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# Assessment of the Bacteriological Quality of Selected Surface Water Resources in Anambra Central Senatorial Zone Anambra State

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## ABSTRACT

This study assessed the bacteriological quality of selected water sources with particular emphasis on coliform bacteria as indicators of faecal contamination. The water samples were collected from 21 towns and villages in Anambra Central Senatorial Zone, Anambra State. They were analyzed for different bacterial groups using standard microbiological procedures. The result revealed that Awka North had the highest total coliform count of 44.33 ± 1.93 with percentage frequency of 16.60 %, Awka South had the highest total faecal *Streptococci* count of 20.00± 0.00 with percentage frequency of 11.84 %, Dunukofia had the lowest total *Staphylococcus* count of 1.33± 0.03 with percentage frequency of 0.58 %, Anaocha had lowest total faecal *Streptococci* count of 1.67± 0.33 with percentage frequency of 1.19 %, Njikoka had the highest total *Pseudomonas* count of 13.00±2.08 with percentage frequency of 4.92 %, Idemili South had the highest total *Bacillus cereus* count of 34.00±3.00 with percentage frequency of 14.49 %, Idemili North had the highest total Salmonella-Shigella count of 69.00±5.70 with percentage frequency of 19.90% respectively. Total coliform counts (TCC) in all samples exceeded the permissible limit of zero total coliforms per 100 mL recommended by the World Health Organization (WHO) for potable water, indicating significant microbial contamination. None of the surface water samples complied with WHO standards, suggesting widespread deterioration of water quality. Elevated faecal coliform and faecal streptococci counts further confirmed substantial faecal pollution, with evidence pointing toward predominant human excreta contamination. Statistical analysis revealed significant differences among sampling sites ($F = 2.789$, $p < 0.0002$) and among bacterial groups ($F = 4.66$, $p < 0.0001$), indicating spatial variability in contamination levels. Overall, the findings demonstrate that the investigated water sources are microbiologically unsafe for direct human consumption without adequate treatment. The study underscores the urgent need for improved sanitation practices, routine monitoring, and effective water treatment interventions to protect public health.

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**Keywords**
Faecal pollution; Public health; Routine monitoring; Sanitary practice; Surface water



## INTRODUCTION

Water pollution refers to the contamination of water bodies when undesirable substances are introduced into them, leading to a deterioration in water quality and making the water harmful to both the environment and human health (Alrumman *et al*., 2016). These pollutants may include physical, chemical, or biological materials that alter the natural characteristics of water, rendering it unsafe for consumption and other uses. As a vital natural resource, water plays a fundamental role in sustaining life. It is essential not only for drinking but also for agriculture, industry, sanitation, and overall socio-economic development. Access to clean and safe drinking water is therefore critical for maintaining public health worldwide (Uba, 2019a; 2019b; 2019c; Uba *et al*. 2019b; 2019c).

Because water is often described as a universal solvent, it has the ability to dissolve a wide range of substances. While this property makes it highly useful, it also increases its vulnerability to contamination. Polluted water can easily carry pathogenic microorganisms, toxic chemicals, and other harmful agents, making it a significant source of infection. According to the World Health Organization (WHO), approximately 80% of diseases in developing regions are linked to waterborne causes. Furthermore, in many countries, drinking water supplies fail to meet the safety standards established by the WHO (Bibi *et al*., 2016), exposing millions of people to serious health risks. It has also been reported that around 3.1% of global deaths are associated with poor sanitation and unsafe water quality (Pawari and Gawande, 2015).

The major contributors to water pollution include the discharge of untreated domestic sewage and industrial effluents into rivers, lakes, and oceans. Additional sources include leakage from storage tanks, improper marine dumping, the disposal of radioactive waste, and atmospheric deposition of pollutants (Owa, 2013; Ubajekwe *et al*., 2025). These activities introduce hazardous substances such as heavy metals, organic chemicals, nutrients, and pathogens into water systems. Consequently, water pollution not only disrupts aquatic ecosystems but also threatens biodiversity, food security, and human well-being (Ekwenze *et al*., 2025). Addressing this issue requires strict environmental regulations, effective wastewater treatment systems, and increased public awareness to ensure the sustainable management of water resources (Uba *et al.*, 2017; Dokubo *et al.*, 2022a; 2022b; Anidu *et al*., 2023; Obiefoka *et al*., 2023; Uba and Obiefuna, 2023).

Microorganisms play a major role in water quality, particularly those associated with waterborne diseases such as *Escherichia coli*, *Shigella* sp., *Salmonella* sp. and *Vibrio cholerae* (Adetunde and Glover, 2010; Umeh *et al.*, 2020; 2021). These microorganisms are responsible for diseases such as typhoid fever, diarrhoea, dysentery, gastroenteritis, and cholera.
The most severe form of water pollution occurs when faecal matter contaminates the water supply. Many of these diseases are transmitted through the faecal–oral route, whereby pathogens shed in human faeces contaminate food or water that is subsequently ingested. The presence of faecal coliforms, particularly *E. coli*, is commonly used as an indicator of potential contamination by waterborne pathogens (Adetunde and Glover, 2010; Uba *et al*., 2020a; 2020b; 2020c; 2020d; 2020e; 2020f; 2020g).

The need for good water quality has been of growing concern in Nigeria and worldwide. Urgent attention is therefore necessary to mitigate water pollution problems in Nigeria, especially through **routine microbial monitoring** and the **enforcement of industrial effluent discharge standards** (Egurefa *et al*. 2020a; 2020b; Okafor *et al*., 2023; Ubani *et al*., 2024a; 2024b; 2025; Okolo *et al.*, 2025; Okpalaunegbu *et al.*, 2025; Obiefuna *et al.* 2025). Waterborne diseases caused by pathogenic bacteria remain a significant public health challenge, particularly in rural and peri-urban communities that depend directly on untreated surface waters for domestic uses such as drinking, cooking, and bathing. Despite this, there is a *dearth of information* on the bacteriological properties of rivers and streams in the **Anambra Central Senatorial Zone, Anambra State,** which hinders effective management and risk assessment.

Understanding the bacterial quality of these water sources is critical because high levels of faecal contamination and pathogenic bacteria can indicate recent pollution and pose serious health risks. This knowledge gap limits policymakers' ability to design targeted interventions and undermines efforts to safeguard public health and environmental quality. Therefore, this study aims to **evaluate the bacteriological characteristics** of selected rivers and streams in the Anambra Central Senatorial Zone, with a focus on **faecal indicator organisms and potential pathogens,** to provide baseline data for water quality management and public health protection.

