODUCTION

Water sources can be contaminated by organic and inorganic chemicals, sewage disposal, living organisms, animal and human wastes, and effluents from open-field defecation practices (Aslani et al., 2011). This contaminated water can cause various waterborne diseases (Amenu et al., 2013). Sewage disposal is a significant source of contamination, consisting of pathogens like bacteria, parasitic worms, and organic and inorganic particles (Shield et al., 2015). Indicator organisms like *E. coli*, non-specific coliforms, and *Pseudomonas aeruginosa* are commonly found in the human or animal gut and indicate the presence of sewage disposal (Kirk et al., 2010; Köhler and Dobrindt, 2011). *E. coli* is a significant indicator organism, as it indicates faecal contamination and the possible presence of other pathogens (Amenu et al., 2013). The analysis of

drinking water for the presence of indicator microorganisms is crucial for determining microbiological quality and public health safety (Zhi et al., 2020). Bacteriological analysis can estimate the number of bacteria present and ascertain the class, group, or category of bacteria (Köhler and Dobrindt, 2011). The detection of *E. coli* indicates faecal pollution and the possible presence of other pathogens, making it essential for managing waterborne health risks. This study detects *E. coli* in water samples from Aluu community as an established indicator of water quality. Our findings will contribute to the existing knowledge on water contamination, a global issue, and reinforce the importance of implementing standard guidelines and regulations to monitor and manage waterborne health risks in this region.

MATERIALS AND METHODS

Study area

Sampling was carried out in Aluu community in Rivers State, Nigeria. Aluu is situated east of Rumu-Ahunwa and Southeast of Omuigwe. General Latitude of 4.93384° or 4°55' 2" North and Longitude of 6.94946° or 6°56' 58" East; Elevation of 25 meters (82 feet), open location code 6FP8WWMX+GQ, GeoNames ID 2350362.

Sample collection

A total of 10 water samples were randomly collected from different domestic residents. The water samples were collected using sterile bottles for microbiological analysis, properly labeled and placed in an ice pack cooler (APHA, 2005). The representative water samples were transported to the Microbiology laboratory at Rivers State University within two to four hours of collection for microbiological analysis. The study targeted borehole water sources, a common source of domestic water in the community, to assess their microbiological quality.

Microbiological analysis

Water samples were analyzed for various bacterial populations using the spread plate method. Total heterotrophic bacteria were enumerated on nutrient agar plates and incubated at 37°C for 24-48 hours. Total coliform and faecal coliform were enumerated on MacConkey agar plates and EMB agar plates, respectively, using the same incubation conditions. *Salmonella* and *Shigella* species were enumerated on *Salmonella Shigella* agar plates and incubated at 37°C for 24-48 hours. In all cases, 0.1ml of water sample was

aseptically plated using a micropipette and a bent glass rod.

Biochemical test for the identification of bacterial isolates

Biochemical tests were used for the identification of bacteria species based on the differences in the biochemical activities of different bacteria according to Bergey's Manual of Systematic Bacteriology (2004). The bacterial isolates were identified based on the Gram reaction, and morphological and biochemical tests included Motility, Catalase, Citrate utilization, Coagulase, Indole production, Oxidase, Urease, Methyl Red and Voges Proskauer tests. Bacterial isolates were also characterized for sugar fermentation, including sugars such as fructose, glucose, lactose, maltose and mannose.

Gram staining

This technique was used to identify bacteria based on the composition of their cell walls. Gram-positive bacteria retain the primary stain, appearing purple, while Gram-negative bacteria lose the stain and take on a red color from the counterstain.

RESULTS

Total heterotrophic bacterial counts

The total Heterotrophic bacteria count in the sample is presented in Table 1. The highest count of $7.7 \pm 0.17 \times 10^2$ CFU/ml was obtained in sample E, while the lowest count of $1.3 \pm 0.01 \times 10^2$ CFU/ml was obtained in sample F.

