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# Evaluation of Bacterial Counts of Drinking Water Sources in Sagbama Local Government Area of Bayelsa State, Nigeria

**[1]Enaregha, Esther Benafegha & [2]Nnodim, Lasbry Chidi**

**[1]Biology Department,**
**Isaac Jasper Boro College of Education Sagbama, Nigeria**
**Email: estherenaregha@yahoo.com/+2347034867531**

**[2]Microbiology Department,**
**Rivers State University, Port Harcourt, Nigeria**
**Email: lasbry.nnodim@ust.edu.ng/2348134150863**

**ABSTRACT**

This study is aimed at evaluating the bacterial counts of drinking water sources in Sagbama Local Government Area (SLGA) in Bayelsa state. The water samples (borehole, river, and sachet waters) were aseptically collected and transported to the Department of Microbiology laboratory at Rivers State University. Total Heterotrophic Bacteria Count (THBC), Total Coliform Count (TCC), Faecal Coliform Count (FCC), Salmonella Count (SMC), Shigella Count (SHC), Staphylococcal Count (STC), Pseudomonad Count (PMC) and Vibriod Count (VBC) were enumerated using standard microbiological methods. The evaluation showed that mean bacterial counts of the water samples ranged from 0.18±0.09 - 5.44±0.40 (LogCFU/ml) with THBC (5.44±0.40) > TCC (5.27±2.35) > FCC (2.74±1.44) >STC (2.66±0.7) > SHC (2.44±1.72) > PMC (0.91±0.21) > SMC (0.60±0.07) > VBC (0.18±0.09). The THBC, FCC, TCC, SMC, SHC, STC, PMC and VBC of borehole water samples ranged from 5.51±0.03 – 6.18±0.02, 0.00 – 4.75±0.21, 3.12±0.02 - 10.36±0.27, 0.00 – 1.30±0.004, 0.00 – 5.40±0.02, 2.27±0.05 – 2.99±0.01, 0.00 – 2.60±0.08 and 0.00 (LogCFU/ml); river water samples ranged from 4.83±0.18 – 5.63±0.03, 0.00 – 3.20±0.01, 3.20±0.01 – 4.83±0.10, 0.00 – 1.63±0.21, 2.33±0.69 – 3.25±0.01, 2.40±0.02 – 2.97±0.04, 0.00 – 2.68±0.04, and 0.00 – 1.24±0.34; and sachet water samples ranged from 5.02±0.03 – 6.17±0.01, 0.00 – 4.15±0.21, 3.94±0.07 – 9.82±0.23, 0.00 – 1.24±0.34, 0.00 – 5.30±0.06, 1.45±0.03 - 4.69±0.12, 0.00, 0.00 - 1.63±0.21 (LogCFU/ml), respectively. The study found a significant negative correlation between THBC/SMC and THBC/SHC, while positive correlation was observed between TCC/FCC, TCC/SHC, TCC/STC, TCC/PMC, SHC/STC, SHC/VBC, and STC/VBC at p-value <0.05. The bacteriological quality of SLGA's drinking water sources is poor and necessitates immediate government intervention due to its public health importance.

**Keywords:** Bacterial counts; Drinking water sources; Borehole water; river water; sachet water

## INTRODUCTION

In recent times, after the year 2022 flood in Bayelsa State, the Bayelsa State government was encouraged to carry out periodic flood assessment studies as nature strikes daily through fires, hurricanes, earthquakes, and flooding (Odubo, 2014), as well as provision of adequate preparedness plans to surmount future occurrences of flood disasters in communities as greater portion are vulnerable to flooding (Berezi & Nwankwoala, 2022); and reports show that 98.8%, 97.8% and 94.9% of the population use rivers, open wells and boreholes respectively as their drinking water sources (Ajumobi *et al*., 2023).

Sagbama Local Government Area is a dynamic settlement in Bayelsa State that, Uzobo *et al*. (2017) reported noticeable migration into Sagbama, and the primary factor contributing to this migration being the influence of kin networks. The presence of institutions established both by private and government also contribute to the migration experienced in Sagbama Local Government Area (SALGA). SALGA is a coastal environment prone to seasonal flooding, which suggests the need for flood risk mapping of the environment (Mmom & Ayakpo, 2014) and the government should prioritize effective control over point sources of pollution in the area to ensure a healthier and cleaner environmental condition for the people (Mustapha *et al*., 2012; Nicholas, 2023; Olaitari, 2020).

The Sagbama river serve as both a source of drinking water and a location for open defecation for coastal communities, with a prevalence of waterborne diseases at 88%, typhoid being the most common at 64% and diarrhoea at 25%. Children under five years have the highest prevalence at 35%, indicating that the Sagbama river poses a significant health risk to its consumers (Ogbole & Oyelana, 2020): which could be attributed to urbanization (Shahabudin & Musa, 2018). Flood risk assessment before borehole installation and remediation of existing flood-prone boreholes to mitigate population exposure to contaminated water; as the greatest public health risk occurs when households are seeking alternative water sources during or following flood season. (Dzodzomenyo *et al*., 2022), suggesting the need to control environmental pollution of the river to keep the environment safe for water organisms and people living in the area who depend on it for their livelihood (Egbere *et al*., 2023; Ezekwe *et al*., 2022). Knowing that most of Nigeria's rural and coastal communities drink from surface water sources where groundwater is inaccessible (Enaregha *et al*., 2022). It is important to remember that without water, there is no food, and without food, there is no security; inferring that to develop and manage water sustainably, the government should provide strong policy, legal and regulatory frameworks, effective organizations and tools, and by being proactive in monitoring and compliance (Olalekan *et al*., 2019). Each water source could show different concentrations of contamination metrics, making them unsafe for human consumption (Sun *et al*., 2016).

A flood is a natural event that is inescapable with frequent occurrences in waterways and natural drainage structures destroying lives, natural resources, and environs together with health challenges and economic loss yearly (Berezi & Nwankwoala, 2022). Naturally occurring disasters (like flooding) are one of the risks brought on by environmental changes and natural disasters that people in society fear the most (Sholihah *et al*., 2020). Flooding also affects the quality of groundwater and surface water resources and can cause supply service interruption due to damaged infrastructures, reduction in groundwater quality and deterioration of stored water quality, which is also due to turbidity, resulting in disease outbreaks (Barbetta *et al*., 2022). This could have resulted in the report of residents suffering from one form of infection or the other (20, 18, 15.3, 13.3, and 12 (%) had suffered from diarrhoea, toilet infections, typhoid, dysentery, and worm infection respectively) (Amawulu, 2020).

This indicates that flooding has been the most devastating natural disaster in the world which has often impacted negatively on the socio-cultural organization of human societies, and recently, the Niger Delta region of Nigeria, particularly Bayelsa State, was severely affected by flooding (Odubo, 2014; Sun *et al*., 2016); with significant health hazards on the residents due to environmental impact of flooding (Olaitari, 2020); especially those water-related diseases causing the death of children under five years worldwide, which are more evident in rural areas of developing countries (Grady *et al*., 2014; Hambati & Smiley, 2019).

Water is essential and its safety is indispensable for life and the well-being of ecosystems, food security, sustainable development, and humanity's future (as approximately 80% of diseases, including those caused by bacteria, viruses, and parasites, are transmitted through contaminated water sources) (KiliÇ, 2021; Kponee *et al*., 2015; Nicholas, 2023). Water is a life-supporting liquid and humans like other living beings require it for their metabolism, domestic and industrial activities (Akpan & Ajayi, 2016; Al-Taa, 2021; Barbetta *et al*., 2022). Thus, a fundamental starting point for food and life, and its scarcity are a critical global issue: as about a billion people lack access to adequate supplies of water and two billion suffer from the consequences of poor sanitation due to contaminated water sources. And about 95% of deadly diseases in the human body is associated with the consumption of liquid content (Olalekan *et al*., 2019). This suggests that, the quality of the water consumed by the people calls into question the water and sanitation

component of the public health system (Anarado *et al*., 2019). Sagbama environs are not exempted as faecal contamination of drinking water is a significant challenge in the oil-bearing communities of the Niger Delta region in Nigeria (Maduka & Ephraim-Emmanuel, 2019).

The suspicion of surface and underground water contamination by many people encouraged the commercialization and consumption of sachet water (to meet with demand for safe and potable water) whether certified or not (Airaodion, 2019). Because it is inexpensive, convenient, and reliably available, sachet water is becoming more and more well-liked and accepted by society. On the other hand, serious questions are raised about its portability, safety, and hygiene; as water taken out of a borehole is the main source of sachet water (Adiotomre & Agbale, 2015). Many researchers have reported the portability and safeness of sachet water sold in some parts of Nigeria (Chiwetalu *et al*., 2022; Dada, 2009), while others have argued that, selling water in sachets to the general public, national surveillance agencies are required to keep an eye on and enforce compliance with microbiological safety regulations (Edema et al., 2011; Emerenini, 2020a; Ifeanyi et al., 2006; Magaji, 2020; Ngwai et al., 2010; Opafola et al., 2020; Udoh et al., 2021).

The quality of the water supply is assessed by bacteriological properties, thus, the presence of these types of bacteria in water sources can lead to health problems for those who consume it (Adesakin *et al*., 2020). Bacterial contamination of drinking water sources has continued to emerge, as an important public health concern across the globe and has been associated with water epidemic outbreaks, especially in rural communities where access to potable water remains a massive challenge (Azuonwu *et al*., 2019). The major indicator of water contamination is high bacterial density (Agedah *et al*., 2015) and in the water network systems, it was reported that a high concentration of heterotrophic bacteria count, correlated with a high concentration of coliforms and faecal streptococci bacteria (Amanidaz *et al*., 2015). The sachet water contaminated with bacteria, such as *Enterobacter* species, *Pseudomonas* species, *Escherichia* coli, and *Klebsiella* species were recommended for proper treatment to provide safe and high-quality packaged drinking fluids (Bukar *et al*., 2015). Low levels of Heterotrophic Plate Count in drinking water indicate effective treatment but an increase in the HPC baseline range signals a change in the treatment process, an interruption or contamination in the distribution system, or a shift in the water's overall bacteriological quality. The HPC test can be used in conjunction with monitoring for Escherichia coli, and Total coliforms, as part of a multi-barrier approach to safe drinking water production (Health Canada, 2012).

