



Comparative Enumeration of Indicator Microorganisms in Two Water Sources in Kolokuma/Opokuma LGA, Bayelsa State

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Article ID: NJBR-BDC26-D009 | Received: 12 April, 2026 | Accepted: 19 April, 2026

ABSTRACT

Access to safe and portable water remains a major public health concern, and these water sources usually contain potential pathogenic organisms responsible for illness such as diarrhoea, cholera and typhoid fever. Hence, this study is aimed at comparing the enumeration of indicator microorganisms in well and borehole water sources in Kolokuma/Opokuma LGA, Bayelsa State. Water samples were collected from Odi and Kaiama, and microbiological analysis was conducted, such as total coliform count, faecal coliform count and microscopic examination. Total coliform counts were found in all the water sources, while the well water sample from Odi, had the highest total coliform count (280 MPN/100 mL). Coliform isolates, including Escherichia coli, Streptococcus faecalis, Salmonella spp, and Pseudomonas aeruginosa were found in the water samples, with E. coli having the highest frequency. This study, though still ongoing, reveals that the two water sources studied were contaminated by the presence of microorganisms, including indicator organisms, above the recommended levels by WHO, for a domestic water source.

Key words: Water, Odi, Kaiama, indicator organisms, total coliform

INTRODUCTION

Water is a crucial natural resource that sustains life and supports a wide range of domestic, agricultural and industrial activities. Despite its importance, access to safe and portable water remains a major public health concern, particularly in developing regions such as Kolokuma/Opokuma Local Government Area of Bayelsa state. In many rural and semi-urban communities in Nigeria, water is commonly sourced from rivers, shallow wells, boreholes and harvested rainwater, often without adequate treatment or routine quality monitoring (Nwidu et al., 2008; Augustine et al., 2025).

The microbiological quality of water is a perilous determinant of its safety for human consumption. Pointer microorganisms, such as total coliforms, faecal coliforms and *Escherichia coli*, are commonly used to evaluate water contamination and the potential presence of pathogenic organisms. These indicators are preferred because they are relatively easy to detect and are associated with faecal pollution, which may harbor disease-causing microorganisms responsible for illness such as diarrhoea, cholera and typhoid fever (Oyedeji et al., 2010). Previous Nigerian studies have reported alarming levels of microbial loads in groundwater sources in the Niger Delta, including Bayelsa state (Nwidu et al., 2008), while Aremu et al. (2011) documented contamination of well water in Ilorin. In regions like Bayelsa state, environmental factors such as flooding, poor sanitation practices, oil exploration activities and improper waste disposal contribute significantly to water contamination. Communities in Kolokuma/Opokuma largely depend on untreated surface and groundwater sources, increasing their vulnerability to water-borne infection. Seasonal variations and anthropogenic activities further influence the microbial load of these water sources (Edokpayi et al., 2017; Egbueri, 2021).

Comparative enumeration of indicator microorganisms across different water sources is therefore essential for evaluating their relative safety and identifying potential health risks. By quantifying and comparing microbial populations in various sources, it becomes possible to determine contamination levels, assess compliance with established water quality standards and provide baseline data for effective water management and intervention strategies (World Health Organization, 2017).

This study aims to comparatively enumerate indicator microorganisms present in different water sources within Kolokuma/Opokuma local government area, with a view to assessing their microbiological quality and implications for public health. The findings are expected to contribute to improving water quality monitoring, policy formation and the promotion of safe water practices in the study area.

MATERIALS AND METHODS

Study Area

The study was conducted in Odi and Kaiama communities located in Kolokuma/Opokuma Local Government Area of Bayelsa State, Nigeria. The area is located within the Niger Delta region and is characterized by a tropical climate, high rainfall, and extensive riverine and wetland systems. The inhabitants largely depend on various water sources such as boreholes, hand-dug wells, rivers, and rainwater for domestic use.

Sample Collection

Well and borehole water samples were collected from Odi and Kaiama in sterile 250 mL bottles, stored in an ice-packed cooler, and transported to the laboratory within 2-4 hours.

Microbiological Analysis

Media Preparation

Seventy-three grams of lactose broth was weighed using an analytical weighing balance and dissolved in 1000 mL of sterile distilled water inside a conical flask. Fifty-two grams of MacConkey agar powder was dissolved in 1000 mL of sterile distilled water, and 36 g of Eosin Methylene Blue powder was prepared in 1000 mL of sterile distilled water. For proper dissolution and homogenization, the media were shaken vigorously and melted using a water bath at a temperature of 45 °C for 40 min before sterilizing in an autoclave at 121 °C for 15 min. Media will be aseptically dispensed into oven-sterilized Petri dishes and allowed to solidify under laminar airflow.

