

# Bacteriological and physicochemical assessment of Bundu and Nembe Creeks, Rivers State, Nigeria

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## ABSTRACT

Surface waters in the Niger Delta are increasingly influenced by anthropogenic activities that may alter their physicochemical and bacteriological characteristics. This study assessed the physicochemical and bacteriological characteristics of Bundu and Nembe Creeks, Rivers State, Nigeria. Water samples were collected from Bundu and Nembe Creeks and analysed for temperature, pH, salinity, electrical conductivity (EC), turbidity, dissolved oxygen (DO), biochemical oxygen demand (BOD<sub>5</sub>), and chemical oxygen demand (COD). Total heterotrophic bacteria (THB) and hydrocarbon-utilizing bacteria (HUB) were enumerated using standard microbiological methods. Representative bacterial isolates were characterized using conventional morphological, biochemical, and physiological procedures. Significant differences were observed between the two creeks in pH, salinity, EC, turbidity, DO, BOD<sub>5</sub>, and COD ( $P < 0.05$ ), whereas temperature did not differ significantly ( $P = 0.215$ ). Bundu Creek recorded higher turbidity ( $10.96 \pm 0.14$  NTU), DO ( $3.58 \pm 0.36$  mg/L), BOD<sub>5</sub> ( $6.83 \pm 0.03$  mg/L), and COD ( $38.13 \pm 0.85$  mg/L), whereas Nembe Creek recorded higher salinity ( $5.58 \pm 0.22\text{‰}$ ) and EC ( $4520.00 \pm 358.89$   $\mu\text{S/cm}$ ). THB and HUB populations were higher in Nembe Creek ( $9.52 \times 10^5 \pm 6.30 \times 10^5$  and  $2.20 \times 10^4 \pm 1.15 \times 10^3$  CFU/mL, respectively) than in Bundu Creek ( $4.36 \times 10^4 \pm 3.82 \times 10^3$  and  $1.20 \times 10^4 \pm 8.16 \times 10^2$  CFU/mL, respectively). Eleven bacterial taxa were recovered from Bundu Creek and six from Nembe Creek, with *Bacillus* sp., *Pseudomonas* sp., *Staphylococcus* sp., *Enterobacter* sp., and *Klebsiella* sp. occurring in both creeks. Overall, Bundu and Nembe Creeks exhibited distinct physicochemical and bacteriological characteristics, with evidence of bacterial contamination and the presence of hydrocarbon-utilizing bacteria. Continued monitoring and appropriate pollution-control measures are recommended to protect the ecological integrity and public-health quality of these aquatic environments.

**Keywords:** Bundu creek, Nembe creek, surface water, physicochemical characteristics, heterotrophic bacteria, hydrocarbon-utilizing bacteria.

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## INTRODUCTION

Surface waters constitute important components of aquatic ecosystems and provide essential ecological and socioeconomic functions, including supporting aquatic organisms and fisheries, facilitating transportation, contributing to nutrient cycling, and sustaining domestic livelihoods. In the Niger Delta region of Nigeria, an extensive network of rivers, creeks, estuaries, and wetlands provides important resources for surrounding communities. However, maintaining the environmental quality of these water bodies remains a significant concern because they are exposed to multiple human activities, while long-term, site-specific monitoring

information for many creeks remains limited. Domestic waste disposal, sewage discharge, agricultural runoff, industrial activities, petroleum exploration and transportation, and other anthropogenic activities can introduce organic matter, microorganisms, hydrocarbons, and other contaminants into receiving waters. These activities are recognized as potential sources of water-quality deterioration within the Niger Delta, although they were not directly measured in the present study and are considered contextual environmental influences. Previous studies conducted in Rivers State and other parts of the Niger Delta have demonstrated the importance of

assessing physicochemical and microbiological characteristics in evaluating the condition of surface waters (Olorode et al., 2015; Ukpaka and Chuku, 2012; Onojake et al., 2017).

Physicochemical parameters are important indicators of aquatic environmental quality. Temperature, pH, turbidity, electrical conductivity, salinity, dissolved oxygen, biochemical oxygen demand, and chemical oxygen demand provide information on the physical and chemical conditions of water and may be influenced by both natural processes and anthropogenic inputs (Patil et al., 2012; Environmental Protection Agency, 2001). Variations in these parameters can affect microbial abundance, distribution, and metabolic activities, making their assessment essential for understanding aquatic ecosystem health.