## MATERIALS AND METHODS

### Sampling Area

The centre region of Nigeria's Bayelsa State is home to the Sagbama Local Government Area. It is situated in the southern part of Nigeria, more precisely in the Niger Delta region. Around 5.1000° N latitude and 6.1167° E longitude are Sagbama's geographic coordinates. The geography of Sagbama is distinguished by low-lying coastal plains, mangrove swamps, and riverine habitats. The region is crisscrossed with streams, rivers, and waterways that are essential for transportation, fishing, and agriculture. The region is well-known for its diverse flora and animals, which are typical of a deltaic environment.

### Sample Collection and Sampling Point

The bacteriological quality of drinking water from the primary sources (river, tap, and sachet) was evaluated in cross-sectional research. Samples were collected from sixteen different locations and grouped into three types of water sources. Five tap water samples (customer taps), six river water samples (1000 ml), respectively and five brands of sachet water were collected from different sites of the distribution system aseptically. The locations where water samples, were collected are Sagbama town (5°9′33"N 6°11′40"E; 5°9′29"N 6°11′43"E), Tungbo (5°7′23"N 6°10′0"E; 5°7′30"N 6°10′5"E), Bolu-Orua (5°6′37"N 6°7′15"E; 5°6′42"N 6°7′11" E), Toru-Angiama (5°8′17"N 6°6′35"E), Ebedebiri (5°8′18"N 6°4′20" E) and Toru-Orua (5°6′10"N 6°3′52"E; 5°6′18"N 6°4′1"E) for river and borehole samples used by the public, respectively; the sachet water samples coded as PA, GG, AQB, EBN and ESE. Each collected water sample was labelled with the temporal code and transported in coolers containing ice cubes within 2-3 hours to the research laboratory located at Rivers State University for analyses (Garkuwa *et al*., 2020; Gemechu *et al*., 2018; Malhotra *et al*., 2015; Solomon *et al*., 2011).

**Microbiological Analyses of Water Samples**

Each water sample for the bacteriological examination (1 ml) was transferred aseptically into 9 ml of 0.1% sterile peptone water, mixed well, and the necessary dilutions were made for the microbiological investigations. Water samples underwent a bacterial examination on media to look for the following categories of bacteria:

***Enumeration of Total Heterotrophic Bacteria***

The Total heterotrophic bacteria counts were made on nutrient agar (28 g/L) by using the spread plate technique method of Edema *et al*. (2011) adapted, from the water sample 0.1ml was aseptically transferred onto the centre of a prepared nutrient agar and a sterile glass rod was used to spread the water sample evenly on the surface of media (Bukar *et al*., 2015), the agar plates were incubated inverted at 37 °C for 48 h. Distinct colonies were counted, which should range from 30 – 300 colonies and the Logarithm of colony forming units per millilitre (LogCFU/ml) of sample was calculated by counting the resulting colonies on the plates (Agedah *et al*., 2015).

***Enumeration of Total Coliform and Faecal Coliform Bacteria***

The Eosine Methylene Blue agar (35.96 g/L) plate was prepared according to standard microbiological practice as employed by Ndayisenga *et al*. (2020) and Taiwo *et al*. (2020) adapted. 0.1 ml of the diluted water samples were aseptically transferred onto the centre of a prepared MacConkey agar and a sterile glass rod was used to spread the water sample evenly on the surface of the media. After complete solidification, the inoculated plates were inverted and incubated under different temperatures according to the targeted bacteria (37°C for 24 - 48 for Total Coliform, which is identified by pinkish colonies; 44.5 °C for 24 - 48 h for faecal coliform, which is identified by metallic sheen colouration. The Total and Faecal coliform count per millilitre in water samples were calculated from the number of colonies obtained.

***Enumeration of Staphylococcal Counts***

Mannitol salt agar (111 g/L) plates were prepared according to the manufacturer's instructions (Abu *et al*., 2020). Aliquots (0.1 ml) from diluted water samples were transferred onto the centre of the media and spread-plated. The inoculated plates were inverted and incubated under the temperature of 37°C for 24 – 48h to assess for the presence of *Staphylococcus* species. Distinct yellow and pink colonies were counted as *Staphylococcus aureus* and non-*Staphylococcus aureus* colonies, respectively.

***Enumeration of Pseudomonad Counts***

Cetrimide agar also known as (Pseudosal Isolation Agar) (45.3 g/L) was used for *Pseudomonas* sp. enumeration of the water samples method employed by Mahmood and Mohamad (2022) slightly adapted. Aliquots (0.1 ml) from diluted water samples were transferred onto the centre of the media and spread-plated. The inoculated plates were inverted and incubated under the temperature of 37°C for 24 – 48h to assess for the presence of *Pseudomonas* species. Distinct yellow and green colonies were counted as *Pseudomonas aeruginosa* and non-*Pseudomonas aeruginosa* colonies, respectively.

***Enumeration of Salmonella, Shigella and Vibrio Counts***

The Salmonella/Shigella agar (60 g/L) was used for *Salmonella* sp. and *Shigella* sp. enumeration, while Thioglycolate Citrate Bile Salt agar (89.08 g/L) was used for Vibriod enumeration method of Abu *et al*. (2020); Adesoji *et al*. (2019) adapted. The media were prepared (by boiling for a minute without autoclaving) according to the manufacturer's instructions. Aliquots (0.1 ml) from diluted water samples were transferred onto the centre of the media and spread-plated. The inoculated plates were inverted and incubated under the temperature of 37°C for 24 – 48h. On Salmonella/Shigella agar, colonies with black eye dots indicate *Salmonella* sp. and pinkish colonies indicate *Shigella* sp. In contrast, on Thioglycolate Citrate Bile Salt agar, yellow colonies indicate *Vibrio cholerae* and green colonies indicate *Vibrio parahaemolyticus*.

**Calculation of Bacterial Cell Population**

The bacterial cell population for each of the media were done in LogCFU/ml.

Bacterial cell population = $\log_{10}\left(\frac{Number\ of\ colonies}{Volume\ plated \times Dilution\ factor}\right)$ (Maes *et al*., 2019).

**Statistical Analysis**

Statistical analyses on the obtained microbiological enumerations results were carried out using Statistical Analysis System software (Minitab®, version 21.4.2, 2023 Minitab LLC). Distribution of the log-transformed enumerations per microbiological parameters was represented by mean and standard deviation for normally distributed value and evaluated using Analysis of Variance (ANOVA), PCA, Cluster analysis and correlation (Maes *et al*., 2019) with slight modification.

## RESULTS

**Mean bacterial counts of drinking water sources in Sagbama Local Government Area.**

The mean bacterial count parameters considered during water analysis are Total heterotrophic bacterial counts (THBC), Faecal Coliform count (FCC), Total coliform counts (TCC), Salmonella counts (SMC), Shigella counts (SHC), Staphylococcal counts (STC), Pseudomonad counts (PMC), and Vibriod counts (VBC) expressed in LogCFU/ml. The comparison of the bacterial counts' parameters of the drinking water sources in Table 1. showed that any water sample obtained from the study areas in Sagbama Local Government Area (SALGA) contained at least an average of THBC (5.44±0.40) > TCC (5.27±2.35) > FCC (2.74±1.44) >STC (2.66±0.7) > SHC (2.44±1.72) > PMC (0.91±0.21) > SMC (0.60±0.07) > VBC (0.18±0.09). The bacterial count parameters showed a significant difference statistically in their mean bacterial counts at P-value <0.0001.

**Table 1: Overall mean bacterial counts (LogCFU/ml) parameters of drinking water samples**

| **Bacterial counts** | **Mean**±Std | **P-value** |
|---|---|---|
| Heterotrophic bacterial count | 5.44±0.40 $^{A}$ | |
| Faecal Coliform Count | 2.74±1.44 $^{B}$ | |
| Total coliform count | 5.27±2.35 $^{A}$ | |
| Salmonella count | 0.60±0.07 $^{C}$ | |
| Shigella count | 2.44±1.72 $^{B}$ | <0.0001 |
| Staphylococcal count | 2.66±0.72 $^{B}$ | |
| Pseudomonad count | 0.91±0.21 $^{C}$ | |
| Vibriod count | 0.18±0.09 $^{C}$ | |

The mean bacterial counts of selected drinking water sources (Borehole water, River water and sachet water) sampled from some communities in SLGA are represented in Table 2. The total heterotrophic bacterial counts (THBC) ranged from 5.19±0.33 – 5.73±0.26 (LogCFU/ml), then recording 5.73±0.26, 5.19±0.33 and 5.46±0.42 (LogCFU/ml) for borehole water, river water and sachet water samples, respectively; borehole water sample recorded the highest value of 5.73±0.26 (LogCFU/ml). Statistically, there is a significant difference in the THBC of the drinking water sources at P-value <0.0001. FCC ranged from 2.60±1.22 - 2.85±1.64 (LogCFU/ml), faecal coliform count of 2.85±1.64, 2.60±1.22 and 2.80±1.61 (LogCFU/ml) were recorded for borehole water, river water and sachet water samples, respectively. Borehole waters had the highest value of 2.85±1.64 (LogCFU/ml), with no statistically significant difference in FCC of the drinking water sources at P-value 0.916. TCC of the drinking water sources ranged from 4.13±0.74 - 6.51±2.66 (LogCFU/ml), while the TCC of 5.40±2.79, 4.13±0.74 and 6.51±2.66 (LogCFU/ml) were recorded for borehole water, river water and sachet water samples, respectively. Sachet water recorded the highest TCC value of 6.51±2.66 (LogCFU/ml). Statistically, there is a significant difference in the TCC of the drinking water sources at a P-value of 0.054. Salmonella counts (SMC) ranged from 0.25±0.53 – 1.18±0.60 (LogCFU/ml), and SMC values of 0.26±0.55, 1.18±0.60 and

0.25±0.53 were reported for borehole water, river water and sachet water, respectively. River water had the highest SMC (1.18±0.60 LogCFU/ml). Statistically, there is a significant difference in the SMC at P-value <0.0001.