## MATERIALS AND METHODS

### Description of Study Area

The studied areas include: Mmiri St John Alor, Mmiri Mgbo Nnobi, Oba Stream in Idemili South Local Government Area, Ukwu Apku Stream Eziowelle, Mmiri Oraukwu Oraukwu, Mbuda Spring Water Abacha in Idemili North, Otti Spring Enugu Ukwu, Abagana Stream, Ogbujilekwe Stream Nimo in Njikoka Local Government Area Umudioka Stream, Ali Ukpo Stream Ukpo, Onyekwena Spring Water Ifitedunu, in Dunukofia Local Government Area, Agulu Lake Agulu, Adazi Nnukwu Stream, Nri Stream in Anaocha Local Government Area, Nkwelle Awka Stream, Abor River in Umuawulu, Umuaba River Nibo in Awka South Local Government Area and Umuife Iyiohia Urum Stream, Araka Stream Mgbakwu, Ogbanabo Stream Isuaniocha in Awka North Local Government Area all located in Anambra Central Senatorial Zone, Anambra State Nigeria. The coordinates of the sampling points were determined using a hand-held Global Positioning System (GPS) with coordinate of Alor latitude 6° 6' 11.98" MN and longitude 6° 57' 17.46" ME, Nnobi latitude 6° 5' 10.30" MN and longitude 6° 56' 7. 30" ME, Oba latitude 6° 2' 32.79" MN and longitude 6° 50' 9.62" ME, Eziowelle latitude 6° 9' 30.70" MN and longitude 6° 57' 40.15" ME, Oraukwu latitude 6° 6' 18.25" MN and longitude 6° 57' 33.51" ME, Abacha latitude 6° 9' 2.30" MN and longitude 6° 57' 47.97" ME, Enugu Ukwu latitude 6° 9' 35.65" MN and longitude 7° 0' 20.53" ME, Abagana latitude 6° 10' 8.09" MN and longitude 6° 57' 44.53" ME, Nimo latitude 6° 7' 6.79" MN and longitude 6° 59' 41.27" ME, Umudioka latitude 6° 11' 44.79" MN and longitude 6° 55' 24.27" ME, Ukpo latitude 6° 12' 2.23" MN and longitude 6° 59' 1.05" ME, Ifitedunu latitude 6° 11' 4.24" MN and longitude 6° 2' 38.38" ME, Agulu latitude 6° 7' 47.20" MN and longitude 7° 2' 0.60" ME, Adazi Nnukwu latitude 6° 7' 12.60" MN and longitude 7° 0' 39.24" ME, Nri latitude 6° 9' 2.79" MN and longitude 7° 1' 0.01" ME, Nkwelle Awka latitude 6° 11' 52.82" MN and longitude 7° 5' 20.35" ME, Umuawulu latitude 6° 9' 28.13" MN and longitude 7° 5' 27.57" ME, Nibo latitude 6° 9' 54.49" MN and longitude 7° 4' 53.40" ME, Urum latitude 6° 17' 15.93" MN and longitude 7° 1' 35.67" ME, Mgbakwu latitud e 6° 17' 24.63" MN and longitude 7° 4' 38.28" ME and Isuaniocha latitude 6° 14' 41.78" MN and longitude 7° 3' 21.37" ME respectively. Anthropogenic activities in the sampling sites revealed that they are source of water supply for domestic and agricultural purposes in the eastern parts of the town despite being exposed to different effluents (Alfred *et al*. 2023; 2025a; 2025b).

### Collection of Water Sample

Samples of Spring and Lake water were aseptically collected in triplicates from each of the seven local government areas (Njikoka, Enugu Ukwu, Idemili North, Abacha, Anaocha, Agulu and Dunukofia, Ifitedunu) using sterile sample bottles. The sampling method used for the rivers and stream water collection was the grab method as described by Dokubo *et al*. 2024); Uba and Okonkwo *et al*. (2025), Uba *et al*. 2025a; Okwonkwo *et al.* (2026) and Uba *et al.* (2026a) at Alor stream, Nnobi stream, Oba stream, Eziowelle stream, Oraukwu river, Abacha Spring Water, Otti Spring Enugu Ukwu, Abagana Stream, Ogbujilekwe Stream Nimo, Ali Ukpo Stream, Onyekwena Spring Water Ifitedunu, Agulu Lake, Adazi Nnukwu Stream, Nri Stream, Nkwelle Awka Stream, Abor River Umuawulu, Umuaba River Nibo, Umuife Iyiohia Urum, Araka Stream Mgbakwu and Ogbanabo Stream Isuaniocha respectively. The river and stream water samples were collected in triplicates from different sampling points; downstream, middle stream and upstream using sterile 5 L cylindrical plastic containers, labeled, placed in a cooler and immediately were transported to the laboratory for analysis as described by Dibua *et al*. (2020), Ibo *et al*. (2020); Chukwura *et al*. (2025); and Dibua *et al*. (2025a); (2025b); (2025c).

**Culture Media**

The following media namely Nutrient agar, Chromocult Coliform Agar (CCA), Bile Aesculin Azide Agar (BAA), Thiosulfate Citrate Bile Salt Sucrose Agar (TCBS), Mannitol Salt Agar (MSA) and Salmonella - Shigella Agar (SSA), Cetrimide Milk Agar (CMA), Bacillus Selective agar (BSA) Buffered Peptone Water and Nutrient Broth were used and prepared according to the manufacturer's specification.

**Sterilization**

As stated in Willey *et al.* (2008), conical flasks (Pyrex), prepared media and other plastic materials were sterilized by autoclaving at 121 ºC for 15 min at a pressure of 15 psi. Glass wares such as pipettes, glass spreader, Petri dishes, measuring cylinder, and other glass materials were sterilized in the laboratory hot air oven at a temperature of 160ºC for 1 hr before use (Nkamigbo *et al*. 2020a; 2020b; Uba, 2019; Okafor *et al*. 2021a; 2021b).

**Bacterial Isolation Technique**

A direct spread plate with volumes of 0.1ml of aliquot was used. A ten-fold serial dilution method was used. Then, 0.1 mL from dilutions $10^{-3}$ were inoculated onto a Nutrient agar, Chromocult Coliform Agar (CCA), Bile Aesculin Azide Agar (BAA), Thiosulfate Citrate Bile Salt Sucrose Agar (TCBS), Mannitol Salt Agar (MSA) and Salmonella - Shigella Agar (SSA), Cetrimide Milk Agar (CMA) and Bacillus Selective agar (BSA) respectively (APHA, 2012; Ifediegwu *et al*. 2023a; 2023b; Ifediegwu *et al.* 2024a, 2024b; 2024c; Nnaka *et al*. 2024).

**Bacteriological Analysis**

**Determination of total heterotrophic aerobic bacterial count**

The total heterotrophic aerobic bacterial counts of the water samples will be obtained using spread plate method. With the aid of a sterile pipette, 0.1 mL aliquots of the $10^{-3}$ dilution were spread plated on the surfaces of the Nutrient Agar (NA) plate in duplicates with the aid of a glass spreader. The spreader was sterilized after each successive spreading by dipping it in 70 % ethanol and then passing it through flame of a Bunsen burner. The inoculated plates were incubated by inversion at 37 °C for 24 hr. The total heterotrophic aerobic bacterial counts were determined after incubation using an electric colony counter and colonies counted were expressed at CFU/mL as described by APHA (2012).

**Determination of total coliform count**

The total coliform counts of the water samples were obtained using spread plate method. With the aid of a sterile pipette, 0.1 mL aliquots of the $10^{-3}$ dilution were spread plated on the surfaces of the Chromocult Coliform Agar (CCA) plate in duplicates with the aid of a glass spreader. The spreader was sterilized after each successive spreading by dipping it in 70 % ethanol and then passing it through flame of a Bunsen burner. The inoculated plates were incubated inverted at 45 °C for 24 hr. The total coliform counts were determined after incubation using an electric colony counter and colonies counted were expressed at CFU/mL as described by APHA (2012).

**Determination of total faecal coliform count**

The total faecal coliform counts of the water samples were obtained using spread plate method. With a sterile pipette, 0.1 mL aliquots of the $10^{-3}$ dilution were spread plated on the surfaces of the Chromocult Coliform Agar (CCA) plate in duplicates with the aid of a glass spreader. The spreader was sterilized after each successive spreading by dipping it in 70 % ethanol and then passing it through flame of a Bunsen burner. The inoculated plates were incubated inverted at 37 °C for 24 hr. The faecal coliform counts were determined after incubation using an electric colony counter and colonies counted were expressed at CFU/mL as described by APHA (2012).

**Determination of total *Salmonella* - *Shigella* count**

The total *Salmonella* - *Shigella* counts of the water samples were obtained using spread plate method. With a sterile pipette, 0.1 ml aliquots of the $10^{-3}$ dilution were spread plated on the surfaces of the *Salmonella* - *Shigella* Agar (SSA) plate in duplicates with the aid of a glass spreader. The spreader was sterilized after each successive spreading by dipping it in 70 % ethanol and then passing it through flame of a Bunsen burner. The inoculated plates were incubated inverted at 37 °C for 24 hr. The *Salmonella* - *Shigella* counts were determined after incubation using an electric colony counter and colonies counted were expressed at CFU/mL as described by APHA (2012).

**Determination of total *Vibrio* count**

The total *Vibrio* counts of the water samples were obtained using spread plate method. With a sterile pipette, 0.1 mL aliquots of the $10^{-3}$ dilution were spread plated on the surfaces of the Thiosulphate Citrate Bile Sucrose Agar (TCBS) plate in duplicates with the aid of a glass spreader. The spreader was sterilized after each successive spreading by dipping it in 70 % ethanol and then passing it through flame of a Bunsen burner. The inoculated plates were incubated inverted at 37 °C for 24 hr. The *Vibrio* counts were determined after incubation using an electric colony counter and colonies counted were expressed at CFU/mL as described by APHA (2012).