The bacteriological characteristics of surface water provide complementary information on environmental quality and potential contamination. Total heterotrophic bacterial populations reflect the overall bacterial community, while the occurrence of different bacterial taxa may indicate variations in nutrient availability, organic matter loading, and prevailing environmental conditions. Previous investigations of rivers and creeks in Nigeria have reported bacterial populations and identified bacterial isolates from surface-water environments (Amosu et al., 2018; Edun et al., 2016).

In the Niger Delta, petroleum-related activities present an additional environmental concern because hydrocarbon contamination can create selective conditions that favour microorganisms capable of degrading petroleum-derived compounds. Consequently, assessing hydrocarbon-utilizing bacteria alongside total heterotrophic bacteria provides valuable information on microbial community characteristics and the natural biodegradation potential of aquatic environments.

Bundu Creek and Nembe Creek were selected because they are important tidal creek systems in Rivers State that support fishing, transportation, and other community activities while representing contrasting environmental settings within the Niger Delta. Comparing these two creeks provides an opportunity to evaluate whether differences in physicochemical conditions are accompanied by differences in bacterial populations and composition under naturally occurring environmental conditions. Although previous studies have examined the physicochemical and microbiological characteristics of rivers and creeks in Rivers State (Olorode et al., 2015; Onojake et al., 2017; Obunwo et al., 2011; Ollor et al., 2018), site-specific comparative information integrating physicochemical characteristics, total heterotrophic bacteria, hydrocarbon-utilizing bacteria, and bacterial isolates from Bundu and Nembe Creeks remains limited. Addressing this gap is important for establishing baseline information on the environmental and microbiological status of these creeks and providing evidence to support

future monitoring and management efforts.

Therefore, this study aimed to compare the physicochemical and bacteriological characteristics of Bundu and Nembe Creeks, Rivers State, Nigeria. Specifically, the study sought to: (i) determine the physicochemical characteristics of water from both creeks; (ii) quantify total heterotrophic bacterial and hydrocarbon-utilizing bacterial populations; and (iii) identify the bacterial taxa present in each creek.

## MATERIALS AND METHODS

### Study area

The study was conducted in Bundu Creek and Nembe Creek in Port Harcourt, Rivers State, Nigeria, within the Niger Delta region. Both creeks are tidal aquatic systems associated with waterfront communities where fishing, transportation, domestic activities, waste disposal, and petroleum-related activities occur in the surrounding environment. These activities were not directly measured in the present study but represent contextual environmental influences that may affect water quality. One representative sampling point was established in each creek for monthly water sampling throughout the study period.

### Study design and sample collection

A cross-sectional sampling design was adopted to evaluate the physicochemical and bacteriological characteristics of water from Bundu and Nembe Creeks. One representative sampling point was established in each creek, and samples were collected monthly over a five-month period, from March to July 2026, resulting in five sampling events per creek.

During each sampling event, approximately 250 mL of water was aseptically collected from each creek using sterile 500-mL sampling bottles, resulting in a total of 10 water samples for bacteriological analysis (five samples from each creek). Before sampling, each bottle was labelled with the creek name, sampling point, and collection date. Samples were collected by immersing the sterile bottle below the water surface while minimizing contamination and disturbance of the surrounding water.

Immediately after collection, the samples were placed in ice-packed insulated containers, protected from direct sunlight, and transported to the Microbiology Laboratory, Rivers State University, for analysis. All samples were processed within 2 h of collection, with no prolonged storage before bacteriological examination. Although the samples were maintained under cooled transport conditions, the transport temperature was not directly measured and is therefore not reported numerically.

### Physicochemical analysis

Water samples were analysed for temperature, pH, salinity, electrical conductivity (EC), turbidity, dissolved oxygen (DO), biochemical oxygen demand (BOD<sub>5</sub>), and chemical oxygen demand (COD) using the Standard Methods for the Examination of Water and Wastewater (APHA, 2017).