Determination of Total Coliform Count

This was determined by the Most Probable Number (MPN) index method using a 5-5-5 regimen. MacConkey broth was used, and positive results were indicated by acid and gas production on incubation at 37 °C for 48 hours (Cheesebrough, 2006).

Determination of Faecal Coliform Count: Faecal coliform count was carried out using Eosin Methylene Blue medium while employing the pour plate technique. On Eosin Methylene Blue (EMB) agar, *E. coli* strains appear as greenish metallic sheen colonies and this was confirmed by the ability of the organism to ferment the lactose (Burnett and Beauchat, 2011).

Morphological Examination and Identification of Isolates on Media

The cultural characteristics of the isolates on different solid agar were examined. The growth patterns, colony size, edge, and elevation on the plates were noted after 48 hours of incubation at 37°C. Gram staining technique was carried out for the identification and differentiation of each

isolated bacterium. (Ryan and Ray, 2008). Microbial identification was performed using the keys provided in Bergey's Manual of Determinative Bacteriology (1994).

Statistical Analysis

Descriptive statistics and analysis of variance were used to analyze data obtained from the study. The level of significance was accepted at $p < 0.05$. The results were presented as mean and standard deviation.

RESULTS

The results show the number of positive McConkey broth tubes in the two water samples and their corresponding coliform counts. The well and borehole water samples all had positive tubes along with coliform counts. The well water had a higher total coliform count (280 and 34 MPN per 100 mL) than the borehole water (9 and 4 MPN/100 mL) (Table 1). Table 2 represents the results of growth morphology and microscopic examination of coliform isolates from the two water sources and the probable coliform bacteria present.

Table 1: Total coliform count of the different domestic water sources

Water Source	No. of positive tubes	MPN/100 mL
WW1	4-4-2	34
WW2	4-5-3	280
BW1	2-1-2	9
BW2	1-1-2	4

Keys: WW1 and WW2: Well water sources; BW1 and BW2: Borehole water sources

Table 2: Growth morphology and microscopic examination results of coliforms isolated from the two water sources

Water source	Gram reaction	Morphology	Colour of colonies on EMBA	Probable isolate
WW1	-ve	Rod	Pink	<i>Escherichia coli</i>
WW2	+ve	Cocci in chain	Colourless	<i>Streptococcus faecalis</i>
WW3	-ve	Rod	Pink	<i>Escherichia coli</i>
BW1	-ve	Rod	Greyish	<i>Pseudomonas aeruginosa</i>
BW2	-ve	Rod	Nil	<i>Salmonella spp</i>
BW3	-ve	Rod	Pink	<i>Escherichia coli</i>

Keys: WW1: Well water sources in triplicate; BW: Borehole water sources in triplicates

The results showed that the well water sample contained the presence of *E. coli* and *S. faecalis*, while the borehole water sample contained the presence of *E. coli*, *P. aeruginosa*, and *Salmonella* spp.

DISCUSSION

The result of the total coliform count showed that the values obtained were all above the WHO standard for coliform bacteria in drinking water, which is zero total coliform per 100 mL (Welch et al., 1993), for all the water sources. The highest total coliform count (280 MPN/100 mL) was recorded in well water. The presence of total coliform counts in water sources is an indication of faecal contamination. None of the water sources examined met the WHO standard, and this is in agreement with previous works by Benka-Coker Ohimain (1995), Idibie et al. (2018), and Ebah et al. (2022), who reported high microbial load in water with higher organic matter. The result also showed that four bacterial isolates were obtained from the different water samples, including *Escherichia coli*, *Streptococcus faecalis*, *Salmonella* spp, and *Pseudomonas aeruginosa*. The result also showed *E. coli* to have the highest occurrence.

CONCLUSION

The results of this investigation show that all the water sources studied were contaminated with microorganisms, including indicator organisms, exceeding the WHO-recommended values. This suggests the possible presence of pathogenic microorganisms in these water sources and makes them unsafe for human consumption, untreated. Comparatively, the water samples from the well were more contaminated, while those of the Borehole water samples were the least contaminated. The presence of these indicator microorganisms poses the danger of potential waterborne diseases. Additionally, research is ongoing to evaluate the total bacteria using a nutrient agar medium and mannitol salt agar for the isolation of *Staphylococcus aureus*, and *Salmonella*-Shigella agar for *Salmonella* spp isolation. Also, the biochemical evaluation is ongoing.

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How to Cite This Article

Augustine U.E., Timipanipiri T.W., Chukwunonso O., Daunemigha J.J., Ijeoma C.O., Basil E., Koki I., Odoronam, J. F., and Thomas A. (2026). Comparative Enumeration of Indicator Microorganisms in Two Water Sources in Kolokuma/Opokuma LGA, Bayelsa State. *NABDA Journal of Biotechnology Research*, 5(5), 74-78.