**Determination of total *Staphylococcus aureus* count**

The total *Staphylococcus aureus* counts of the water samples were obtained using spread plate method. With a sterile pipette, 0.1 mL aliquots of the $10^{-3}$ dilution were spread plated on the surfaces of the Mannitol Salt agar (MSA) plate in duplicates with the aid of a glass spreader. The spreader was sterilized after each successive spreading by dipping it in 70 % ethanol and then passing it through blue flame of a Bunsen burner. The inoculated plates were incubated inverted at 37 °C for 24 hr. The *Staphylococcus aureus* counts were determined after incubation using an electric colony counter and colonies counted were expressed at CFU/mL as described by APHA (2012).

**Determination of total faecal streptococcal count**

The total faecal streptococcal counts of the water samples were obtained using spread plate method. With a sterile pipette, 0.1 ml aliquots of the $10^{-3}$ dilution were spread plated on the surfaces of the Bile Aesculin Azide Agar (BAA) plate in duplicates with the aid of a glass spreader. The spreader was sterilized after each successive spreading by dipping it in 70 % ethanol and then passing it through flame of a Bunsen burner. The inoculated plates were incubated inverted at 37 °C for 24 hr. The total faecal streptococcal counts were determined after incubation using an electric colony counter and colonies counted were expressed at CFU/mL as described by APHA (2012).

**Determination of total *Pseudomonas aeruginosa* count**

The total *Pseudomonas aeruginosa* counts of the water samples were obtained using spread plate method. With a sterile pipette, 0.1 mL aliquots of the $10^{-3}$ dilution were spread plated on the surfaces of the Cetrimide Milk Agar (CMA) plate in duplicates with the aid of a glass spreader. The spreader was sterilized after each successive spreading by dipping it in 70 % ethanol and then passing it through flame of a Bunsen burner. The inoculated plates were incubated inverted at 37 °C for 24 hr. The *Pseudomonas aeruginosa* counts were determined after incubation using an electric colony counter and colonies counted were expressed at CFU/mL as described by APHA (2012).

**Determination of total spore forming Bacilli count**

The total spore forming bacilli counts of the water samples were obtained using spread plate method. With a sterile pipette, 0.1 mL aliquots of the $10^{-3}$ dilution were spread plated on the surfaces of the Bacillus Selective agar (BSA) plate in duplicates with the aid of a glass spreader. The spreader was sterilized after each successive spreading by dipping it in 70 % ethanol and then passing it through flame of a Bunsen burner. The inoculated plates were incubated inverted at 37 °C for 24 hr. The spore forming bacilli counts were determined after incubation using an electric colony counter and colonies counted were expressed at CFU/mL as described by APHA (2012).

**Purification and Preservation of Bacterial Strains**

The distinct colonies were sub-cultured onto another sterile nutrient agar plates and incubated at 37 °C for 24 hr. After 24 hr of incubation, the colonies were inoculated onto agar slants and re-incubated again. The agar slants were preserved in refrigerator at the temperature of 4 °C as described by Uba *et al*. (2026b) and (2026c).

**Characterization and Identification of Bacterial Strains**

The bacterial strains were characterized and identified using their morphological and biochemical characteristics vis-à-vis: Gram and spore staining, oxidase test, catalase test, urease test, indole test, starch hydrolysis test, Nitrate reduction test, Methyl Red – Voges Proskauer (MR-VP) test, Motility test, and sugar fermentation test (Chesbrough, 2006; Iheukwumere *et al*., 2012a; 2012b; Mundi *et al*., 2013; 2014; Okoye *et al*., 2014; 2020a; 2020b; 2020c; ; Uba *et al*., 2024; Uba *et al*., 2025; Dokubo and Uba, 2023; Nwigwe *et al*. 2022, Nwigwe *et al*. 2023, Ibe *et al*. 2023, Alfred *et al.* 2023, Ofunwa *et al*. 2024; Njoku *et al*., 2019a; 2019b; Alfred *et al.* 2025; Okolo *et al*. 2025; Anameze *et al*., 2023; ; Ele *et al*., 2025; Ezeamama *et al*., 2025a; 2025b). The isolate was identified using key of identification as contained in Bergey's Manual for Determinative Bacteriology by Holt *et al.* (1994).

**Statistical Analysis**

The results of the data generated were expressed as mean ± standard deviation (SD) using GraphPad Prism version 8.0.2. The data means were analyzed by two-way Analysis of Variance (ANOVA) followed by Tukey's to compare differences in the diversity of the pathogen composition of the three sampling sites and different sampling points. Threshold values less than 5 % ($p < 0.05$) were considered statistically significant at 95 % confidence interval (Emmy – Egbe *et al*., 2015; Uba and Chukwura, 2016; Uba *et al*. 2016; 2018a; 2018b; 2018c; 2019d; 2019e; Alisa *et al*., 2020; Anukam *et al*., 2020a; 2020b; Uba *et al.*, 2021a; 2021b; Enemchukwu *et al*., 2026a; 2026b).

## RESULTS

The result of the mean bacterial distribution count of water sample collected from different sampling site at Awka North Local Government is represented in Table 1. From the result Mgbakwu stream had the highest total heterotrophic aerobic count of 275.00 ± 13.58 logCFU/mL with percentage frequency of 53.75 % and highest total coliform count of 103.00 ± 2.51 logCFU/mL with percentage frequency of 20.14 %. Isuaniocha stream had the lowest total coliform count of 00.00 ± 00.00 logCFU/mL with percentage frequency of 00.00 %, Uurm Iyioha stream had the highest total *Vibrio* count of 4.00 ± 0.48 logCFU/mL with percentage frequency of 2.23 % respectively.

The result of the mean bacterial count of water sample collected from different sampling sites at Awka South Local Government is represented in Table 2. From the result Nkwelle Awka had the highest total heterotrophic aerobic bacteria count of 123.00 ± 9.88 with percentage frequency of 63.57 %, Nibo stream had the highest total *Staphylococcus* count of 17.00 ± 1.00 with percentage frequency of 12.32 %, Umuawullu had the highest total faecal Streptococci count of 66.00 ±0.00 with percentage frequency of 34.27% and total *Bacillus cereus* count of 22.00 ± 0.50 with percentage frequency of 12.62 % respectively.

The result of the mean bacterial count of water sample collected from different sampling sites at Dunukofia Local Government is represented in Table 3. From the result Ukpo stream had the highest total heterotrophic aerobic bacteria count of 190.00 ± 7.00 with percentage frequency of 81.89 %, Ifitedunu spring water had the lowest total *Staphylococcus* count of 3.00 ± 0.50 with percentage frequency of 6.52 %, Umudioka stream had the highest total faecal Streptoccoci count of 66.00 ±3.00 with percentage frequency of 25.10% and total *Bacillus cereus* count of 45.10 ± 1.50 with percentage frequency of 18.87 % respectively.

The result of the mean bacterial count of water sample collected from different sampling sites at Anaocha Local Government is represented in Table 4. From the result Adazi Nnukwu stream had the highest total heterotrophic aerobic bacteria count of 130.00 ± 5.00 with percentage frequency of 68.78 % and total *Bacillus cereus* count of 35.10 ± 2.50 with percentage frequency of 18.57 %, Nri stream had the highest total coliform count of 4.00 ± 0.60 with percentage frequency of 3.10 %. Agulu Lake had the lowest total *Salmonella Shigella* count of 1.00 ± 0.10 with percentage frequency of 0.81% respectively.

The result of the mean bacterial count of water sample collected from different sampling sites at Njikoka Local Government is represented in Table 5. From the result Nimo stream had the highest total heterotrophic aerobic bacteria count of 186.00 ± 5.00 with percentage frequency of 83.04 %, Enugu Ukwu spring water had the lowest total coliform count of 0.00 ± 3.00 with percentage frequency of 0.00%, Abagana had the highest highest total coliform count of 70.00 ± 3.60 with percentage frequency of 15.80 % and total *Salmonella Shigella* count of 100.00 ± 12.10 with percentage frequency of 22.57% respectively.