Temperature, pH, salinity, and electrical conductivity were measured in situ using calibrated digital meters, while turbidity was measured using a calibrated turbidity meter and expressed in nephelometric turbidity units (NTU).

Dissolved oxygen was determined using the Winkler titrimetric method. Biochemical oxygen demand (BOD<sub>5</sub>) was determined by measuring the initial dissolved oxygen (DO<sub>0</sub>), incubating the samples in the dark at 20 ± 1°C for five days, and subsequently measuring the final dissolved oxygen (DO<sub>5</sub>). BOD<sub>5</sub> was calculated as:

$$\text{BOD}_5 \text{ (mg/L)} = (\text{DO}_0 - \text{DO}_5) \times \text{Dilution Factor}$$

Chemical oxygen demand (COD) was determined using the dichromate open-reflux method. Samples were refluxed with potassium dichromate and concentrated sulfuric acid, after which the excess dichromate was titrated with standard ferrous ammonium sulfate using ferroin as the indicator. A reagent blank was analysed concurrently.

$$\text{COD (mg/L)} = \frac{(A - B) \times N \times 8000}{V}$$

where *A* is the titrant volume for the blank, *B* is the titrant volume for the sample, *N* is the normality of the ferrous ammonium sulfate solution, and *V* is the sample volume (mL).

### Bacteriological analysis

All bacteriological analyses were performed using aseptic techniques.

#### *Enumeration of total heterotrophic bacteria*

Total heterotrophic bacteria (THB) were enumerated using the viable plate count method. One millilitre of each water sample was aseptically transferred into 9 mL of sterile normal saline and serially diluted ten-fold. Aliquots (0.1 mL) from appropriate dilutions were spread in duplicate onto sterile Nutrient Agar plates using a sterile glass spreader. The plates were incubated at ambient laboratory temperature (approximately 24–32°C) for 24–48 h. Plates containing countable colonies were selected,

and bacterial populations were expressed as colony-forming units per millilitre (CFU/mL).

#### *Enumeration of hydrocarbon-utilizing bacteria*

Hydrocarbon-utilizing bacteria (HUB) were enumerated using Mineral Salt Agar (MSA), which provides inorganic nutrients while petroleum hydrocarbons serve as the principal carbon and energy source. The medium was prepared according to the method described by Odokuma and Dickson (2003).

Appropriate serial dilutions of the water samples were inoculated in duplicate onto MSA plates. Petroleum hydrocarbons were supplied using the vapour-phase transfer technique described by Ebuehi et al. (2005). The plates were incubated at ambient laboratory temperature for five days, after which colonies exhibiting growth on the hydrocarbon-containing medium were counted and expressed as CFU/mL.

#### *Isolation and identification of bacterial isolates*

Representative, morphologically distinct colonies recovered from both THB and HUB enumeration plates were repeatedly subcultured on Nutrient Agar using the streak-plate technique until pure cultures were obtained. Pure isolates were maintained on Nutrient Agar slants at 4°C until characterization.

The isolates were characterized based on colonial morphology, cellular morphology, Gram reaction, motility, and biochemical and physiological tests. These included catalase, oxidase, coagulase, indole, methyl red, Voges-Proskauer, citrate utilization, starch hydrolysis, lecithinase production, lipase production, growth in 7% NaCl, and carbohydrate fermentation using glucose, glycerol, lactose, maltose, mannitol, sucrose, and xylose. Identification was based on phenotypic characteristics and standard bacteriological procedures described by Amosu et al. (2018).

#### *Data analysis*

Data obtained from the physicochemical and bacteriological analyses were summarized using descriptive statistics and presented as mean ± standard deviation. Mean physicochemical parameters, total heterotrophic bacterial (THB) populations, and hydrocarbon-utilizing bacterial (HUB) populations were compared between Bundu and Nembe Creeks using an independent-samples *t*-test, with statistical significance set at *P* < 0.05. Statistical analyses were performed using IBM SPSS Statistics, and the results were presented in tables.