Shigella counts (SHC) of the drinking water sources ranged from 1.72±2.34 – 3.02±0.40 (LogCFU/ml), of which borehole water, river water and sachet water recorded SHC of 1.72±2.34, 3.02±0.40 and 2.47±1.88 (LogCFU/ml), respectively. In contrast, the highest SHC is recorded from river water (3.02±0.40 LogCFU/ml). Statistically, there is no significant difference in the SHC at a P-value of 0.220. Staphylococcal counts (STC) of the drinking water sources ranged from 2.59±1.26 – 2.72±0.33 (LogCFU/ml), with borehole waters, river waters and sachet waters recording mean count of 2.72±0.33, 2.66±0.24 and 2.59±1.26, respectively, and borehole waters recording the highest STC (2.72±0.33 LogCFU/ml). Statistically, there is no significant difference in the STC at a P-value of 0.928. Pseudomonad counts (PMC) of the drinking water sources ranged from 0.00 – 1.99±0.98 (LogCFU/ml), with the drinking water sources: borehole water, rivers water and sachet water recording mean counts of 0.52±0.09, 1.99±0.98 and 0.00 (LogCFU/ml), respectively; and river water recorded the highest count of 1.99±0.98 (LogCFU/ml). Statistically, there is a significant difference in the PMC at P-value <0.0001. Vibriod counts (VBC) of the drinking water sources ranged from 0.00 – 0.33±0.69 (LogCFU/ml), with the drinking water sources: borehole water, river water and sachet water recording mean counts of 0.00, 0.21±0.49 and 0.33±0.69 (LogCFU/ml), respectively; and sachet water recorded highest count of 0.33±0.69 (LogCFU/ml). Statistically, there is no significant difference in the VBC at P-value 0.335.

**Table 2: Mean Bacterial Counts (LogCFU/ml) of drinking water sources of some communities in SLGA**.

| Drinking Water Sources | Total Heterotrophic Bacteria Count | Faecal Coliform Count | Total Coliform Count | Salmonella Count | Shigella Count | Staphylococcal Count | Pseudomonad Count | Vibriod Count |
|---|---|---|---|---|---|---|---|---|
| Borehole water | 5.73±0.26$^{A}$ | 2.85±1.64$^{AB}$ | 5.40±2.79$^{AB}$ | 0.26±0.55$^{B}$ | 1.72±2.34$^{A}$ | 2.72±0.33$^{A}$ | 0.52±0.09$^{B}$ | 0.00$^{A}$ |
| River water | 5.19±0.33$^{B}$ | 2.60±1.22$^{A}$ | 4.13±0.74$^{B}$ | 1.18±0.60$^{A}$ | 3.02±0.40$^{A}$ | 2.66±0.24$^{A}$ | 1.99±0.98$^{A}$ | 0.21±0.49$^{A}$ |
| Sachet water | 5.46±0.42$^{AB}$ | 2.80±1.61$^{A}$ | 6.51±2.66$^{A}$ | 0.25±0.53$^{B}$ | 2.47±1.88$^{A}$ | 2.59±1.26$^{A}$ | 0.00$^{B}$ | 0.33±0.69$^{A}$ |
| **P-value** | **0.005** | **0.916** | **0.054** | **<0.0001** | **0.220** | **0.928** | **<0.0001** | **0.335** |

**Bacterial Counts of Borehole Water Sampled from different Communities in SLGA.**

The bacterial counts of borehole water samples sampled from Bolu-Orua, Ebedebiri, Sagbama town, Toru-Orua, and Tungbo communities in Sagbama LGA are illustrated in Table 3. The THBC of the borehole water samples ranged from 5.51±0.03 – 6.18±0.02 (LogCFU/ml). Bolu-Orua, Ebedebiri, Sagbama town, Toru-Orua, and Tungbo communities recorded THBC of 5.51±0.03, 6.18±0.02, 5.68±0.05, 5.74±0.03 and 5.52±0.06 (LogCFU/ml), respectively; Ebedebiri community (6.18±0.02 LogCFU/ml) recorded the highest THBC. Statistically, there is a significant difference in the THBC means at a P-value <0.0001. The FCC of the borehole water samples ranged from 0.00 – 4.75±0.21 (LogCFU/ml) and Bolu-Orua, Ebedebiri, Sagbama town, Toru-Orua, and Tungbo communities recorded FCC of 4.75±0.21, 3.12±0.02, 3.23±0.07, 0.00 and 3.13±0.05 (LogCFU/ml), respectively; Bolu-Orua community (4.75±0.21 LogCFU/ml) recorded the highest FCC. Statistically, there is a significant difference in the FCC means at P-value <0.0001. The TCC of the borehole water samples ranged from 3.12±0.02 - 10.36±0.27 (LogCFU/ml) and Bolu-Orua, Ebedebiri, Sagbama town, Toru-Orua, and Tungbo communities recorded TCC of 10.36±0.27, 3.12±0.02, 3.23±0.07, 5.44±0.08, and 4.84±0.38 (LogCFU/ml), respectively; Bolu-Orua community (10.36±0.27 LogCFU/ml) recorded the highest TCC. Statistically, there is a significant difference in the TCC means at P-value <0.0001. The SMC of the borehole water samples ranged from 0.00 – 1.30±0.004 (LogCFU/ml),

and only the Bolu-Orua community recorded 1.30±0.004 (LogCFU/ml) SMC. The SHC of the borehole water samples ranged from 0.00 – 5.40±0.02 (LogCFU/ml), but only Bolu-Orua and Toru-Orua recorded SHC of 3.22±0.01 and 5.40±0.02 (LogCFU/ml), respectively. The STC of the borehole water samples ranged from 2.27±0.05 – 2.99±0.01 (LogCFU/ml), the towns Bolu-Orua, Ebedebiri, Sagbama town, Toru-Orua, and Tungbo communities recorded STC of 2.94±0.04, 2.99±0.01, 2.27±0.05, 2.98±0.03 and 2.44±0.05 (LogCFU/ml), respectively. Statistically, there is a significant difference in the STC means at P-value <0.0001. The VBC of the borehole water samples was recorded as 0.00 (LogCFU/ml). The PMC of the borehole water samples ranged from 0.00 – 2.60±0.08 (LogCFU/ml), and only the Ebedebiri community recorded 2.60±0.08 (LogCFU/ml).

**Table 3: Mean bacterial counts (LogCFU/ml) of borehole water of some communities in SLGA**.

| Water sample | Total Heterotrophic bacterial counts | Faecal Coliform counts | Total Coliform counts | Salmonella counts | Shigella counts | Staphylococcal counts | Pseudomonad counts | Vibriod count |
|---|---|---|---|---|---|---|---|---|
| Bolu-Orua Borehole | $5.51\pm0.03^{C}$ | $4.75\pm0.21^{A}$ | $10.36\pm0.27^{A}$ | 1.30±0.004 | 3.22±0.01 | $2.94\pm0.04^{A}$ | 0.00 | 0.00 |
| Ebedebiri borehole | $6.18\pm0.02^{A}$ | $3.12\pm0.02^{B}$ | $3.12\pm0.02^{C}$ | 0.00 | 0.00 | $2.99\pm0.01^{A}$ | 2.60±0.08 | 0.00 |
| Sagbama town borehole | $5.68\pm0.05^{B}$ | $3.23\pm0.07^{B}$ | $3.23\pm0.07^{C}$ | 0.00 | 0.00 | $2.27\pm0.05^{C}$ | 0.00 | 0.00 |
| Toru-Orua borehole | $5.74\pm0.03^{B}$ | $0.00^{C}$ | $5.44\pm0.08^{B}$ | 0.00 | 5.40±0.02 | $2.98\pm0.03^{A}$ | 0.0 | 0.00 |
| Tungbo borehole | $5.52\pm0.06^{C}$ | $3.13\pm0.05^{B}$ | $4.84\pm0.38^{B}$ | 0.00 | 0.00 | $2.44\pm0.05^{B}$ | 0.00 | 0.00 |
| **P-value** | **<0.0001** | **<0.0001** | **<0.0001** | | | <0.0001 | | |

**Bacterial Counts of River Water Sampled from different Communities in SLGA.**

The bacterial counts of water samples sampled from rivers located in the selected communities in Sagbama LGA are shown below in Table 4. The THBC of the river water samples ranged from 4.83±0.18 – 5.63±0.03 (LogCFU/ml). The THBC of river water samples from Bolu-Orua, Ebedebiri, Sagbama town, Toru-Angiama, Toru-Orua, and Tungbo communities recorded the count of 5.15±0.04, 4.87±0.12, 4.83±0.18, 5.63±0.03, 5.56±0.01 and 5.14±0.13 (LogCFU/ml), respectively; and Toru-Angiama community (5.63±0.03 LogCFU/ml) recorded the highest THBC. Statistically, there is a significant difference in the means of THBC at a P-value of 0.001. The FCC of the river water samples ranged from 0.00 – 3.20±0.01 (LogCFU/ml). The FCC of river water samples from Bolu-Orua, Ebedebiri, Sagbama town, Toru-Angiama, Toru-Orua, and Tungbo communities recorded the count of 3.20±0.01, 0.00, 3.03±0.05, 3.06±0.02, 3.12±0.04 and 3.18±0.01 (LogCFU/ml), respectively; and Bolu-Orua community river (3.20±0.01 LogCFU/ml) recorded the highest FCC. Statistically, there is a significant difference in the means of FCC at P-value <0.0001. The TCC of the river water samples ranged from 3.20±0.01 – 4.83±0.10 (LogCFU/ml). The TCC of river water samples from Bolu-Orua, Ebedebiri, Sagbama town, Toru-Angiama, Toru-Orua, and Tungbo communities recorded the count of 3.20±0.01, 4.74±0.06, 4.83±0.10, 4.30±0.32, 3.12±0.04, and 4.57±0.13 (LogCFU/ml), respectively; and Sagbama town community river (4.83±0.10 LogCFU/ml) recorded the highest TCC. Statistically, there is a significant difference in the means of TCC at P-value <0.0001. The SMC of the river water samples ranged from 0.00 – 1.63±0.21 (LogCFU/ml). The SMC of river water samples from Bolu-Orua, Ebedebiri, Sagbama town, Toru-Angiama, Toru-Orua, and Tungbo communities recorded the count of 1.63±0.21, 1.54±0.09, 1.15±0.21, 1.59±0.16, 0.00 and 1.15±0.21 (LogCFU/ml), respectively; and Bolu-Orua community river (1.63±0.21 LogCFU/ml) recorded the highest count of SMC. Statistically, there is a significant difference in the means of SMC at P-value <0.0001.