The result of the mean bacterial count of water sample collected from different sampling sites at Idemili South Local Government is represented in Table 6. From the result Oba stream had the highest total heterotrophic aerobic bacteria count of 150.00 ± 11.00 with percentage frequency of 48.86 % and the highest total *Vibrio* count of 30.00 ± 3.00 with percentage frequency of 9.77 %, Nnobi stream had the highest total *Bacillus cereus* count of 45.00 ± 3.00 with percentage frequency of 22.17 %, Alor stream had the highest total *Salmonella Shigella* count of 40.00 ± 2.00 with percentage frequency of 16.67 % respectively.

The result of the mean bacterial count of water sample collected from different sampling sites at Idemili North Local Government is represented in Table 7. From the result Eziowelle stream had the highest total heterotrophic aerobic bacteria count of 300.00 ± 13.00 with percentage frequency of 51.28 % and total *Salmonella Shigella* count of 95.00 ± 7.00 logCFU/mL with percentage frequency of 16.03 %, Abacha spring water had the highest total *Pseudomonas* count of 25.00 ± 4.25 logCFU/mL with percentage frequency of 7.72 %, Oraukwu had the highest total faecal Streptoccoci count of 14.00 ± 3.00 logCFU/mL with percentage frequency of 10.29% respectively. Statistically, there were significant ($F = 2.789$, $p < 0.0002$) differences detected among the sampling sites and mean bacterial group ($p < 0.05$, $F = 4.66$, $p < 0.0001$).

Cumulatively as presented in Tables 8 and 9, Awka North had the highest total coliform count of 44.33 ± 1.93 with percentage frequency of 16.60 %, Awka South had the highest total faecal Streptococci count of 20.00± 0.00 with percentage frequency of 11.84 %, Dunukofia had the lowest total *Staphylococcus* count of 1.33± 0.03 with percentage frequency of 0.58 %, Anaocha had lowest total faecal Streptococci count of 1.67± 0.33 with percentage frequency of 1.19 %, Njikoka had the highest total *Pseudomonas* count of 13.00±2.08 with percentage frequency of 4.92 %, Idemili South had the highest total *Bacillus cereus* count of 34.00±3.00 with percentage frequency of 14.49 %, Idemili North had the highest total *Salmonella Shigella* count of 69.00±5.70 with percentage frequency of 19.90% respectively. Statistically, there were significant ($F = 55.42$, $p < 0.0001$) differences detected among mean bacterial group and Local Government sampling site ($p < 0.05$, $F = 3.048$, $p = 0.0132$).

Table 1: Mean bacterial counts of water samples collected from different sampling points at Awka North LGA sampling site

| Microbial group | Urum (LogCFU/mL ×$10^4$) | Relative frequency (%) | Mgbakwu (LogCFU/mL ×$10^4$) | Relative frequency (%) | Isuaniocha (LogCFU/mL ×$10^4$) | Relative frequency (%) | WHO standard |
|---|---|---|---|---|---|---|---|
| **THABC** | 70.00 ± 3.98 | 39.12 | 275.00 ± 13.58 | 53.76 | 60.00 ± 3.00 | 56.60 | 1.0 × $10^2$ /mL |
| **TCC** | 30.00 ± 3.44 | 16.79 | 103.00 ± 2.51 | 20.14 | 0.00 ± 0.00 | 0.00 | Zero per 100 mL |
| **TFCC** | 03.00 ±0.04 | 1.68 | 05.00 ± 0.06 | 0.09 | 0.00 ±0.00 | 0.00 | Zero |
| **TSSC** | 56.00 ± 2.95 | 31.28 | 80.00 ± 2.14 | 15.64 | 36.00 ± 5.0 | 33.96 | Zero |
| **TVC** | 4.00 ± 0.48 | 2.23 | 0.00 ± 0.00 | 0.60 | 0.00 ± 0.00 | 0.00 | Zero |
| **TPC** | 5.00 ± 0.71 | 2.79 | 3.00 ± 0.70 | 0.59 | 3.50 ± 1.00 | 3.30 | — |
| **TFSC** | 0.00 ± 0.00 | 0.00 | 6.00 ± 0.50 | 1.17 | 0.00 ± 0.00 | 0.00 | — |
| **TSC** | 2.00 ± 0.19 | 1.12 | 17.00 ± 1.00 | 3.32 | 2.50 ± 2.00 | 2.36 | — |
| **TBCC** | 9.00 ± 0.20 | 5.03 | 27.00± 1.50 | 5.28 | 4.00 ± 3.50 | 3.77 | __ |
| **Total** | 179 ± 8.59 | | 511.5 ± 21.99 | | 106 ±14.5 | | |

N.B: THABC = Total heterotrophic aerobic bacterial count; TCC = Total coliform count; TFCC = Total faecal coliform count; TSSC = Total *Salmonella Shigella* count; TVC = Total *Vibrio* count; TPC = Total *Pseudomonas* count; TFSC = Total faecal Streptococci; TSC = Total *Staphylococcus* count; Total *Bacillus cereus* count; CFU = Colony forming unit per millimeter; % = Percentage; LGA = Local Government Area; WHO = World Health Organization.

Table 2: Mean bacterial counts of water samples collected from different sampling points at Awka South LGA sampling site

| Microbial group | Nkwelle Awka (LogCFU/mL ×$10^4$) | Relative frequency (%) | Nibo (LogCFU/mL ×$10^4$) | Relative frequency (%) | Umuawulu (LogCFU/mL ×$10^4$) | Relative frequency (%) | WHO standard |
|---|---|---|---|---|---|---|---|
| THABC | 123.00 ± 9.88 | 63.57 | 75.00 ± 3.58 | 54.35 | 86.00 ± 5.00 | 49.11 | 1.0 × $10^2$ /mL |
| TCC | 30.00 ± 3.21 | 15.50 | 23.00 ± 6.51 | 16.67 | 0.00 ± 3.00 | 0.00 | Zero per 100 mL |
| TFCC | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | 0.00 ±0.00 | 0.00 | Zero |
| TSSC | 12.50 ± 1.24 | 6.46 | 8.00 ± 8.14 | 5.79 | 1.00 ± 2.95 | 0.57 | Zero |
| TVC | 1.00 ± 0.05 | 0.52 | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | Zero |
| TPC | 4.00 ± 0.09 | 2.07 | 3.00 ± 0.70 | 2.17 | 3.50 ±1.00 | 1.99 | — |
| TFSC | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | 60.00 ± 0.00 | 34.27 | — |
| TSC | 10.00 ± 1.18 | 5.17 | 17.00 ± 1.00 | 12.32 | 2.50 ± 0.70 | 1.43 | — |
| TBCC | 13.00 ± 0.20 | 6.72 | 12.00± 1.50 | 8.69 | 22.10± 0.50 | 12.62 | __ |
| Total | 193.50 ± 7.76 | | 138.00± 21.53 | | 175.10 ± 13.15 | | |

N.B: THABC = Total heterotrophic aerobic bacterial count; TCC = Total coliform count; TFCC = Total faecal coliform count; TSSC = Total *Salmonella Shigella* count; TVC = Total *Vibrio* count; TPC = Total *Pseudomonas* count; TFSC = Total faecal Streptococci; TSC = Total *Staphylococcus* count;; Total *Bacillus cereus* count; CFU = Colony forming unit per millimeter; % = Percentage; LGA = Local Government Area; WHO = World Health Organization.