## RESULTS

The physicochemical characteristics of Bundu and Nembe Creeks are presented in Table 1. The values represent the mean  $\pm$  standard deviation of five monthly observations per creek ( $n = 5$ ). The mean temperature was comparable between Bundu Creek ( $27.25 \pm 0.96^\circ\text{C}$ ) and Nembe Creek ( $28.00 \pm 0.00^\circ\text{C}$ ), with no significant difference between the two creeks (independent-samples  $t$ -test,  $P = 0.215$ ). Nembe Creek recorded significantly higher mean pH ( $6.84 \pm 0.13$ ), salinity ( $5.58 \pm 0.22\text{‰}$ ), and electrical conductivity ( $4520.00 \pm 358.89 \mu\text{S/cm}$ ) than Bundu Creek, which recorded values of  $6.61 \pm 0.01$ ,  $2.74 \pm 0.03\text{‰}$ , and  $1532.50 \pm 27.54 \mu\text{S/cm}$ , respectively ( $P < 0.05$ ). Conversely, Bundu Creek recorded significantly higher turbidity ( $10.96 \pm 0.14 \text{ NTU}$ ), dissolved oxygen ( $3.58 \pm 0.36 \text{ mg/L}$ ),  $\text{BOD}_5$  ( $6.83 \pm 0.03 \text{ mg/L}$ ), and COD ( $38.13 \pm 0.85 \text{ mg/L}$ ) than Nembe Creek, which recorded  $0.12 \pm 0.00 \text{ NTU}$ ,  $2.03 \pm 0.13 \text{ mg/L}$ ,  $0.15 \pm 0.06 \text{ mg/L}$ , and  $0.18 \pm 0.01 \text{ mg/L}$ , respectively ( $P < 0.05$ ).

The bacterial populations of Bundu and Nembe Creeks

are presented in Table 2. The total heterotrophic bacterial population was higher in Nembe Creek ( $9.52 \times 10^5 \pm 6.30 \times 10^5 \text{ CFU/mL}$ ) than in Bundu Creek ( $4.36 \times 10^4 \pm 3.82 \times 10^3 \text{ CFU/mL}$ ). Similarly, hydrocarbon-utilizing bacteria were more abundant in Nembe Creek ( $2.20 \times 10^4 \pm 1.15 \times 10^3 \text{ CFU/mL}$ ) than in Bundu Creek ( $1.20 \times 10^4 \pm 8.16 \times 10^2 \text{ CFU/mL}$ ).

A total of 12 bacterial taxa were recovered from the two creeks (Table 3). Bundu Creek yielded *Escherichia coli*, *Bacillus* sp., *Salmonella* sp., *Enterobacter* sp., *Pseudomonas* sp., *Shigella* sp., *Vibrio* sp., *Klebsiella* sp., *Staphylococcus* sp., *Proteus* sp., and *Citrobacter* sp., Nembe Creek yielded *Bacillus* sp., *Pseudomonas* sp., *Staphylococcus* sp., *Micrococcus* sp., *Enterobacter* sp., and *Klebsiella* sp. Thus, *Bacillus* sp., *Pseudomonas* sp., *Staphylococcus* sp., *Enterobacter* sp., and *Klebsiella* sp. were common to both creeks, whereas *Escherichia coli*, *Salmonella* sp., *Shigella* sp., *Vibrio* sp., *Proteus* sp., and *Citrobacter* sp. were recovered only from Bundu Creek, while *Micrococcus* sp. was recovered only from Nembe Creek.