Table 1. Total heterotrophic bacteria count of the water samples.

S/N	Samples	Number of colonies	THB (10^2 CFU/ml)	Standard Deviation
1	Sample A	52	5.2	± 0.017
2	Sample B	34	3.4	± 0.04
3	Sample C	41	4.1	± 0.01
4	Sample D	49	4.9	± 0.04
5	Sample E	77	7.7	± 0.17
6	Sample F	13	1.3	± 0.01
7	Sample G	35	3.5	± 0.02
8	Sample H	31	3.1	± 0.01
9	Sample I	30	3.0	± 0.08
10	Sample J	75	7.5	± 0.14

Total coliform counts

The population of total coliform is presented in Table 2.

The highest coliform count of $28.8 \pm 0.04 \times 10^2$ CFU/ml was recorded in sample D, while the lowest count of $0.3 \pm 0.02 \times 10^2$ CFU/ml was recorded in sample G.

Table 2. Total coliform counts of the water samples.

S/N	Sample	Number of colonies	$\times 10^2$ CFU/ml	Standard Deviation
1	Sample A	7	0.7	± 0.02
2	Sample B	42	4.2	± 0.02
3	Sample C	13	1.3	± 0.01
4	Sample D	288	28.8	± 0.04
5	Sample E	19	1.9	± 0.17
6	Sample F	20	2.0	± 0.01
7	Sample G	3	0.3	± 0.02
8	Sample H	6	0.6	± 0.04
9	Sample I	41	4.1	± 0.17
10	Sample J	45	4.5	± 0.14

Faecal coliform counts

The population of faecal coliform are presented in Table 3. The highest faecal coliform count is $17.8 \pm 0.75 \times 10^2$ CFU/ml recorded in sample H, while samples B, E, F and I recorded no faecal coliform counts.

Salmonella and Shigella counts

Salmonella and *Shigella* species counts for the

samples are presented in Table 4. The highest count was recorded in sample A which is $1.5 \pm 0.1 \times 10^2$ CFU/ml, while samples B, C, F, G, H, I and J recorded no counts.

Result of biochemical test and identification of *E. coli*

Results of the biochemical test of *E. coli* from domestic borehole water samples are shown in Table 5.

Table 3. Faecal coliform counts of the water samples.

S/N	Sample	Number of colonies	$\times 10^2$ CFU/ml	Standard Deviation
1	Sample A	18	1.8	± 0.02
2	Sample B	18	1.8	± 0.17
3	Sample C	No growth	0	
4	Sample D	168	16.8	± 0.75
5	Sample E	No growth	0	
6	Sample F	No growth	0	
7	Sample G	104	10.4	± 0.75
8	Sample H	178	17.8	± 0.75
9	Sample I	No growth	0	
10	Sample J	2	0.2	± 0.0

Table 4. *Salmonella* and *Shigella* bacterial isolate counts of the water samples.

S/N	Samples	Number of colonies	$\times 10^2$ CFU/ml	Standard Deviation
1	Sample A	15	1.5	± 0.1
2	Sample B	No growth	0	
3	Sample C	2	0.2	± 0.0
4	Sample D	No growth	0	
5	Sample E	5	0.5	± 0.0
6	Sample F	No growth	0	
7	Sample G	No growth	0	
8	Sample H	No growth	0	
9	Sample I	No growth	0	
10	Sample J	No growth	0	

Table 5. Biochemical characteristics of *E. coli*.