The SHC of the river water samples ranged from 2.33±0.69 – 3.25±0.01 (LogCFU/ml). The SHC of river water samples from Bolu-Orua, Ebedebiri, Sagbama town, Toru-Angiama, Toru-Orua, and Tungbo communities recorded the count of 3.24±0.002, 3.15±0.01, 3.18±0.01, 3.25±0.01, 2.96±0.05, and

2.33±0.69 (LogCFU/ml), respectively; Toru-Angiama community's river (3.25±0.01 LogCFU/ml) recorded the highest SHC. Statistically, there is no significant difference in the means of STC at a P-value of 0.102. The STC of the river water samples ranged from 2.40±0.02 – 2.97±0.04 (LogCFU/ml). The STC of river water samples from Bolu-Orua, Ebedebiri, Sagbama town, Toru-Angiama, Toru-Orua, and Tungbo communities recorded the count of 2.53±0.04, 2.97±0.04, 2.43±0.05, 2.40±0.02, 2.93±0.08, and 2.72±0.03 (LogCFU/ml), respectively; Ebedebiri community river (2.97±0.04 LogCFU/ml) recorded the highest STC. Statistically, there is a significant difference in the means of STC at P-value <0.0001. The PMC of the river water samples ranged from 0.00 – 2.68±0.04 (LogCFU/ml). The PMC of river water samples from Bolu-Orua, Ebedebiri, Sagbama town, Toru-Angiama, Toru-Orua, and Tungbo communities recorded the count of 2.68±0.04, 0.00, 2.45±0.02, 1.78±0.25, 2.59±0.08, and 2.45±0.03 (LogCFU/ml), respectively; and Bolu-Orua community river (2.68±0.04 LogCFU/ml) recorded the highest PMC. Statistically, there is a significant difference in the means of PMC at P-value <0.0001. The VBC of the river water samples ranged from 0.00 – 1.24±0.34 (LogCFU/ml), and only the Ebedebiri community river recorded 1.24±0.34 (LogCFU/ml).

**Table 4: Mean Bacterial Counts (LogCFU/ml) of River Water of some Communities in SLGA.**

| Water sample | Total Heterotrophic bacterial counts | Faecal Coliform counts | Total Coliform counts | Salmonella counts | Shigella counts | Staphylococcal counts | Pseudomonad counts | Vibriod count |
|---|---|---|---|---|---|---|---|---|
| Bolu-Orua river | $5.15\pm0.04^{BC}$ | $3.20\pm0.01^{A}$ | $3.20\pm0.01^{B}$ | $1.63\pm0.21^{A}$ | $3.24\pm0.002^{A}$ | $2.53\pm0.04^{C}$ | $2.68\pm0.04^{A}$ | 0.00 |
| Ebedebiri river | $4.87\pm0.12^{C}$ | $0.00^{C}$ | $4.74\pm0.06^{A}$ | $1.54\pm0.09^{A}$ | $3.15\pm0.01^{A}$ | $2.97\pm0.04^{A}$ | $0.00^{C}$ | 1.24±0.34 |
| Sagbama town river | $4.83\pm0.18^{C}$ | $3.03\pm0.05^{B}$ | $4.83\pm0.10^{A}$ | $1.15\pm0.21^{A}$ | $3.18\pm0.01^{A}$ | $2.43\pm0.05^{C}$ | $2.45\pm0.02^{A}$ | 0.00 |
| Toru-Angiama River | $5.63\pm0.03^{A}$ | $3.06\pm0.02^{B}$ | $4.30\pm0.32^{A}$ | $1.59\pm0.16^{A}$ | $3.25\pm0.01^{A}$ | $2.40\pm0.02^{C}$ | $1.78\pm0.25^{B}$ | 0.00 |
| Toru-Orua River | $5.56\pm0.01^{AB}$ | $3.12\pm0.04^{AB}$ | $3.12\pm0.04^{B}$ | $0.00^{B}$ | $2.96\pm0.05^{A}$ | $2.93\pm0.08^{A}$ | $2.59\pm0.08^{A}$ | 0.00 |
| Tungbo river | $5.14\pm0.13^{C}$ | $3.18\pm0.01^{A}$ | $4.57\pm0.13^{A}$ | $1.15\pm0.21^{A}$ | $2.33\pm0.69^{A}$ | $2.72\pm0.03^{B}$ | $2.45\pm0.03^{A}$ | 0.00 |
| **P-value** | **0.001** | **<0.0001** | **<0.0001** | **<0.0001** | **0.102** | **<0.0001** | **<0.0001** | |

**Bacterial Counts Of Sachet Water were Sampled from some Communities in SLGA.**

The bacterial counts of five sachet water brands sold in some communities in Sagbama LGA are shown in Table 5., which are coded as AQB, EBM, ESE, GG, and PA. The THBC of the sachet water samples ranged from 5.02±0.03 – 6.17±0.01 (LogCFU/ml). AQB, EBM, ESE, GG, and PA sachet water THBC are as follows, 5.50±0.04, 6.17±0.01, 5.45±0.04, 5.02±0.03, and 5.15±0.11 (LogCFU/ml), respectively; with EBM sachet water (6.17±0.01 LogCFU/ml) recording the highest THBC. Statistically, there is a significant difference in the means of THBC at P-value <0.0001. The FCC ranged from 0.00 – 4.15±0.21 (LogCFU/ml). AQB, EBM, ESE, GG, and PA sachet water FCC are as follows, 4.15±0.21, 0.00, 3.15±0.10, 2.55±0.05, and 4.15±0.21 (LogCFU/ml), respectively; AQB and PA sachet waters (4.15±0.21 LogCFU/ml) recording the highest FCC. Statistically, there is a significant difference in the means of FCC at P-value <0.0001. The TCC ranged from 3.94±0.07 – 9.82±0.23 (LogCFU/ml). AQB, EBM, ESE, GG, and PA sachet water TCC are as follows, 9.82±0.23, 4.80±0.14, 4.65±0.38, 3.94±0.07, and 9.32±0.09 (LogCFU/ml), respectively; AQB (9.82±0.23 LogCFU/ml) and PA (9.32±0.09 LogCFU/ml) sachet waters recording the highest TCC. Statistically, there is a significant difference in the means of TCC at P-value <0.0001. The SMC ranged from 0.00 – 1.24±0.34 (LogCFU/ml), and only PA sachet water recorded an SMC of 1.24±0.34 (LogCFU/ml).

The SHC ranged from 0.00 – 5.30±0.06 (LogCFU/ml). AQB, EBM, ESE, GG, and PA sachet water SHC are as follows, 5.30±0.06, 0.00, 1.45±0.21, 2.27±0.02, and 3.32±0.02 (LogCFU/ml), respectively; AQB sachet water (5.30±0.06 LogCFU/ml) recorded the highest SHC. Statistically, there is a significant difference in the means of SHC at a P-value <0.0001. The STC ranged from 1.45±0.03 - 4.69±0.12 (LogCFU/ml). AQB, EBM, ESE, GG, and PA sachet water STC are as follows, 4.69±0.12, 2.36±0.03, 1.45±0.21, 1.50±0.28, and 2.97±0.03 (LogCFU/ml), respectively; AQB sachet water (4.69±0.12 LogCFU/ml) recorded the highest STC. Statistically, there is a significant difference in the means of STC

at P-value <0.0001. The PMC of the sachet water samples were 0.00 (LogCFU/ml). While the VBC ranged from 0.00 - 1.63±0.21 (LogCFU/ml), with only AQB sachet water recording a VBC of 1.63±0.21 (LogCFU/ml).

**Table 5: Bacterial Counts (LogCFU/ml) of Sachet Water Sampled from some Communities in SLGA.**

| Water sample | Total Heterotrophic bacterial counts | Faecal Coliform counts | Total Coliform counts | Salmonella counts | Shigella counts | Staphylococcal counts | Pseudomonad counts | Vibriod count |
|---|---|---|---|---|---|---|---|---|
| AQB sachet water | 5.50±0.04$^{B}$ | 4.15±0.21$^{A}$ | 9.82±0.23$^{A}$ | 0.00 | 5.30±0.06$^{A}$ | 4.69±0.12$^{A}$ | 0.00 | 1.63±0.21 |
| EBM sachet water | 6.17±0.01$^{A}$ | 0.00$^{D}$ | 4.80±0.14$^{B}$ | 0.00 | 0.00$^{E}$ | 2.36±0.03$^{B}$ | 0.00 | 0.00 |
| ESE sachet water | 5.45±0.04$^{B}$ | 3.15±0.10$^{B}$ | 4.65±0.38$^{B}$ | 0.00 | 1.45±0.21$^{D}$ | 1.45±0.21$^{C}$ | 0.00 | 0.00 |
| GG sachet water | 5.02±0.03$^{C}$ | 2.55±0.05$^{C}$ | 3.94±0.07$^{B}$ | 0.00 | 2.27±0.02$^{C}$ | 1.50±0.28$^{C}$ | 0.00 | 0.00 |
| PA sachet water | 5.15±0.11$^{C}$ | 4.15±0.21$^{A}$ | 9.32±0.09$^{A}$ | 1.24±0.34 | 3.32±0.02$^{B}$ | 2.97±0.03$^{B}$ | 0.00 | 0.00 |
| **P-value** | **<0.0001** | **<0.0001** | **<0.0001** | | **<0.0001** | **<0.0001** | | |