Table 3: Mean bacterial counts of water samples collected from different sampling points at Dunukofia LGA sampling site

| Microbial group | Ukpo (LogCFU/mL ×$10^4$) | Relative frequency (%) | Ifitedunu (LogCFU/mL ×$10^4$) | Relative frequency (%) | Umudioka (LogCFU/mL ×$10^4$) | Relative frequency (%) | WHO standard |
|---|---|---|---|---|---|---|---|
| THABC | 190.00 ± 7.0 | 81.89 | 35.00 ± 2.58 | 76.09 | 126.00 ± 12.00 | 52.72 | 1.0 × $10^2$ /mL |
| TCC | 3.00 ± 0.06 | 1.21 | 1.00 ± 1.00 | 2.17 | 0.00 ± 0.00 | 0.00 | Zero per 100 mL |
| TFCC | 1.00 ± 0.08 | 0.43 | 1.00 ± 0.20 | 2.17 | 0.00 ±0.00 | 0.00 | Zero |
| TSSC | 2.00 ± 0.07 | 0.86 | 1.00 ± 0.14 | 2.17 | 1.00 ± 0.05 | 0.42 | Zero |
| TVC | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | Zero |
| TPC | 2.00 ± 0.05 | 0.86 | 3.00 ± 0.50 | 6.52 | 2.50 ±1.00 | 1.05 | — |
| TFSC | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | 60.00 ± 3.00 | 25.10 | — |
| TSC | 7.00 ± 0.10 | 3.02 | 3.00 ± 0.50 | 6.52 | 4.50 ± 0.40 | 1.88 | — |
| TBCC | 23.00 ± 0.30 | 9.91 | 2.00± 0.50 | 4.35 | 45.10± 1.50 | 18.87 | __ |
| Total | 232 ± 7.76 | | 46.00 ± 5.42 | | 239 ± 17.95 | | |

N.B: THABC = Total heterotrophic aerobic bacterial count; TCC = Total coliform count; TFCC = Total faecal coliform count; TSSC = Total *Salmonella Shigella* count; TVC = Total *Vibrio* count; TPC = Total *Pseudomonas* count; TFSC = Total faecal Streptococci; TSC = Total *Staphylococcus* count; Total *Bacillus cereus* count; CFU = Colony forming unit per millimeter; % = Percentage; LGA = Local Government Area; WHO = World Health Organization.

Table 4: Mean bacterial counts of water samples collected from different sampling points at Anaocha LGA sampling site

| Microbial group | Nri (LogCFU/mL ×$10^4$) | Relative frequency (%) | Agulu (LogCFU/mL ×$10^4$) | Relative frequency (%) | Adazi Nnukwu (LogCFU/mL ×$10^4$) | Relative frequency (%) | WHO standard |
|---|---|---|---|---|---|---|---|
| THABC | 90.00 ± 6.0 | 69.77 | 70.00 ± 4.00 | 56.45 | 130.00 ± 5.00 | 68.78 | 1.0 × $10^2$ /mL |
| TCC | 4.00 ± 0.60 | 3.10 | 2.00 ± 0.50 | 1.61 | 0.00 ± 0.00 | 0.00 | Zero per 100 mL |
| TFCC | 1.00 ± 0.50 | 0.78 | 1.00 ± 0.20 | 0.81 | 0.00 ±0.00 | 0.00 | Zero |
| TSSC | 3.00 ± 0.10 | 2.33 | 1.00 ± 0.10 | 0.81 | 8.00 ± 0.50 | 4.23 | Zero |
| TVC | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | Zero |
| TPC | 5.00 ± 0.25 | 3.88 | 0.00 ± 0.00 | 0.00 | 2.00 ±1.00 | 1.06 | — |
| TFSC | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | 5.00 ± 1.00 | 2.65 | — |
| TSC | 7.00 ± 0.20 | 5.43 | 6.00 ± 0.60 | 4.84 | 9.0 ± 0.40 | 4.76 | — |
| TBCC | 19.00 ± 1.30 | 14.73 | 24.00± 1.50 | 19.34 | 35.10± 2.50 | 18.57 | __ |
| Total | 129.00±8.95 | | 124.00±6.90 | | 189.00±10.40 | | |

N.B: THABC = Total heterotrophic aerobic bacterial count; TCC = Total coliform count; TFCC = Total faecal coliform count; TSSC = Total *Salmonella Shigella* count; TVC = Total *Vibrio* count; TPC = Total *Pseudomonas* count; TFSC = Total faecal Streptococci; TSC = Total *Staphylococcus* count; Total *Bacillus cereus* count; CFU = Colony forming unit per millimeter; % = Percentage; LGA = Local Government Area; WHO = World Health Organization.

Table 5: Mean bacterial counts of water samples collected from different sampling points at Njikoka LGA sampling site

| Microbial group | Abagana (LogCFU/mL ×10$^4$) | Relative frequency (%) | Enugu Ukwu (LogCFU/mL ×10$^4$) | Relative frequency (%) | Nimo (LogCFU/mL ×10$^4$) | Relative frequency (%) | WHO standard |
|---|---|---|---|---|---|---|---|
| **THABC** | 180.00 ± 16.00 | 40.63 | 70.00 ± 5.00 | 53.43 | 186.00 ± 5.00 | 83.04 | 1.0 × 10$^2$ /mL |
| **TCC** | 70.00 ± 3.60 | 15.80 | 0.00 ± 0.00 | 0.00 | 2.00 ± 1.00 | 0.89 | Zero per 100 mL |
| **TFCC** | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | 0.00 ±0.00 | 0.00 | Zero |
| **TSSC** | 100.00 ± 12.10 | 22.57 | 15.00 ± 2.00 | 11.45 | 0.00 ± 0.00 | 0.00 | Zero |
| **TVC** | 1.00 ± 0.70 | 0.23 | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | Zero |
| **TPC** | 25.00 ± 4.25 | 5.64 | 6.00 ± 1.00 | 6.11 | 8.00 ±1.00 | 3.57 | — |
| **TFSC** | 1.00 ± 0.50 | 0.23 | 0.00 ± 0.00 | 0.00 | 4.00 ± 1.00 | 1.79 | — |
| **TSC** | 17.00 ± 1.20 | 3.84 | 9.00 ± 2.00 | 6.87 | 9.0 ± 3.50 | 4.02 | — |
| **TBCC** | 49.00 ± 3.00 | 11.06 | 25.00 ± 4.00 | 19.08 | 15.00± 2.00 | 6.70 | __ |
| **Total** | 443.00±41.35 | | 131.00±1.50 | | 224.00±13.50 | | |

N.B: THABC = Total heterotrophic aerobic bacterial count; TCC = Total coliform count; TFCC = Total faecal coliform count; TSSC = Total *Salmonella Shigella* count; TVC = Total *Vibrio* count; TPC = Total *Pseudomonas* count; TFSC = Total faecal Streptococci; TSC = Total *Staphylococcus* count; Total *Bacillus cereus* count; CFU = Colony forming unit per millimeter; % = Percentage; LGA = Local Government Area; WHO = World Health Organization.

Table 6: Mean bacterial counts of water samples collected from different sampling points at Idemili South LGA sampling site

| Microbial group | Oba (LogCFU/mL ×10$^4$) | Relative frequency (%) | Nnobi (LogCFU/mL ×10$^4$) | Relative frequency (%) | Alor (LogCFU/mL ×10$^4$) | Relative frequency (%) | WHO standard |
|---|---|---|---|---|---|---|---|
| **THABC** | 150.00 ± 11.00 | 48.86 | 140.00 ± 5.00 | 68.97 | 70.00 ± 4.00 | 38.89 | 1.0 × 10$^2$ /mL |
| **TCC** | 50.00 ± 3.00 | 16.29 | 0.00 ± 0.00 | 0.00 | 30.00 ± 2.00 | 16.67 | Zero per 100 mL |
| **TFCC** | 1.00 ± 0.00 | 0.33 | 0.00 ± 0.00 | 0.00 | 0.00 ±0.00 | 0.00 | Zero |
| **TSSC** | 16.00 ± 2.00 | 5.21 | 2.00 ± 0.00 | 0.99 | 40.00 ± 2.00 | 22.22 | Zero |
| **TVC** | 30.00 ± 3.00 | 9.77 | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | Zero |
| **TPC** | 25.00 ± 4.00 | 8.14 | 6.00 ± 1.00 | 2.96 | 8.00 ±1.00 | 4.44 | — |
| **TFSC** | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | — |
| **TSC** | 13.00 ± 2.20 | 4.23 | 12.00 ± 2.00 | 5.91 | 9.0 ± 2.00 | 5.00 | — |
| **TBCC** | 34.00 ± 3.00 | 11.07 | 45.00 ± 3.00 | 22.17 | 23.00± 3.00 | 12.78 | __ |
| **Total** | 307.00±28.00 | | 203.00±11.00 | | 180.00±14.00 | | |

N.B: THABC = Total heterotrophic aerobic bacterial count; TCC = Total coliform count; TFCC = Total faecal coliform count; TSSC = Total *Salmonella Shigella* count; TVC = Total *Vibrio* count; TPC = Total *Pseudomonas* count; TFSC = Total faecal Streptococci; TSC = Total *Staphylococcus* count; Total *Bacillus cereus* count; CFU = Colony forming unit per millimeter; % = Percentage; LGA = Local Government Area; WHO = World Health Organization.

