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Microbiological Quality of Surface Water and Sediment from Amadi Creek, Port Harcourt, Rivers State, Nigeria: An Evolving Public Health Risk

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ABSTRACT

The microbiological quality of an environment is one of the elements to its safety usage and ecological integrity. This study assessed the microbiological quality of surface water and sediment from Amadi Creek, Port Harcourt, Rivers State, Nigeria. Surface water and sediment samples were collected monthly for 3 months (June-August, 2023) from three stations (Marine base jetty, Niger Delta Development Commission (NDDC) water front, and Eastern bye-pass bridge) using standard methods. Counts of *Escherichia coli*, Total *Salmonella Shigella*, Total Bacteria, and Total coliform were analysed using standard microbiological methods. The results revealed no spatial variations (ANOVA, $p>0.05$) for microbiological qualities in surface water and sediment. A Comparison of microbiological counts in the matrices, indicated that only total bacteria count was significantly higher in sediment than surface water (student's *t*-test) across the stations. A comparison with standard values showed that microbiological counts in surface water exceeded with several magnitudes compared to the European Union estuary and harbour basin water standard, suggesting high microbial contamination. In conclusion, Amadi creek is highly contaminated with microorganisms which might be influenced by the various anthropogenic activities in the study stations. The elevated microbial counts with values which exceeded with several magnitude the EU estuarine and habour basin water standard indicated the extent of the contamination. Consuming seafood or using water from Amadi Creek without adequate treatment is an evolving public health risk. Hence, there is need for immediate intervention that will safeguard the ecological integrity and safety of the creek.

Keywords: Creek, Anthropogenic Activities, Microbial Contamination, *E. coli*, Total Coliform, Public Health Risk.

Introduction

The microbiological quality of surface water and sediment is one of the determinant factors to its safety usage and ecological integrity (Ajibade *et al.*, 2008). Microorganism contaminants in the water can affect the quality and consequently, the human health directly or indirectly (Marcheggiani and Mancini, 2011; Williams and Madise, 2018). Water is an essential resource that supports life and sustains various ecosystems and all aquatic organisms require water as a support system and as a medium for total well-being (Sikoki and Veen (2004). However, the increasing pressures from urbanization, industrialization, and other practices have led to significant degradation of water quality worldwide(Chebet *et al.*, 2020).

In Nigeria, particularly in Port Harcourt, Rivers State, the situation is even more aggravated by the presence of illegal oil refineries and other activities that contribute to the pollution of surface waters and sediments with toxic chemicals, nutrients and microorganisms (Anaero-Nweke, 2018, Moslen *et al.*, 2018; Williams and Madise, 2018; Onwuala-John and Offodile, 2023; Amachree *et al.*, 2025). This pollution poses serious risks to public health, aquatic life, and the overall environment (Chibuike *et al.*, 2023).

Like many coastal environments within the Niger Delta, surface water and sediment of Amadi Creek serve as an important resource for both the industries and locals. However, several anthropogenic pressures have raised concerns about the creek's water quality and overall ecological health.

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While the water serves as the point of release of contaminants, the sediments act as reservoirs due to their capacity to retain pollutants within the layers of the matrix thus giving rise to suitable habitats for the growth of particular species of microbes, mostly anaerobes (Davies *et al*., 1995; Robles *et al.*, 2000; Desmarais, *et al.*, 2002). Microbiological quality of an environment is a critical indicator of its safety usage and ecological integrity. Microorganisms are essential for nutrient cycling but can also harbour harmful pathogens that affect quality of surface water and sediment (Williams and Madise, 2018; Feng *et al.*, 2023). Estimates suggested that there are up to 10^4 bacterial species per gram sediment, of which at least half (and perhaps as many as 95%) are yet unculturable. Although, it is very difficult to find general indicators that characterize the health of an ecosystem, a rich biodiversity, for example indicates a healthy system, but in some cases, it can also be a symptom of disturbance when high amounts of nutrients in an aquatic ecosystem cause enhancement of microbial growth (Marcheggiani and Mancini, 2011). Pathogenic microorganisms can thrive in polluted environments, leading to diseases and ecological imbalances (Ajibade *et al.,* 2008). Microorganisms are the main sources of fertility and degradation of organic matter and pollutants in sediments. Their complex biochemical diversity enables them to exist in various habitats throughout the planet where they are essential for the geochemical cycle of many elements and the elimination of many pollutants (Marcheggiani and Mancini, 2011). Due to their ubiquitous presence, microorganisms are very important as environmental indicators of contamination and provide an excellent subject for the establishment of quality guidelines (Mancini *et al.*, 2008).

The assessment of microbiological characteristics in both surface water and sediment are therefore crucial for understanding the extent of microbial contamination and its implications for health and environmental sustainability.

Furthermore, communities depending on the creek for seafoods and recreational purposes are at increased risk of exposure to microorganisms' contamination hence, having profound implications on public health. There is paucity of reports in the literature on microbial assessment on Amadi creek.