**Comparative Bacterial Counts of the Drinking Water Source from some Communities in Sagbama LGA**

A comparative study of the bacterial counts of each water sample from the three drinking water sources identified in Sagbama LGA is shown in Table 6. Considering the statistical grouping of the water samples based on their bacterial load using alphabetical superscript. The THBC (LogCFU/ml) of water samples, shows that statistically, Ebedebiri borehole water (6.18±0.02) and EBM sachet water sample (6.17±0.01); AQB sachet water (5.50±0.04), Bolu-Orua Borehole water (5.51±0.03), Sagbama town borehole water (5.68±0.01), Toru-Angiama river water (5.63±0.03), Toru-Orua borehole water (5.74±0.03), Toru-Orua river water (5.56±0.01), and Tungbo borehole water (5.52±0.06); Bolu-Orua river water (5.15±0.04), Ebedebiri river water (4.87±0.12), ESE sachet water (5.44±0.04), GG sachet water (5.02±0.03), PA sachet water (5.15±0.11), Sagbama town river water (4.83±0.18), Tungbo river water (5.14±0.13) recorded the same THBC, respectively. The FCC (LogCFU/ml) of water samples, shows that statistically, Bolu-Orua Borehole water (4.75±0.21) had the highest count, while AQB sachet water (4.15±0.21) and PA sachet water (4.15±0.21); Bolu-Orua river water (3.19±0.01), Ebedebiri borehole water (3.12±0.02), ESE sachet water (3.15±0.09), Sagbama town borehole water (3.23±0.07), Sagbama town river water (3.03±0.05), Toru-Angiama river water (3.06±0.02), Toru-Orua river water (3.12±0.04), Tungbo borehole water (3.13±0.05), and Tungbo river water (3.18±0.01) recorded the same FCC, respectively. The TCC (LogCFU/ml) of water samples, shows that statistically, AQB sachet water (9.82±0.23) and Bolu-Orua Borehole water (10.36±0.27); Ebedebiri river water (4.74±0.06), EBM sachet water (4.80±0.14), Sagbama town river water (4.83±0.10), Tungbo borehole water (4.84±0.38), and Tungbo river water (4.57±0.13); Bolu-Orua river water (3.20±0.01), ESE sachet water (4.65±0.38), GG sachet water (3.94±0.07), Sagbama town borehole water (3.23±0.07), and Toru-Angiama river water (4.30±0.32) recorded the same TCC, respectively. The SMC (LogCFU/ml) of water samples, shows that Bolu-Orua Borehole water (1.30±0.00), Bolu-Orua river water (1.63±0.21), Ebedebiri river water (5.4±0.09), PA sachet water (1.24±0.34), Sagbama town river water (1.15±0.21), Toru-Angiama River water (1.58±0.16), Tungbo river water (1.15±0.21) recorded SMC. The SHC (LogCFU/ml) of water samples, shows that statistically, AQB sachet water (5.30±0.06) and Toru-Orua borehole water (5.40±0.02); Bolu-Orua Borehole water (3.22±0.02), Bolu-Orua river water (3.24±0.01), Ebedebiri river water (3.15±0.01), PA sachet water (3.32±0.02), Sagbama town river water (3.18±0.01), Toru-Angiama river water (3.2±0.01), and Toru-Orua river water (2.96±0.05); GG sachet water (2.27±0.02), Toru-Orua river water (2.96±0.05), and Tungbo river water (2.33±0.69) recorded the same SHC, respectively. The STC (LogCFU/ml) of the water samples, shows that statistically, AQB sachet water (4.69±0.13) recorded the highest STC, while Bolu-Orua Borehole water (2.94±0.04), Ebedebiri borehole water (2.97±0.01), Ebedebiri river water (2.97±0.04), PA sachet water

(2.97±0.03), Toru-Orua borehole water (2.98±0.03), Toru-Orua river water (2.93±0.08), and Tungbo river water (2.72±0.03); Bolu-Orua river water (2.53±0.04), EBM sachet water (2.36±0.03), Sagbama town borehole water (2.27±0.05), Sagbama town river water (2.43±0.05), Toru-Angiama river water (2.40±0.02), Tungbo borehole water (2.44±0.06), Tungbo river water (2.72±0.03) recorded the same STC, respectively.

The PMC (LogCFU/ml) of water samples, shows that Bolu-Orua river water (2.68±0.04), Ebedebiri borehole water (2.60±0.08), Sagbama town river water (2.50±0.022), Toru-Angiama River water (1.78±0.25), Toru-Orua River water (2.59±0.08), and Tungbo river water (2.45±0.03) are in the group. The VBC (LogCFU/ml) of the water samples indicate that AQB sachet water (1.63±0.21) and Ebedebiri river water (1.24±0.34) are in the same group.

**Table 6: Comparative Bacterial Counts (LogCFU/ml) of the Drinking Water Source from some Communities in Sagbama LGA**

| Water Sample | Total Heterotrophic Bacteria Count | Faecal Coliform Count | Total Coliform Count | Salmonella Count | Shigella Count | Staphylococcal Count | Pseudomonad Count | Vibriod Count |
|---|---|---|---|---|---|---|---|---|
| AQB sachet water | $5.50\pm0.04^{B}$ | $4.15\pm0.21^{B}$ | $9.82\pm0.23^{AB}$ | 0.00 | $5.30\pm0.06^{A}$ | $4.69\pm0.13^{A}$ | 0.00 | 1.63±0.21 |
| Bolu-Orua Borehole water | $5.51\pm0.03^{B}$ | $4.75\pm0.21^{A}$ | $10.36\pm0.27^{A}$ | 1.30±0.00 | $3.22\pm0.02^{B}$ | $2.94\pm0.04^{B}$ | 0.00 | 0.00 |
| Bolu-Orua river water | $5.15\pm0.04^{CD}$ | $3.19\pm0.01^{C}$ | $3.20\pm0.01^{FG}$ | 1.63±0.21 | $3.24\pm0.01^{B}$ | $2.53\pm0.04^{CDE}$ | 2.68±0.04 | 0.00 |
| Ebedebiri borehole water | $6.18\pm0.02^{A}$ | $3.12\pm0.02^{C}$ | $3.12\pm0.02^{G}$ | 0.00 | $0.00^{E}$ | $2.97\pm0.01^{B}$ | 2.60±0.08 | 0.00 |
| Ebedebiri river water | $4.87\pm0.12^{DE}$ | $0.00^{E}$ | $4.74\pm0.06^{CD}$ | 1.54±0.09 | $3.15\pm0.01^{B}$ | $2.97\pm0.04^{B}$ | 0.00 | 1.24±0.34 |
| EBM sachet water | $6.17\pm0.01^{A}$ | $0.00^{E}$ | $4.80\pm0.14^{CD}$ | 0.00 | $0.00^{E}$ | $2.36\pm0.03^{DE}$ | 0.00 | 0.00 |
| ESE sachet water | $5.44\pm0.04^{BC}$ | $3.15\pm0.09^{C}$ | $4.65\pm0.38^{DE}$ | 0.00 | $1.45\pm0.21^{D}$ | $1.45\pm0.21^{F}$ | 0.00 | 0.00 |
| GG sachet water | $5.02\pm0.03^{DE}$ | $2.55\pm0.05^{D}$ | $3.94\pm0.07^{EF}$ | 0.00 | $2.27\pm0.02^{C}$ | $1.50\pm0.28^{F}$ | 0.00 | 0.00 |
| PA sachet water | $5.15\pm0.11^{CD}$ | $4.15\pm0.21^{B}$ | $9.32\pm0.09^{B}$ | 1.24±0.34 | $3.32\pm0.02^{B}$ | $2.97\pm0.03^{B}$ | 0.00 | 0.00 |
| Sagbama town borehole water | $5.68\pm0.01^{B}$ | $3.23\pm0.07^{C}$ | $3.23\pm0.07^{FG}$ | 0.00 | $0.00^{E}$ | $2.27\pm0.05^{E}$ | 0.00 | 0.00 |
| Sagbama town river water | $4.83\pm0.18^{E}$ | $3.03\pm0.05^{C}$ | $4.83\pm0.10^{CD}$ | 1.15±0.21 | $3.18\pm0.01^{B}$ | $2.43\pm0.05^{DE}$ | 2.50±0.022 | 0.00 |
| Toru-Angiama River water | $5.63\pm0.03^{B}$ | $3.06\pm0.02^{C}$ | $4.30\pm0.32^{DE}$ | 1.58±0.16 | $3.25\pm0.01^{B}$ | $2.40\pm0.02^{DE}$ | 1.78±0.25 | 0.00 |
| Toru-Orua borehole water | $5.74\pm0.03^{B}$ | $0.00^{E}$ | $5.44\pm0.08^{C}$ | 0.00 | $5.40\pm0.02^{A}$ | $2.98\pm0.03^{B}$ | 0.00 | 0.00 |
| Toru-Orua River water | $5.56\pm0.01^{B}$ | $3.12\pm0.04^{C}$ | $3.12\pm0.04^{G}$ | 0.00 | $2.96\pm0.05^{BC}$ | $2.93\pm0.08^{BC}$ | 2.59±0.08 | 0.00 |
| Tungbo borehole water | $5.52\pm0.06^{B}$ | $3.13\pm0.05^{C}$ | $4.84\pm0.38^{CD}$ | 0.00 | $0.00^{E}$ | $2.44\pm0.06^{DE}$ | 0.00 | 0.00 |
| Tungbo river water | $5.14\pm0.13^{D}$ | $3.18\pm0.01^{C}$ | $4.57\pm0.13^{D}$ | 1.15±0.21 | $2.33\pm0.69^{C}$ | $2.72\pm0.03^{BCD}$ | 2.45±0.03 | 0.00 |
| **P-value** | **<0.0001** | **<0.0001** | **<0.0001** | | **<0.0001** | **<0.0001** | | |

**Cluster variable analysis of bacterial counts and sample location variables**.

Classification of the bacterial counts and location variables based on the similarity in bacterial load is illustrated in Figure 1 – 2. The bacterial count variables grouping shown in Figure 1 are classified into four clusters: cluster 1 (Heterotrophic bacterial count); Cluster 2 (FCC); Cluster 3 (Total coliform count, Shigella count, Staphylococcal count, and Vibriod count) and Cluster 4 (Salmonella count and Pseudomonad count). The location variables (Figure 2) are grouped into four clusters: cluster 1 (AQB sachet water, PA sachet water, Bolu-Orua Borehole water; cluster 2 (EBM sachet water); cluster 3 (ESE sachet water, GG sachet water, Ebedebiri borehole water, Sagbama town borehole water, Tungbo borehole water, Bolu-Orua river water, Sagbama town river water, Toru-Angiama river water, Tungbo river water and Toru-Orua river water) and cluster 4 (Toru-Orua borehole water and Ebedebiri river water).