Table 7: Mean bacterial counts of water samples collected from different sampling points at Idemili North LGA sampling site

| Microbial Group | Abacha (LogCFU/mL ×10$^4$) | Relative frequency (%) | Eziowelle (LogCFU/mL ×10$^4$) | Relative frequency (%) | Oraukwu (LogCFU/mL ×10$^4$) | Relative frequency (%) | WHO standard |
|---|---|---|---|---|---|---|---|
| **THABC** | 150.00 ± 16.00 | 46.27 | 300.00 ± 13.00 | 51.28 | 80.00 ± 4.00 | 58.82 | 1.0 × 10$^2$ /mL |
| **TCC** | 18.00 ± 3.60 | 5.56 | 0.00 ± 0.00 | 0.00 | 3.00 ± 1.00 | 2.21 | Zero per 100 mL |
| **TFCC** | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | 1.00 ±0.00 | 0.74 | Zero |
| **TSSC** | 87.00 ± 7.10 | 26.86 | 95.00 ± 7.00 | 16.38 | 25.00 ± 3.00 | 18.38 | Zero |
| **TVC** | 0.00 ± 0.00 | 0.00 | 93.00 ± 8.00 | 16.03 | 0.00 ± 0.00 | 0.00 | Zero |
| **TPC** | 25.00 ± 4.25 | 7.72 | 6.00 ± 2.00 | 1.03 | 3.00 ± 1.00 | 2.21 | — |
| **TFSC** | 0.00 ± 0.00 | 0.00 | 14.00 ± 3.00 | 2.41 | 14.00 ± 3.00 | 10.29 | — |
| **TSC** | 7.00 ± 1.20 | 2.16 | 19.00 ± 3.00 | 3.28 | 2.0 ± 0.00 | 1.47 | — |
| **TBCC** | 37.00 ± 3.00 | 11.42 | 53.00 ± 4.00 | 9.14 | 8.00± 2.00 | 5.88 | __ |
| **Total** | 324.00±35.50 | | 580.00±40.00 | | 136.00±14.00 | | |

N.B: THABC = Total heterotrophic aerobic bacterial count; TCC = Total coliform count; TFCC = Total faecal coliform count; TSSC = Total *Salmonella Shigella* count; TVC = Total *Vibrio* count; TPC = Total *Pseudomonas* count; TFSC = Total faecal Streptococci; TSC = Total *Staphylococcus* count; Total *Bacillus cereus* count; CFU = Colony forming unit per millimeter; % = Percentage; LGA = Local Government Area; WHO = World Health Organization.

Table 8: Cumulative mean bacterial counts of water samples collected from different sampling sites at Awka North, Awka South, Dunokofia and Anaocha Local Government Areas

| **Microbial group** | **Awka North (LogCFU/mL ×10⁵)** | **Relative frequency (%)** | **Awka South (LogCFU/mL ×10⁵)** | **Relative frequency (%)** | **Dunokofia (LogCFU/mL ×10⁵)** | **Relative frequency (%)** | **Anaocha (LogCFU/mL ×10⁵)** | **Relative frequency (%)** | **WHO standard** |
|---|---|---|---|---|---|---|---|---|---|
| **THABC** | 135.00 ± 6.85 | 50.56 | 94.67 ± 6.15 | 56.08 | 117 ± 7.19 | 51.42 | 96.67 ± 5.00 | 68.71 | $1.0 \times 10^2$ /mL |
| **TCC** | 44.33 ± 1.93 | 16.60 | 17.67 ± 4.24 | 0.10 | 1.33 ± 0.35 | 0.58 | 2.00 ± 0.37 | 1 42 | Zero per 100 mL |
| **TFCC** | 2.67 ± 0.03 | 1.00 | 0.00 ± 0.00 | 0.00 | 0.67 ± 0.09 | 0.29 | 0.67 ± 0.23 | 0.48 | Zero |
| **TSSC** | 57.33 ± 3.36 | 21.47 | 7.17 ± 4.11 | 4.25 | 1.33 ± 0.09 | 0.58 | 4.00 ± 0.23 | 2.84 | Zero |
| **TVC** | 1.33 ± 0.16 | 0.50 | 0.33 ± 0.02 | 0.20 | 0.00 ± 0.00 | 0.00 | 0.00 ± 0.00 | 0.00 | Zero |
| **TPC** | 3.83 ± 0.80 | 1.43 | 3.50 ± 0.60 | 2.07 | 2.50 ± 0.37 | 1.20 | 2.33 ± 0.42 | 1.66 | — |
| **TFSC** | 2.00 ± 0.17 | 0.75 | 20.00 ± 0.00 | 11.84 | 20.00 ± 0.00 | 8.79 | 1.67 ± 0.33 | 1.19 | — |
| **TSC** | 7.17 ± 1.06 | 2.69 | 9.83 ± 0.96 | 5.82 | 1.33 ± 0.03 | 0.58 | 7.33 ± 0.28 | 5.21 | — |
| **TBCC** | 13.33 ± 1.73 | 4.99 | 15.7 ± 0.73 | 9.30 | 23.37 ± 0.77 | 10.27 | 26.03 ± 1.77 | 18.50 | — |
| **Total** | 266.99±16.09 | | 168.80±16.81 | | 227.53±8.54 | | 140.70±8.63 | | |

N.B: THABC = Total heterotrophic aerobic bacterial count; TCC = Total coliform count; TFCC = Total faecal coliform count; TSSC = Total *Salmonella Shigella* count; TVC = Total *Vibrio* count; TPC = Total *Pseudomonas* count; TFSC = Total faecal Streptococci; TSC = Total *Staphylococcus* count; Total *Bacillus cereus* count; CFU = Colony forming unit per millimeter; % = Percentage; LGA = Local Government Area; WHO = World Health Organization.

Table 9: Cumulative mean bacterial counts of water samples collected from different sampling sites at Njikoka, Idemili South and Idemili North Local Government Areas

| **Microbial group** | **Njikoka (LogCFU/mL ×10⁴)** | **Relative frequency (%)** | **Idemili South (LogCFU/mL ×10⁴)** | **Relative frequency (%)** | **Idemili North (LogCFU/mL ×10⁴)** | **Relative frequency (%)** | **WHO standard** |
|---|---|---|---|---|---|---|---|
| **THABC** | 145.33 ± 8.67 | 55.05 | 120.00 ± 6.67 | 51.14 | 176.69 ± 11.00 | 50.97 | $1.0 \times 10^2$ /mL |
| **TCC** | 24.00 ± 1.53 | 9.09 | 26.67 ± 1.67 | 11.37 | 7.00 ± 1.53 | 2.02 | Zero per 100 mL |
| **TFCC** | 0.00 ± 0.00 | 0.00 | 0.33 ± 0.00 | 0.14 | 0.33 ± 0.00 | 0.10 | Zero |
| **TSSC** | 38.33 ± 4.70 | 14.52 | 19.33 ± 1.33 | 8.24 | 69.00 ± 5.70 | 19.90 | Zero |
| **TVC** | 0.33 ± 0.23 | 0.13 | 10.00 ± 1.00 | 4.26 | 31.00 ± 2.67 | 8.94 | Zero |
| **TPC** | 13.00 ± 2.03 | 4.92 | 13.00 ± 2.00 | 5.54 | 11.33 ± 2.42 | 3.27 | — |
| **TFSC** | 1.67 ± 0.50 | 0.63 | 0.00 ± 0.00 | 0.00 | 9.33 ± 2.00 | 2.69 | — |
| **TSC** | 11.67 ± 2.23 | 4.42 | 11.33 ± 2.07 | 4.84 | 9.33 ± 1.40 | 2.69 | — |
| **TBCC** | 29.67 ± 3.00 | 11.24 | 34.00 ± 3.00 | 14.49 | 32.69 ± 3.00 | 9.43 | __ |
| **Total** | 264.00±22.94 | | 234.66±15.74 | | 346.68±29.59 | | |

N.B: THABC = Total heterotrophic aerobic bacterial count; TCC = Total coliform count; TFCC = Total faecal coliform count; TSSC = Total *Salmonella Shigella* count; TVC = Total *Vibrio* count; TPC = Total *Pseudomonas* count; TFSC = Total faecal Streptococci; TSC = Total *Staphylococcus* count; Total *Bacillus cereus* count; CFU = Colony forming unit per millimeter; % = Percentage; LGA = Local Government Area; WHO = World Health Organization.