**Table 1.** Physicochemical characteristics of water samples from Bundu and Nembe Creeks.

| Parameter                        | Bundu Creek (Mean $\pm$ SD) | Nembe Creek (Mean $\pm$ SD) | Overall Mean $\pm$ SD | P-value |
|----------------------------------|-----------------------------|-----------------------------|-----------------------|---------|
| Temperature ( $^\circ\text{C}$ ) | $27.25 \pm 0.96$            | $28.00 \pm 0.00$            | $27.63 \pm 0.74$      | 0.215   |
| pH                               | $6.61 \pm 0.01$             | $6.84 \pm 0.13$             | $6.73 \pm 0.15$       | 0.035   |
| Salinity (‰)                     | $2.74 \pm 0.03$             | $5.58 \pm 0.22$             | $4.16 \pm 1.52$       | <0.001  |
| EC ( $\mu\text{S/cm}$ )          | $1532.50 \pm 27.54$         | $4520.00 \pm 358.89$        | $3026.25 \pm 1614.18$ | <0.001  |
| Turbidity (NTU)                  | $10.96 \pm 0.14$            | $0.12 \pm 0.00$             | $5.54 \pm 5.79$       | <0.001  |
| DO (mg/L)                        | $3.58 \pm 0.36$             | $2.03 \pm 0.13$             | $2.80 \pm 0.87$       | 0.002   |
| $\text{BOD}_5$ (mg/L)            | $6.83 \pm 0.03$             | $0.15 \pm 0.06$             | $3.49 \pm 3.57$       | <0.001  |
| COD (mg/L)                       | $38.13 \pm 0.85$            | $0.18 \pm 0.01$             | $19.15 \pm 20.29$     | <0.001  |

**Table 2.** Total heterotrophic bacterial and hydrocarbon-utilizing bacterial populations of Bundu and Nembe Creeks.

| Sampling location | THB (CFU/mL)                            | HUB (CFU/mL)                            |
|-------------------|-----------------------------------------|-----------------------------------------|
| Bundu Creek       | $4.36 \times 10^4 \pm 3.82 \times 10^3$ | $1.20 \times 10^4 \pm 8.16 \times 10^2$ |
| Nembe Creek       | $9.52 \times 10^5 \pm 6.30 \times 10^5$ | $2.20 \times 10^4 \pm 1.15 \times 10^3$ |

**Table 3.** Bacterial isolates recovered from Bundu and Nembe Creeks.

| Bacterial isolate         | Bundu Creek | Nembe Creek |
|---------------------------|-------------|-------------|
| <i>Escherichia coli</i>   | ✓           | —           |
| <i>Bacillus</i> sp.       | ✓           | ✓           |
| <i>Salmonella</i> sp.     | ✓           | —           |
| <i>Enterobacter</i> sp.   | ✓           | ✓           |
| <i>Pseudomonas</i> sp.    | ✓           | ✓           |
| <i>Shigella</i> sp.       | ✓           | —           |
| <i>Vibrio</i> sp.         | ✓           | —           |
| <i>Klebsiella</i> sp.     | ✓           | ✓           |
| <i>Staphylococcus</i> sp. | ✓           | ✓           |
| <i>Proteus</i> sp.        | ✓           | —           |
| <i>Citrobacter</i> sp.    | ✓           | —           |
| <i>Micrococcus</i> sp.    | —           | ✓           |

## DISCUSSION

The physicochemical characteristics observed in Bundu and Nembe Creeks indicate marked differences in the environmental conditions of the two aquatic systems. Such differences are expected in surface waters because physicochemical characteristics are influenced by hydrological conditions, tidal influence, surrounding land use, organic inputs, and other environmental factors. Although human activities occur around both creeks, these activities were not directly assessed in the present study and are therefore considered possible influences rather than measured drivers of the observed patterns. Physicochemical parameters remain useful indicators for evaluating the ecological condition of aquatic ecosystems (Patil et al., 2012).

The mean temperature recorded in the two creeks was comparable, with no significant difference between Bundu and Nembe Creeks. The similarity in temperature suggests that both water bodies experienced broadly comparable ambient climatic conditions during the study period. Water temperature influences microbial metabolism, dissolved oxygen availability, chemical reactions, and biological processes in aquatic environments (Patil et al., 2012). The values recorded fall within the range commonly reported for tropical surface waters and are comparable with observations from other Nigerian aquatic systems (Fafioye et al., 2005; Silas et al., 2018).

The significantly higher pH observed in Nembe Creek indicates differences in the acid–base characteristics of the two water bodies, although both remained slightly acidic to near-neutral. Such variation may reflect differences in organic matter decomposition, mineral composition, photosynthetic activity, or other natural environmental processes. Similar spatial variations in pH have been reported in surface waters in Rivers State (Olorode et al., 2015; Ollor et al., 2018). Consequently, the lower pH recorded in Bundu Creek may reflect differences in the materials entering the creek, although the specific sources were not evaluated in this study.