Biochemical characteristics	<i>Escherichia coli</i>
Gram stain	Negative
Shape	Rod
Motility	Mobile
Capsule	Variably capsulated
Spore	Non spore former
Flagella	Flagellated
Catalase	Positive
Methyl red(MR)	Positive
Indole	Positive
Citrate	Negative
Sugar fermentation	
Fructose	Positive
Glucose	Positive
Lactose	Positive
Maltose	Positive
Mannose	Positive

DISCUSSION

This study was conducted to investigate the presence of microbial contamination of coliform bacteria, particularly *E. coli*, in water used for domestic purposes in Aluu communities, Rivers State, Nigeria. The results of this study indicate varying levels of bacterial contamination in the water samples collected from Aluu Community in Rivers State, Nigeria. The total heterotrophic bacterial counts suggest that samples E and F have the highest and lowest levels of general bacterial contamination, respectively. This is consistent with previous studies that have reported varying levels of bacterial contamination in water sources in Nigeria (Ademola et al., 2019; Oladipo et al., 2020). The total coliform counts indicate that sample D has the highest level of coliform contamination, while sample G has the lowest. This agrees with a study conducted in Lagos, Nigeria, which reported high levels of coliform contamination in water sources (Adeyemo et al., 2018). Coliform bacteria are indicators of faecal contamination and can pose health risks to consumers (WHO, 2019). The faecal coliform counts suggest that sample H has the highest level of faecal contamination, while samples B, E, F, and I show no faecal coliform presence. This is consistent with a study conducted in Port Harcourt, Nigeria, which reported high levels of faecal coliform contamination in water sources (Nwanyanwu et al., 2019). Faecal coliform bacteria can cause waterborne diseases such as cholera, typhoid, and dysentery (CDC, 2020). *Salmonella* and *Shigella* species were detected only in sample A, indicating potential health risks. *Salmonella* and *Shigella* are pathogens that can cause waterborne diseases such as typhoid fever and dysentery (WHO, 2018; CDC, 2020).

The isolation of *Escherichia coli*, *Shigella sonnie*, *Staphylococcus* sp, *Citrobacter koseri*, and *Serratia marcescens* from some samples in Aluu community is a

significant public health concern. *E. coli* is a common indicator of faecal contamination and can cause waterborne diseases like urinary tract infections, diarrhoea, and pneumonia (CDC, 2020). *Shigella sonnie* is a pathogen that can cause shigellosis, a bacterial diarrhoea that can lead to severe complications like dehydration and death, especially in vulnerable populations like children and the elderly (WHO, 2019). *Staphylococcus* sp is a common cause of skin infections, pneumonia, and bloodstream infections (CDC, 2020). *Citrobacter koseri* is a pathogen that can cause urinary tract infections, septicemia, and meningitis, especially in neonates and immunocompromised individuals (CDC, 2020). *Serratia marcescens* is a multidrug-resistant pathogen that can cause various infections, including pneumonia, urinary tract infections, and bloodstream infections (CDC, 2020). The presence of these pathogens in water sources is a public health concern and requires proper treatment and management to ensure safe drinking water. The possible existence of these pathogenic bacteria isolates may indicate failure of treatment and lack of maintenance of borehole water after construction (Abu-Sini et al., 2023). The presence of *E. coli* in water samples intended for drinking and domestic purposes is a serious health risk to the inhabitants of the community, particularly to the immune-suppressed individuals and presents a risk of acquiring infections (Frampton and Restaino, 2003; Kirk et al., 2010; Sarantuya et al., 2011).

CONCLUSION AND RECOMMENDATION

The study found that *E. coli* is a reliable indicator of faecal contamination in drinking water, and its presence in water samples from Aluu community, Rivers state, indicates a high risk of waterborne diseases. The detection of *E. coli* and other indicator microorganisms in most water samples suggests that the water sources are contaminated with faecal matter, posing a significant public health risk. To ensure safe drinking water the following measures should be taken: improve water treatment methods, employ community-managed drinking water systems, regularly test and properly handle water quality, implement control measures by regulatory authorities, conduct regular monitoring and inspection, provide community education on hygiene practices, and perform follow-up demonstrations and monitoring to ensure effectiveness.

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- Citation:** Ogbuleka NAC, Aleruchi O, Kueniode OL, Awari VG, 2024. Evaluation of bacterial contamination in domestic water sources in Aluu community in Rivers State, Nigeria. *Microbiol Res Int*, 12(3): 73-77.
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