The microscopic and biochemical features of dominant bacteria strains isolated from the twenty-one sampling sites are presented in Tables 10. From the Table 10 most of the isolates were Gram negative, short rod shaped, positive to catalase, motility, citrate, nitrate reduction test, rhamnose, galactose, sorbitol, mannose, glucose, lactose and sucrose but negative to indole, oxidase, urease and coagulase respectively.

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Table 10: Microscopic and biochemical feature of the selected pathogenic bacterial strains isolated from the twenty-one sampling sites in the seven local Government Areas in Anambra State

| Isolate code | Gram reaction | Cellular shape | CAT | MOT | IND | H2S | OXI | URE | CIT | NRT | MR | VP | RHA | GAL | SOR | ARA | MAN | XYL | INO | GLU | LAC | SUC | COG | IDENTITY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **SAL1** | Gram - | Rod | + | + | — | + | — | — | + | + | — | + | + | + | + | + | + | + | — | + | — | — | — | *Salmonella* sp. |
| **SAL2** | Gram - | Rod | + | + | — | + | — | — | + | + | + | — | + | + | + | + | + | + | + | + | — | — | — | *Salmonella enterica* |
| **SAL3** | Gram - | Rod | + | + | — | + | — | — | + | + | + | — | — | + | + | — | + | + | — | + | — | — | — | *Salmonella typhi* |
| **SAL4** | Gram - | Rod | + | + | — | — | — | — | + | + | — | — | + | + | + | — | + | — | + | + | — | — | — | *Shigella* sp. |
| **PA1** | Gram - | Rod | + | + | — | — | + | — | + | — | + | + | + | + | + | — | + | + | + | — | — | — | — | *Pseudomonas fluorescens* |
| **PA2** | Gram - | Rod | + | + | — | — | + | — | + | + | — | — | — | — | — | — | + | — | — | — | — | — | — | *Pseudomonas aeruginosa* |
| **PA3** | Gram - | Rod | + | + | — | — | + | — | + | + | — | — | — | — | — | — | + | — | + | — | — | — | — | *Pseudomonas aeruginosa* |
| **PA4** | Gram - | Rod | + | + | — | — | + | — | + | + | — | + | + | + | + | + | + | + | + | — | — | — | — | *Pseudomonas* sp. |
| **EC1** | Gram - | Rod | + | + | — | + | — | + | + | + | + | — | + | + | + | — | + | + | + | + | + | + | — | *Citrobacter* sp. |
| **EC2** | Gram - | Rod | + | + | + | — | — | — | — | + | + | — | + | + | + | + | + | — | — | + | + | + | — | *Escherichia coli* |
| **EC3** | Gram - | Rod | + | + | — | + | — | — | + | + | — | + | + | + | + | — | + | + | + | + | + | + | — | *Enterobacter faecalis* |
| **EC4** | Gram - | Rod | + | + | — | + | — | — | + | + | — | + | + | + | + | + | — | + | + | + | + | + | — | *Enterobacter faecalis* |
| **VS1** | Gram - | Rod | + | + | + | + | + | — | + | + | — | — | + | + | + | + | + | + | + | + | + | + | — | *Vibrio* sp. |
| **VS2** | Gram - | Rod | + | + | + | + | + | — | + | + | — | — | + | + | + | + | + | + | + | + | + | + | — | *Vibrio* sp. |
| **VS3** | Gram - | Rod | + | + | + | — | + | — | + | + | — | — | + | + | + | + | + | — | + | + | + | + | — | *Vibrio* sp. |
| **VS4** | Gram - | Rod | + | + | + | — | + | — | + | + | — | + | — | + | + | + | + | — | — | — | + | + | — | *Vibrio alginolyticus* |

N.B. CAT = catalase, MOT = motility, IN = indole, $H_2S$ = Hydrogen sulphide, OXI = Oxidase, UR = urease, CIT = citrate, NRT = nitrate reduction test, M.R = methyl red, V.P = Voges Proskauer, RHA= Rhamnose, GLU = glucose, GAL = Galactose, SOR = Sorbitol, ARA = Arabinose, MAN = mannitol, XYL = xylose, INO = inositol, GLU = Glucose, LAC = Lactose, SUC = Sucrose, COG = Coagulase; + = positive, — = negative, Gram + = Gram positive, Gram — = Gram negative

Table 10: Continued

| Isolate code | Gram reaction | Cellular shape | CAT | MOT | IND | H2S | OXI | URE | CIT | NRT | MR | VP | RHA | GAL | SOR | ARA | MAN | XYL | INO | GLU | LAC | SUC | COG | IDENTITY |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **VS5** | Gram - | Rod | + | + | + | — | + | — | + | + | — | + | — | + | — | — | + | — | — | + | + | + | — | *Vibrio cholera* |
| **VS6** | Gram - | Rod | + | + | + | — | + | — | + | + | — | — | + | + | — | — | + | — | + | + | + | — | — | *Vibrio mimicus* |
| **SA1** | Gram + | Coccus | + | — | — | — | — | + | + | + | + | + | — | + | — | — | + | — | — | + | + | + | — | *Staphylococcus simulans* |
| **SA2** | Gram + | Coccus | + | — | — | — | — | + | + | + | + | — | + | + | + | + | + | — | + | + | + | + | — | *Staphylococcus* sp. |
| **SA3** | Gram + | Coccus | + | — | — | — | — | + | + | + | + | + | + | + | + | — | + | + | + | + | + | + | + | *Staphylococcus intermedius* |
| **SA4** | Gram + | Coccus | + | — | — | — | — | + | + | + | + | + | + | + | + | — | + | — | + | + | + | + | + | *Staphylococcus aureus* |
| **SA5** | Gram + | Coccus | + | — | — | — | — | + | + | + | + | — | + | + | + | + | + | + | + | + | + | + | — | *Staphylococcus* sp. |
| **SF1** | Gram + | Coccus | — | — | — | — | — | — | — | + | + | + | + | + | + | — | + | + | — | + | + | — | — | *Enterococcus asini* |
| **SF2** | Gram + | Coccus | — | — | — | — | — | — | — | + | + | + | + | + | + | + | + | — | — | + | + | — | — | *Enterococcus faecium* |
| **SF3** | Gram + | Coccus | — | — | — | — | — | — | — | + | — | + | — | + | + | — | + | — | — | + | + | — | — | *Enterococcus faecalis* |
| **SF4** | Gram + | Coccus | — | — | — | — | — | — | — | + | + | + | — | + | + | — | + | — | — | + | + | — | — | *Enterococcus faecalis* |
| **BAC1** | Gram + | Rod | + | + | — | — | — | — | + | + | — | + | — | — | — | — | — | — | — | + | — | + | — | *Bacillus cereus* |
| **BAC2** | Gram + | Rod | + | + | — | — | — | — | + | + | — | + | — | — | — | — | — | — | + | + | — | + | — | *Bacillus cereus* |
| **BAC3** | Gram + | Rod | + | + | — | — | — | — | + | + | — | + | — | + | + | + | + | + | + | + | + | + | + | *Bacillus subtilis* |

N.B. CAT = catalase, MOT = motility, IN = indole, $H_2S$ = Hydrogen sulphide, OXI = Oxidase, UR = urease, CIT = citrate, NRT = nitrate reduction test, M.R = methyl red, V.P = Voges Proskauer, RHA= Rhamnose, GLU = glucose, GAL = Galactose, SOR = Sorbitol, ARA = Arabinose, MAN = mannitol, XYL = xylose, INO = inositol, GLU = Glucose, LAC = Lactose, SUC = Sucrose, COG = Coagulase; + = positive, — = negative, Gram + = Gram positive, Gram — = Gram negative