Salinity and electrical conductivity were substantially higher in Nembe Creek, suggesting stronger saline or tidal influence than in Bundu Creek. These parameters are strongly influenced by tidal exchange, freshwater dilution, evaporation, and dissolved ionic content and are recognized as important determinants of microbial distribution in estuarine environments. Similar spatial variability has been reported within the Bonny/New Calabar River Estuary (Onojake et al., 2017) and other water bodies in Rivers State (Ukpaka and Chuku, 2012; Olorode et al., 2015). The findings therefore emphasize the importance of local hydrological conditions when comparing neighbouring creeks.

In contrast, turbidity was markedly higher in Bundu Creek. Elevated turbidity generally reflects increased concentrations of suspended particles, including silt, clay, organic matter, microorganisms, and other particulate materials. The higher turbidity observed in Bundu Creek may indicate greater suspended-solid inputs, sediment disturbance, runoff, or other environmental influences around the creek, although these potential sources were not directly investigated. Previous studies have similarly demonstrated that environmental disturbances can influence turbidity and related water-quality characteristics (Obunwo et al., 2011; Hemant et al., 2012).

Dissolved oxygen was significantly higher in Bundu Creek than in Nembe Creek. Dissolved oxygen is essential for aerobic microbial activity and aquatic life and often reflects the balance between oxygen consumption and replenishment. The lower dissolved oxygen

concentration observed in Nembe Creek may reflect differences in oxygen demand, water movement, or reaeration characteristics rather than a single identifiable cause. Nevertheless, the relatively low dissolved oxygen concentrations recorded in both creeks suggest environmental conditions that warrant continued monitoring (Koshy and Nayar, 1999; Onojake et al., 2017).

BOD<sub>5</sub> differed markedly between the two creeks, with Bundu Creek recording substantially higher values than Nembe Creek. Because BOD<sub>5</sub> reflects the oxygen required for the microbial decomposition of biodegradable organic matter, the higher values observed in Bundu Creek suggest a greater biodegradable organic load during the sampling period. This pattern may be consistent with increased organic inputs from surrounding environmental sources, including runoff or other organic materials, although these sources were not directly measured. Similar relationships between elevated BOD<sub>5</sub> and environmental disturbances have been reported in previous studies (Hemant et al., 2012; Obunwo et al., 2011).

Chemical oxygen demand showed a similar pattern, with Bundu Creek recording substantially higher values than Nembe Creek. The combination of elevated turbidity, BOD<sub>5</sub>, and COD suggests that Bundu Creek contained a greater oxygen-demanding load than Nembe Creek during the sampling period. While this observation may reflect differences in organic and particulate inputs, the present study did not directly identify the contributing sources. Comparable spatial variations in oxygen-demand parameters have been reported in other Niger Delta aquatic environments (Olorode et al., 2015; Onojake et al., 2017; Obunwo et al., 2011).

The bacteriological findings further demonstrated differences in the microbial characteristics of the two creeks. Total heterotrophic bacterial populations were considerably higher in Nembe Creek than in Bundu Creek. Because THB represents the abundance of viable, culturable bacteria capable of utilizing available nutrients, differences between the two creeks may reflect variations in physicochemical conditions, nutrient availability, and other environmental factors rather than any single environmental source. Similar spatial variability in microbial populations has been reported in Niger Delta aquatic environments (Edun et al., 2016; Nwabueze, 2011).

Hydrocarbon-utilizing bacteria were detected in both creeks, with Nembe Creek recording higher HUB populations. Their presence demonstrates that microorganisms capable of utilizing hydrocarbon compounds occur in both aquatic environments and indicates microbial potential for hydrocarbon utilization. However, these findings should be interpreted cautiously because HUB counts alone do not quantify petroleum contamination or confirm greater hydrocarbon pollution.

The higher HUB population in Nembe Creek may reflect favourable environmental conditions for these organisms, long-term microbial adaptation, or the availability of naturally occurring hydrocarbon substrates. Consequently, the HUB results provide evidence of ecological potential for hydrocarbon utilization rather than a direct measure of contamination intensity.