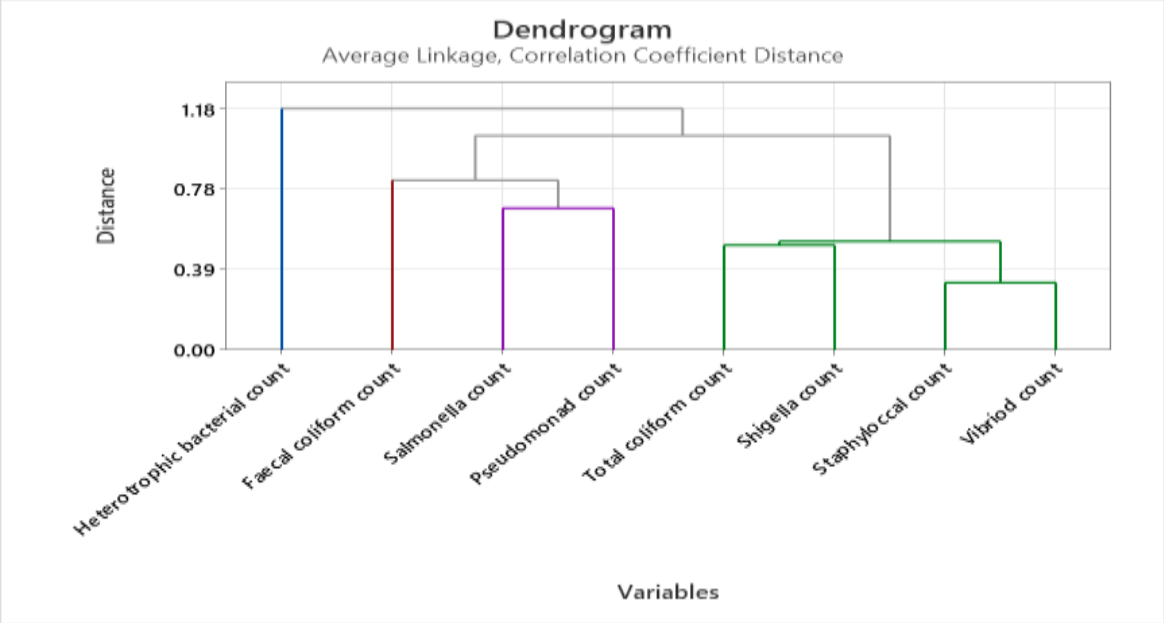


Figure 1. Dendrogram showing similarity in bacterial load among the bacterial count variables.

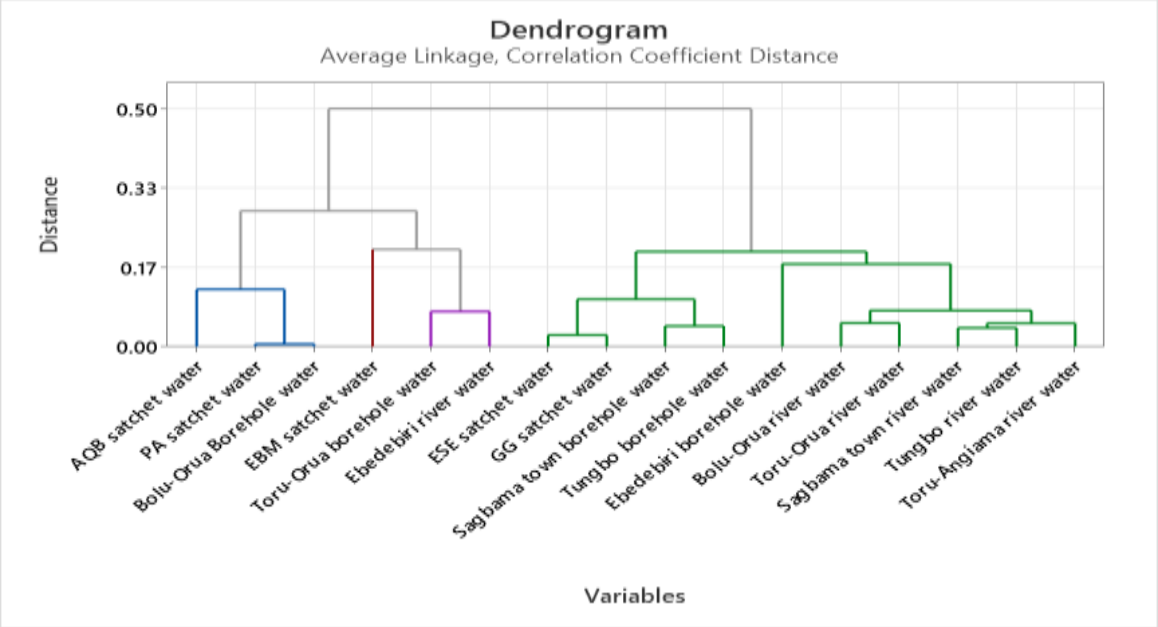


Figure 2. Dendrogram showing similarity in bacterial load among the sample location variables.

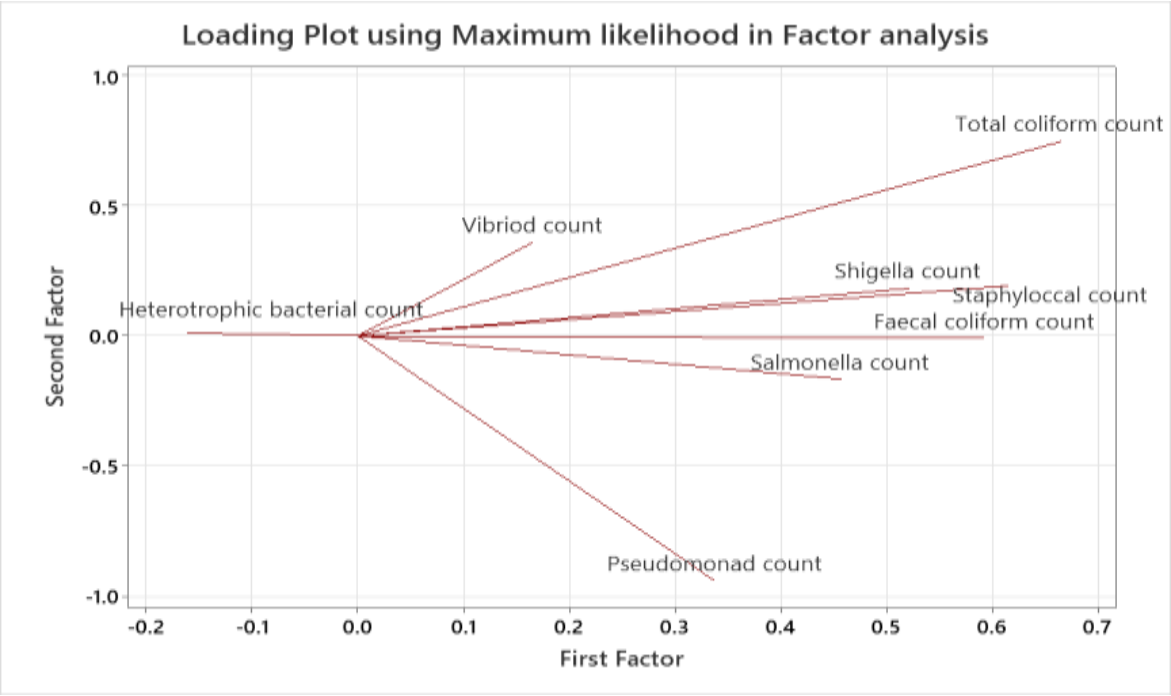


Figure 3. Loading plot using maximum likelihood in Factor analysis

The correlation between the bacterial counts' parameters using maximum likelihood in Factor analysis and pairwise Pearson correlation is shown in Figure 3 and Table 6 respectively. The Factor analysis illustrates that there is a positive correlation between the TCC, FCC, SMC, SHC, STC, PMC, and VBC parameters: TCC, SHC, STC, FCC, and SMC are strongly positively correlated; while the VBC and PMC have weak negative correlation, but THBC have a strong negative correlation with the other bacterial count parameters.

The Pearson correlation is shown in Table 7 representing the statistical presentation of the correlation between the parameters. The Pearson correlation coefficient value with negative and positive values indicates a negative and positive correlation, respectively; while a P-value $\leq 0.05$ indicates a significant correlation coefficient and $> 0.05$ is a non-significant correlation coefficient.

**Table 7: Pairwise Pearson correlation coefficient of the bacterial counts' parameters**

| Sample 1 | Sample 2 | Correlation | P-Value |
|---|---|---|---|
| Faecal coliform count | Heterotrophic bacterial count | -0.140 | 0.445 |
| Total coliform count | Heterotrophic bacterial count | -0.098 | 0.595 |
| Salmonella count | Heterotrophic bacterial count | **-0.536** | **0.002** |
| Shigella count | Heterotrophic bacterial count | **-0.402** | **0.022** |
| Staphylococcal count | Heterotrophic bacterial count | 0.117 | 0.524 |
| Pseudomonad count | Heterotrophic bacterial count | -0.065 | 0.724 |
| Vibriod count | Heterotrophic bacterial count | -0.193 | 0.289 |
| Total coliform count | Faecal Coliform Count | **0.386** | **0.029** |
| Salmonella count | Faecal Coliform Count | 0.141 | 0.443 |
| Shigella count | Faecal Coliform Count | 0.028 | 0.881 |
| Staphylococcal count | Faecal Coliform Count | 0.153 | 0.402 |
| Pseudomonad count | Faecal Coliform Count | 0.207 | 0.256 |
| Vibriod count | Faecal coliform count | -0.098 | 0.595 |
| Salmonella count | Total coliform count | 0.179 | 0.328 |
| Shigella count | Total coliform count | **0.482** | **0.005** |
| Staphylococcal count | Total coliform count | **0.552** | **0.001** |
| Pseudomonad count | Total coliform count | **-0.481** | **0.005** |
| Vibriod count | Total coliform count | 0.378 | **0.033** |
| Shigella count | Salmonella count | 0.338 | 0.058 |
| Staphylococcal count | Salmonella count | 0.053 | 0.772 |
| Pseudomonad count | Salmonella count | 0.310 | 0.084 |
| Vibriod count | Salmonella count | 0.032 | 0.862 |
| Staphylococcal count | Shigella count | **0.518** | **0.002** |
| Pseudomonad count | Shigella count | 0.003 | 0.987 |
| Vibriod count | Shigella count | **0.421** | **0.016** |
| Pseudomonad count | Staphylococcal count | 0.025 | 0.891 |
| Vibriod count | Staphylococcal count | **0.672** | **0.000** |
| Vibriod count | Pseudomonad count | -0.283 | 0.117 |