## DISCUSSION

In this research on the basis of the Tables 1 - 9 results obtained from twenty-one freshwater bodies Urum, Mgbakwu, Isuaniocha, Nkwelle Awka, Nibo, Umuawullu, Ukpo, Ifitedunu, Umudioka, Nri, Agulu, Adazi-Nnukwu, Abagana, Enugu-Ukwu,Nimo, Oba, Nnobi, Alor, Abacha, Eziowelle, Oraukwu in Anambra Central Senetorial zone, Nigeria. The mean total heterotrophic aerobic bacteria count was between 70.00 ± 3.98 logCFU/mL for Urum, 275.00 ± 13.58 logCFU/mL for Mgbakwu, 60.00 ± 3.00 logCFU/mL for Isuaniocha, 123.00 ± 9.88 logCFU/mL for Nkwelle Awka, 75.00 ± 3.58 logCFU/mL for Nibo, 86.00 ± 5.00 logCFU/mL for Umawullu, 190.00 ± 7.00 logCFU/mL for Ukpo, 35.00 ± 2.58 logCFU/mL for Ifitedunu, 126.00 ± 12.00 logCFU/mL for Umudoka, 90.00 ± 6.00 logCFU/mL for Nri, 70.00 ± 4.00 logCFU/mL for Agulu, 130.00 ± 5.00 logCFU/mL for Adazi-Nnukwu, 180.00 ± 16.00 logCFU/mL for Abagana, 70.00 ± 5.00 logCFU/mL for Enugu-Ukwu, 186.00 ± 5.00 logCFU/mL for Nimo, 150.00 ± 11.00 logCFU/mL for Oba, 140.00 ± 5.00 logCFU/mL for Nnobi, 70.00 ± 4.00 logCFU/mL for Alor, 150.00 ± 16.00 logCFU/mL for Abacha, 300.00 ± 13.00 logCFU/mL for Eziowelle and 80.00 ± 4.00 logCFU/mL for Oraukwu, respectively indicating high level of pollution of fresh water due to human and animal activities. The observed microbial counts were higher than the permissible limit of 0 CFU/mL for potable water as specified by the Nigerian Industrial Standards (NIS, 2007), indicating potential public health risks. Such elevated bacterial loads may be attributed to multiple contamination pathways. Environmental factors such as surface runoff, particularly during rainfall events, can transport soil particles, organic matter, and microorganisms into water bodies. In addition, animal waste deposition and grazing activities in surrounding pastures may introduce enteric bacteria into the water sources. Furthermore, anthropogenic activities including swimming, indiscriminate waste disposal, domestic washing, and faecal discharge (Egberongbe *et al*., 2012) significantly contribute to microbial contamination. These activities not only introduce pathogenic and non-pathogenic microorganisms but also enrich the water with organic nutrients. The increased nutrient load enhances microbial proliferation, thereby sustaining and amplifying bacterial populations across the various water sources. Consequently, the microbiological quality of the water may be compromised, rendering it unsuitable for direct human consumption without adequate treatment

Coliform bacteria are widely recognized as reliable indicators of microbiological water quality and the extent of environmental contamination. In the present study, the total coliform counts (TCC) recorded in all samples exceeded the permissible limit of zero total coliforms per 100 mL established by the World Health Organization (WHO) (2012) for potable water. This non-compliance clearly indicates microbiological deterioration and renders the water unsuitable for direct human consumption without adequate treatment. The detection of coliform organisms strongly suggests faecal contamination, as these bacteria are commonly associated with the intestinal tract of humans and warm-blooded animals. The failure of all surface water samples to meet WHO (2012) standards is consistent with previous reports, including the findings of Onajite *et al*. (2018), who attributed elevated microbial loads in surface waters to increased organic matter and anthropogenic influences. Surface water bodies are particularly vulnerable to contamination due to direct exposure to runoff, agricultural activities, open defecation, and improper waste disposal practices. Such inputs introduce both microorganisms and biodegradable organic matter, thereby creating favorable conditions for bacterial survival and proliferation.

The isolation of pathogenic organisms such as *Salmonella* spp., *Pseudomonas* spp., *Vibrio* spp., and *Staphylococcus aureus* from both water sources is of significant public health concern. These organisms have been implicated in a variety of infections, including gastroenteritis, typhoid fever, cholera-like illnesses, urinary tract infections, wound infections, septicemia, and respiratory tract infections, particularly among vulnerable populations such as children, the elderly, and immunocompromised individuals (Brook *et al.,* 2013). Their presence not only confirms faecal contamination but also suggests the possible circulation of enteric pathogens within the study area.

Furthermore, faecal streptococci (enterococci) are considered more specific indicators of human faecal pollution compared to total coliforms, as they are less likely to multiply in the external environment. The markedly elevated faecal streptococci count observed in this study suggest substantial contamination from human excreta rather than solely from animal sources. The consistently high faecal coliform values across all sampling points reinforce the conclusion that the water bodies are heavily impacted by faecal pollution and aligned with the published works of Alfred *et al.* (2025) and Uba *et al*. (2025). Statistical analysis further demonstrated significant spatial variation in microbial contamination among the sampling sites ($F = 2.789$, $p < 0.0002$) and among the different bacterial groups ($F = 4.66$, $p < 0.0001$). These statistically significant differences ($p < 0.05$) indicate that contamination levels are not uniformly distributed, likely reflecting variations in land use practices, proximity to human settlements, sanitation infrastructure, and local hydrological conditions.

The results presented in Tables 4.10 revealed that the dominant bacterial isolates from the selected sampling sites included *Bacillus cereus, Escherichia coli, Pseudomonas aeruginosa, Staphylococcus aureus, Salmonella enterica subsp. enterica, Enterococcus faecalis, and Vibrio cholerae*. These findings are consistent with the published work of Ike *et al*. (2021), who conducted a bacteriological examination of Obibia Stream during the wet and dry seasons in Awka, Anambra State, Nigeria. Their study identified the presence of *Shigella*, *Salmonella*, *Escherichia coli*, *Vibrio, Enterobacter*, *Klebsiella*, *Enterococcus, Staphylococcus*, *Pseudomonas*, and *Serratia*, with respective frequencies of occurrence of 4.55%, 18.18%, 13.64%, 27.27%, 4.5%, 9.09%, 4.55%, 4.55%, 9.09%, and 4.55%. Similarly, some of these bacteria were also isolated in the study conducted by Agbabiaka *et al*. (2012) on Foma River, Ilorin. The similar microorganisms reported included *Pseudomonas aeruginosa*, *Escherichia coli*, and *Bacillus cereus*. The recurrence of these organisms across different freshwater systems suggests a widespread pattern of microbial contamination in surface waters within the region. The detection of *Escherichia coli* and *Enterococcus faecalis*, which are widely recognized indicators of fecal contamination, strongly implies the introduction of domestic sewage, agricultural runoff, and open defecation into the water bodies. Likewise, the presence of *Salmonella enterica* and *Vibrio cholerae* is of significant public health concern, as these organisms are associated with gastrointestinal infections, typhoid fever, and cholera outbreaks, particularly in areas with inadequate water treatment and sanitation facilities.

Furthermore, the isolation of opportunistic pathogens such as *Pseudomonas aeruginosa* and *Staphylococcus aureus* may reflect contamination from hospital effluents, washing activities, animal waste, and other anthropogenic sources. *Bacillus cereus*, a spore-forming bacterium commonly found in soil, may have entered the freshwater system through surface runoff, especially during periods of heavy rainfall. Overall, the presence of these microorganisms in the freshwater bodies can be strongly linked to human-related activities such as improper waste disposal, agricultural practices, bathing, washing, and discharge of untreated wastewater, as supported by Agbabiaka *et al*. (2012).

## CONCLUSION

Overall, the findings highlight serious microbiological impairment of the investigated water sources and underscore the urgent need for effective water treatment, improved sanitation practices, proper waste management strategies and continuous microbiological monitoring of freshwater sources to safeguard public health.

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