The bacterial isolation results demonstrated greater phenotypically identified bacterial diversity in Bundu Creek than in Nembe Creek. Bundu Creek yielded *Escherichia coli*, *Bacillus* sp., *Salmonella* sp., *Enterobacter* sp., *Pseudomonas* sp., *Shigella* sp., *Vibrio* sp., *Klebsiella* sp., *Staphylococcus* sp., *Proteus* sp., and *Citrobacter* sp., whereas Nembe Creek yielded *Bacillus* sp., *Pseudomonas* sp., *Staphylococcus* sp., *Micrococcus* sp., *Enterobacter* sp., and *Klebsiella* sp. The occurrence of these genera indicates that the two creeks support microbiologically distinct bacterial communities under the environmental conditions observed during the study period.

The detection of *Escherichia coli* in Bundu Creek is noteworthy because the organism is widely recognized as an indicator of faecal contamination (Odonkor and Ampofo, 2013). Its occurrence therefore suggests the possible presence of faecal inputs at the time of sampling. However, its absence from the Nembe Creek isolates should not be interpreted as evidence that faecal contamination was absent, since bacterial recovery depends on sampling conditions, microbial abundance, environmental survival, and the analytical methods employed.

The recovery of *Salmonella* sp., *Shigella* sp., *Vibrio* sp., *Proteus* sp., and *Citrobacter* sp. from Bundu Creek is environmentally relevant because these genera include species that may be associated with enteric or opportunistic infections. However, the present study relied on phenotypic identification; therefore, their detection should be interpreted as evidence of the occurrence of these genera rather than confirmation of specific pathogenic species or disease risk. Their presence indicates environmental bacterial diversity and highlights the value of continued microbiological monitoring, particularly where communities have frequent contact with surface waters (Odonkor and Ampofo, 2013; Pal and Gupta, 2011).

The occurrence of *Enterobacter* sp. and *Klebsiella* sp. in both creeks further demonstrates the presence of bacteria commonly associated with both environmental and intestinal habitats. Because these genera occur naturally in soil, water, vegetation, and animal-associated environments, their detection alone should not be interpreted as confirmation of a specific contamination source. Instead, they contribute to understanding the overall microbiological composition of the two aquatic systems (El-Jakee et al., 2009).

Similarly, the occurrence of *Pseudomonas* sp. and *Bacillus* sp. in both creeks is consistent with their broad

environmental distribution. These genera are well known for their ecological versatility and ability to survive under diverse environmental conditions. The occurrence of *Pseudomonas* sp. alongside hydrocarbon-utilizing bacteria is also noteworthy because some members of the genus possess hydrocarbon-degrading capabilities; however, the present study did not determine whether the recovered isolates possessed this specific functional ability.

Bundu and Nembe Creeks exhibited distinct physicochemical and bacteriological characteristics despite being located within the same broader Niger Delta environment. Bundu Creek was characterized by higher turbidity, dissolved oxygen, BOD<sub>5</sub>, and COD, whereas Nembe Creek had higher pH, salinity, electrical conductivity, and THB and HUB populations. Greater phenotypically identified bacterial diversity was observed in Bundu Creek, including the detection of *E. coli* and other genera commonly associated with environmental or faecal sources. These findings highlight spatial differences between the two creeks and demonstrate that combined physicochemical and bacteriological assessments provide valuable baseline information for environmental monitoring and future investigations of aquatic ecosystems in Rivers State (Olorode et al., 2015; Ollor et al., 2018; Onojake et al., 2017).

## CONCLUSION

Bundu and Nembe Creeks exhibited distinct physicochemical and bacteriological characteristics. Bundu Creek recorded higher turbidity, dissolved oxygen (DO), biochemical oxygen demand (BOD<sub>5</sub>), and chemical oxygen demand (COD), whereas Nembe Creek had higher salinity, electrical conductivity (EC), total heterotrophic bacterial (THB) counts, and hydrocarbon-utilizing bacterial (HUB) counts. The recovery of indicator and potentially pathogenic bacterial taxa, particularly from Bundu Creek, suggests bacteriological contamination and a potential public-health concern. Given these findings, regular monitoring of the physicochemical and bacteriological quality of both creeks, together with appropriate pollution-control and waste-management measures, is recommended to minimize further deterioration and protect the ecological and public-health value of these creek systems.

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