## DISCUSSION

The use of water sources such as surface water (rivers), groundwater (borehole) and sachet water is a common practice, and the quality of water sources is mostly evaluated by their bacteriological properties which determine the contamination level of drinking water sources (Cabral, 2010), and the occurrence of several bacterial genera in drinking water sources are considered potential health risk to the consumers (Adesakin *et al*., 2020). Considering the overall mean bacterial counts (Table 1), the drinking water sources in Sagbama Local Government Area are contaminated with a high heterogeneous bacteria load. The mean bacterial count and heterogeneity indicate environmental contamination due to anthropogenic activities or environmental disasters. This finding agrees with the studies conducted by Agedah *et al*. (2015) and Omari and Yeboah-Manu (2012) that reported of high bacteria density in drinking water source in Bayelsa State and bacterial contamination of different drinking water sources in Mpraeso, Ghana,

respectively: attributed to anthropogenic activities (Amanidaz *et al*., 2015; Dangi *et al*., 2017); Poor water supply infrastructures (Boakye-Ansah *et al*., 2016); poor environmental sanitation and personal hygiene practice (Agwaranze *et al*., 2017; Berezi & Nwankwoala, 2022; Gwimbi *et al*., 2019); climatic adverse effects on the environment (Ajumobi *et al*., 2023; Jung *et al*., 2014), storage of water (Lavanya & Ravichandran, 2013), biofouling of water pipeline (Yu *et al*., 2012) and seasonal (raining or dry) change (Akrong *et al*., 2019).

The study showed that, there is variation in bacterial count parameters of the drinking water sources. The finding agrees with studies carried out by several researchers (Abbas Bakhiet & Zaroug, 2020; Aslan *et al*., 2020; Bissonnette *et al*., 1975). The cause of the variation could be due to the physicochemical properties, eutrophication from runoff water or/and natural disaster (like flood) introducing microbial contaminant, inadequate water treatment into the water sources and poor water distribution facility (Agedah *et al*., 2015; Gwimbi *et al*., 2019) and the bacterial genera enumerated were reported as the main bacterial contaminant of water sources (Omari & Yeboah-Manu, 2012; Otorkpa, 2019). The mean bacterial counts recorded for each genius are above the WHO-recommended bacterial load. My finding is in agreement with the report of $10^5$ - $10^7$ (Adesakin *et al*., 2020), 1.8 x $10^3$ to 7.0 x $10^3$ (CFU/ml) (Otajevwo & Tamaramiene, 2020) and over 500 (CFU/ml) of THBC in drinking water which indicates poor drinking water source quality (Amanidaz *et al*., 2015), > 1 to 3 MPN/100ml for FCC (Garkuwa *et al*., 2020; Sitotaw *et al*., 2021; Syamsussabri *et al*., 2019; Yari *et al*., 2018). Pathogenic bacterial species like *Salmonella* sp., *Shigella* spp., and *Staphylococcus* sp. were enumerated (Angelopoulou *et al*., 2021; Anochie *et al*., 2018; Busgang *et al*., 2018), while *Pseudomonas* spp. and *Vibrio* spp. were also implicated (Abu *et al*., 2020; Baghal *et al*., 2013; Briancesco *et al*., 2020; Deji-Agboola *et al*., 2017; Djaouda *et al*., 2013). This agrees and correlates with the report of Bayelsans suffering from diarrhoea, toilet infections, typhoid, and dysentery (Amawulu, 2020; Olaitari, 2020), which are attributed to poor water quality, due to the presence of indicators and some as pathogens (Kristanti *et al*., 2022); thus, could be inevitable crises and insecurity in the state, due to lack of potable water (Odubo, 2014; Olalekan *et al*., 2019).

The three drinking water sources (borehole water, river water and sachet water) examined for their bacteriological quality showed high bacterial counts (Table 2.) which is above the WHO-recommended microbiological criteria for potable water. This finding is in agreement with the report that there is an overlook in the microbial quality and equal distribution of contamination in drinking water sources accessible (Boakye-Ansah *et al*., 2016), as unimproved drinking water sources are reservoirs of contaminant resulting from a lack of community-led sanitation and hygiene education and practice, and water source protection (Gwimbi *et al*., 2019). Nwaiwu *et al*. (2019) reported the need to enhance communities' water quality structures to meet the WHO's sustainable development goals on water sanitation.

The several microbial count results obtained agree with the suggestion that regulatory bodies should take proactive actions to enforce production and ensure the availability of safe drinking water, as interventions along the drinking water sources value chain are looked for to protect public health (Angnunavuri *et al*., 2022). The finding of this study agrees with the report of Bahago *et al*. (2019) that there is a need to re-evaluate the complaints of licensed water producers (to World Health Organization (WHO) standards for drinking water to promote public health), including their industrial facilities and the potential health impact of their products (Emerenini, 2020b). The drinking water sources sampled did not meet the WHO standards. The results of my study complement the report of borehole and sachet water samples not meeting the WHO standard (Adegoke *et al*., 2012; Adetunde *et al*., 2014; Adewoye *et al*., 2013; Adiotomre & Agbale, 2015; Adogo *et al*., 2016; Ahmed *et al*., 2019; Bahago *et al*., 2019; Bashir *et al*., 2018; Bello *et al*., 2013; Duru *et al*., 2012; Eboh *et al*., 2017). High bacterial count in sachet water that exceeds WHO standard collaborate with the report from Edo State (Idibie *et al*., 2018; Nwand1kor & Okolo, 2016), in Maiduguri, 66.6% of the packaged water sold is either not treated properly or produced in unhygienic environments: thus, regulatory agencies are to closely monitor and enforce Good Manufacturing Practice (GMP) for quality drinking water (Jethro *et al*., 2020; Miner *et al*., 2014). The finding collaborated with the report of high microbial counts in borehole and surface water that exceed the level they are regarded as safe by the Kenyan regulatory body and WHO standards for potable water

(Onyango *et al*., 2018; Oyedeji *et al*., 2010). It was revealed that most of the sachet water faecal contamination was from the major source, and location-specific treatment, and other quality control (QC) measures should be enforced to reduce the water security menace (Tenebe *et al*., 2023; Udoh *et al*., 2021). The findings from the study correlate with the report by Jung *et al*. (2014) and Kristanti *et al*. (2022) that microbial pollution in aquatic environments is a vital subject concerning the sanitary state of water bodies utilized as drinking water supply due to potential contamination by bacteria contaminants.

The river water recorded bacterial counts suggest bacterial contamination of river water. My finding agrees with the reports of several researchers (Abu *et al*., 2020; Alam *et al*., 2023; Asabia *et al*., 2021; Ebong *et al*., 2018; Garcia-Armisen & Servais, 2004; Obioma *et al*., 2017; Olalemi & Ogundare, 2022; Olorunjuwon *et al*., 2023; Paulse *et al*., 2007; Sampson *et al*., 2022; Santo Domingo *et al*., 2000; Ugbaja & Otokunefor, 2015; Ukwuoma *et al*., 2022; Wose Kinge & Mbewe, 2010; Yamaguchi *et al*., 1997) of high bacterial counts due to sewage contamination (Feresu & Sickle, 1990), urbanization (Olayemi, 1994), microbial adaptability (Santo Domingo *et al*., 2000) to environmental dynamics (Sampson *et al*., 2022), and duration of water storage and water storage system (Lavanya & Ravichandran, 2013).

In Nigeria, most of the local population relies on borehole water as the primary source of water for drinking and domestic use, as only a few people can afford to buy treated water (Adogo *et al*., 2016) and microbial contamination of borehole water is a common occurrence (Asabia *et al*., 2021). The major contaminants of borehole water according to my findings are heterotrophic bacteria, faecal coliforms, and Total coliforms (Table 3). This finding agrees with the report of bacterial load recovered from (the Wamakko Local Government Area, Sokoto State) borehole water was above the WHO standard for bacterial loads, and high coliform content which could be due to anthropogenic activities and the purity level of water that percolate to the underground water as a function of the geological conditions of the soil (Bashir *et al*., 2018; Bello *et al*., 2013; Duru *et al*., 2012; Ebong *et al*., 2018). The proximity of septic tanks to the borehole water source influences the heterotrophic bacteria and enteric bacteria load (Fubara-Manuel & Jumbo, 2014), organic compound soil pollution (Wilsona *et al*., 1983). However, there is a disagreement with the report, there was no bacteria contamination of borehole water located in Oroworukwu, Port Harcourt which indicated that the borehole water is microbiologically safe (Akinfolarin & Chukwuji, 2020).

The bacterial genera enumerated agree with bacterial genera identified such as Total heterotrophic bacterial count in the borehole water sample (Adogo *et al*., 2016) which could be bacteria isolates like *Aeromonas* sp., *Acinetobacter* sp., *Aureobacterium* sp., *Bacillus* sp., *Chryseobacterium* sp., *Corynebacterium* sp., *Klebsiella* sp., *Moraxella* sp., *Pseudomonas* sp., *Staphylococcus* sp., and *Vibrio* sp. Total and faecal coliforms such as *Escherichia coli*, *Salmonella* sp., *Shigella* sp., *Pseudomonas aeruginosa* and *Staphylococcus aureus* were isolated from the borehole water samples (Bello *et al*., 2013; Eboh *et al*., 2017); *Pseudomonas* sp., *E. coli*, *Salmonella* sp., and *Staphylococcus* sp., isolates occurred in borehole water (Duru *et al*., 2012); *Salmonella* sp., *Shigella* sp., and *Vibrio* spp. (Olalemi *et al*., 2021; Ugbaja & Otokunefor, 2015; Uzoigwe, 2012).

In most rural communities, the major sources of water apart from rainfall are surface water such as river water (Obioma *et al*., 2017) and contamination of natural water sources is a major health problem globally (Borja-Serrano *et al*., 2020). Considering the bacterial load from the bacterial counts (Table 4.) the river waters in Sagbama which do not measure up to the WHO standard for potable water pose a critical hazard to the people using it as a drinking water source. My finding collaborates with the report of poor water quality due to microbial contamination found in water (Rakesh *et al*., 2022). FCC and TCC higher than WHO recommended standard (permissible limit) in river water was reported by Abu *et al*. (2020) and Divya and Solomon (2016), and Enterobacteriaceae exists in the unhygienic and polluted situation of rivers which is a clear representation of uncontrolled hazardous activity (Alam *et al*., 2023; Feresu & Sickle, 1990).

The counts of Salmonella, Shigella, Staphylococcus, Pseudomonas and Vibrio were higher than the WHO-recommended standard. My finding agrees with the report that the quality of Owena Metropolis river water did not conform to the drinking water standard of WHO, due to the presence of some pathogenic microorganisms (Ayo & Arotupin, 2017; Garcia-Armisen & Servais, 2004), like *E. coli* pathotypes (EIEC,

EHEC, and EAEC) (Borja-Serrano *et al*., 2020), *Proteus* spp., *Citrobacter* spp., *Klebsiella* spp. *Pseudomonas* spp., *Bacillus* spp., *Enterobacter* spp., *Streptococcus* spp., *Salmonella* spp. (Ekhaise & Omoigberale, 2011) *Shigella* spp., and *Vibrio* spp. (Okwelle, 2020).

Sachet water is the ultimate source of drinking water in Nigeria (Daniel & Daodu, 2016 ). The five sachet water brands commonly distributed among the people of Sagbama LGA (Table 5.) did not meet its essence of alleviating the stress of poor and inadequate water supply due to poor and inadequate water supply infrastructure (Dada, 2009). As the bacterial counts THBC, FCC, and TCC are above the WHO permissible limit for potable water, which could result from lack of or improper water treatment process or technique, faecal contamination either from water source or humans during packaging. This finding agrees with the report of inappropriate treatment processes in packaged drinking waters (Bukar *et al*., 2015), thus the enforcement of routine monitoring of producers of sachet water is essential (Daniel & Daodu, 2016 ), as the microbial quality of their product did not meet WHO permissible limit, due poor microbial quality. Sachet water brands sold in metropolises with high FCC and TCC were reported (Bahago et al., 2019; Emerenini, 2020a; Gyasi et al., 2019; Ifeanyi et al., 2006).

Inconsistency in the microbial quality of the sachet water brands of drinking water was reported (Adegoke *et al*., 2012; Adetunde *et al*., 2014; Adiotomre & Agbale, 2015; Anyamene & Ojiagu, 2014; Miner *et al*., 2014; Wuni & Adetunde, 2015), which could be due to improper storage (under sun storage) or in a hot environment enhancing microbial proliferation in sachet water (Adewoye *et al*., 2013; Angnunavuri *et al*., 2022), inadequate disinfection process or technique due to biofilm formation or leakage of the pipelines used to fill these packages (Aslan *et al*., 2020), poor personal hygiene standard of water vendors (Magaji, 2020), poor hygiene during processing and packaging (Okolafor & Idemudia, 2022). But my finding disagrees with the reports on safe microbial water quality sold in Nnewi, South East, Nigeria (Ezeugwunne *et al*., 2009); sachet drinking water produced or sold in Ibadan metropolis of good quality and hygienic for consumption (Airaodion, 2019); absence of biological contamination in sachet water brands and considered safe for consumption (Chiwetalu *et al*., 2022); sachet water produced with no indication of contamination from sewage or animal waste (Giwa *et al*., 2015).

Bacterial genera (SMC, SHC, STC, and VBC) were isolated and enumerated from sachet drinking water, except PMC. My results collaborate with the report of identification of water-borne bacterial pathogens isolated from sachet water (Oladipo *et al*., 2009), like pathogenic *Escherichia coli* and *Salmonella* sp. (Ahmed *et al*., 2019; Edema *et al*., 2011), *Pseudomonas* sp. (Giwa *et al*., 2015; Mgbakor *et al*., 2011), *Staphylococcus aureus* (Maduka *et al*., 2014; Muhammed *et al*., 2021) *Staphylococcus aureus* and *Pseudomonas aeruginosa* (Mmuoegbulam *et al*., 2019; Ngwai *et al*., 2010), *Pseudomonas aeruginosa* and *Salmonella* sp. (Muazu *et al*., 2012), *Staphylococcus aureus* and *Vibrio cholerae* (Oluwafemi & Oluwole, 2012) and *Staphylococcus aureus, Salmonella enterica* and *Shigella* spp. (Busgang *et al*., 2018). The main route of transmission of bacterial pathogens to man is through drinking contaminated water consumption of inadequately cooked aquatic food products (Osunla & Okoh, 2017), and poor sanitary and personal hygienic practices (Onohuean *et al*., 2021). The absence of Pseudomonad counts in sachet drinking water was recorded. This finding agrees with the report of Buchanan-Mappin and Wall (1986) that *Pseudomonas* sp. are majorly found in stream waters. However, *Pseudomonas* sp. biofilms can grow under cold water environments on domestic plumbing materials, as a reservoir and persist in that habitats mostly in a viable but non-culturable state (Wingender *et al*., 2009).

Bacterial contamination of drinking water sources is a major public health delinquent in rural areas of sub-Saharan Africa, thus community-led sanitation and hygiene education and better water source protection are urgently needed (Gwimbi *et al*., 2019). The bacteriological quality of drinking water sources (borehole, river, and sachet) sampled in Sagbama LGA is unsafe for consumption, considering the high bacterial load (Table 6.) of indicator microorganisms (THBC, TCC and FCC) and pathogenic microorganisms (SMC, SHC, STC, PMC and VBC) associated with the drinking water sources. My finding is like the report on bacterial contamination of drinking water sources in rural villages of Mohale Basin, Lesotho (Gwimbi *et al*., 2019) such as groundwater sources and surface water suggesting the need for treatment before consumption (Omari & Yeboah-Manu, 2012). The prevalence of disease-causing microorganisms further confirms that the majority of the drinking waters considered safe for consumption across Nigeria are not fit

for human consumption (Otorkpa, 2019). The prevalence of microorganisms in drinking water sources could be a function of sediment types (particle size and organic carbon content) which act as a reservoir of pathogenic bacteria and exhibit potential health hazards from possible resuspension and subsequent ingestion, and its transport characteristics (Jung *et al*., 2014; Lavanya & Ravichandran, 2013).

The bacterial count variables are classified into three clusters representing the three groups (or classes) of the bacterial counts obtained from water samples, which are THBC cluster, FCC, SMC, and PMC cluster and TCC, SHC, STC and VBC cluster of the dendrogram showing complete linkage correlation (Figure 1.). The findings of this study collaborate with the reports of several researchers (Adesakin *et al*., 2020; Agedah *et al*., 2015; Amanidaz *et al*., 2015). Having multiple clusters indicates the magnitude of microbial loads associated with the bacterial counts' variables in drinking water sources in the communities, thus inferring a lack of portability due to a lack of proper water treatment (Chowdhury, 2012; Health Canada, 2012). The mean TCC, SHC, STC and VBC showed similarity in bacterial load. My findings disagree with the report of Mahalakshmi *et al*. (2011) that there is a relationship between TCC and VBC, but my finding agrees with the report of Baghal *et al*. (2013) that there is no relationship between THBC and PMC and the report of Shahryari *et al*. (2017) that there is the relationship between FCC and SMC. A report on the relationship between other bacterial count variables has not been reported.

The classifying of the sampled drinking water sources based on similarity in bacterial counts showed that some sachet water samples are as contaminated and hold several bacterial communities as the river water samples and borehole water samples, respectively and verse versa (Figure 2). My finding agrees with the reports of several researchers (Angnunavuri et al., 2022; Bahago et al., 2019; Emerenini, 2020b; Idibie et al., 2018; Jethro et al., 2020; Miner et al., 2014), which could be due to poor and inadequate storage, poor hygienic production conditions or lack of or inadequate water treatment. The contamination of river waters and boreholes could be due to environmental faecal pollution that is washed from riparian to water bodies or linked down to the underground water (Cabral, 2010; Gwimbi *et al*., 2019; Omari & Yeboah-Manu, 2012; Otorkpa, 2019) and microbial response to physicochemical properties of drinking water sources (X. Guo *et al*., 2022; Y. Guo *et al*., 2022; Qin *et al*., 2016; Wang *et al*., 2021; Wang *et al*., 2022).

Concerning the relationship between the bacterial count variables as analysed using Pearson's Correlation (Table 7) and maximum likelihood in Factor analysis (Figure 3), there is a significant positive correlation between enteric pathogenic bacteria and faecal indicator microorganisms, and a significant negative correlation between pathogenic microorganisms and Total heterotrophic bacteria count. This is an indication that the presence of indicator microorganisms in water suggests the presence of pathogenic microorganisms. This finding agrees with the report of a positive correlation between *Salmonella* sp. and *Escherichia coli* presence in drinking water (Shahryari *et al*., 2017), which could be introduced into the water body due to runoff water or flood (Ajumobi *et al*., 2023; Amawulu, 2020; Jung *et al*., 2014; Olaitari, 2020).

## CONCLUSION

The bacteriological quality of drinking water sources in the Sagbama Local Government Area calls for serious concern and government interventions, as the bacterial counts associated with the drinking water sources (sachet water, borehole water and river water) are of a public health concern as pathogenic bacteria like *Salmonella* sp., *Pseudomonas* sp., *Shigella* sp., *Vibrio* sp., and *Staphylococcus* sp. isolates were isolated from all the water samples sampled from the communities studied. This is an indication that the government agencies saddled with the responsibility of monitoring the safety and quality of water produced and consumed are passive rather than active as there is no difference in the bacterial counts (THBC, FCC and TCC) of the drinking water sources sampled in the various communities. This study shows that the flood in the year 2022 had severe impacts on the drinking water sources in Sagbama LGA.

## RECOMMENDATIONS

Based on the findings obtained from the study, it was recommended that:

1. A public enlightenment system needs to be created to alert people of the danger of drinking bacteria polluted water in most part of sagbama local government area.

2. Government should provide adequate bore hole system in various communities in other to supply lean and pure water for local consumptions.

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