Previous studies on Amadi creek and surrounding creeks have documented contamination of microorganisms (Williams and Madise, 2018; Kpikpi, 2023). These studies emphasize the importance of continuous monitoring of the microbiological characteristics in the creek. Hence, the present study aimed to evaluate the microbiological characteristics of surface water and sediment from Amadi Creek. By analyzing samples collected at different points along the creek, this research seeks to identify microbial populations present and add to existing literatures data that can inform future monitoring and intervention efforts.

Materials and Methods

Study Area

The study was carried out along Amadi Creek a tidal, brackish water creek in Port Harcourt Local Government Area (PHALGA) of Rivers State. Amadi creek flows from Okrika town down to Mini-Ewa, Rumuobiakani through Woji, Oginigba, Okujagu communities and then empties into the Bonny River, en route to the Atlantic Ocean (Ezeilo and Kingdom, 2012). Amadi Creek is an important resource to the industries and communities around it.

Sampling Stations

Three sampling stations were established within the study area (Figure 1). The stations were chosen based on ecological settings and human activities in the area. The stations are: Station 1 (Marine base Jetty) with latitude 4°46'8"N and longitude 7°1'49"E is an open water area. Activities found within station 1 includes human settlement, waste disposal, boat fabrication, industrial waste discharge, transportation and fishing; Station 2 (NDDC water front) with latitude 4°46'18"N and longitude 7°1'17"E is an area with a dead end (i.e., water movement occurs through a single route). Activities within station 2 includes; human settlement, block industry, boat fabrication and repair, direct sewage and domestic disposal, and fishing activities and; Station 3 (Eastern bypass bridge,) with latitude 4°47'11"N and longitude 7°1'16"E is located beneath the Eastern Bypass Bridge around the Koko-Ama community axis. Activities includes; human settlement, waste disposal, recreational and fishing activities. A Map of the study area and sampling stations is shown in Figure 1.

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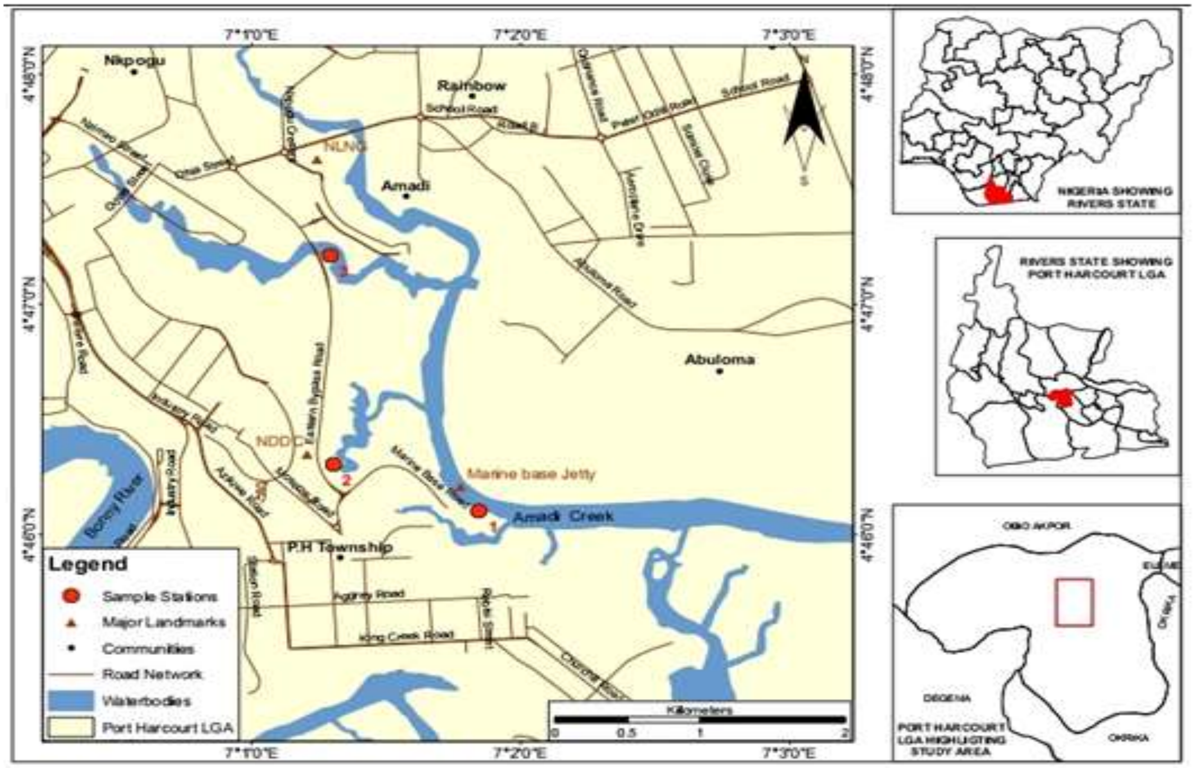

Fig. 1: Map of study area and sampling stations

Sample collection and determination of Microbiological qualities

Water and sediment samples were monitored for microbiological qualities in the three stations from June-August 2023. Samples were collected monthly during ebb tide.

Sample preparation and Isolation of Microorganisms

Surface water and sediment samples were collected in pre-washed and sterilised (95% ethanol) plastic containers. Surface water sample were collected approximately 10 cm below surface water facing upstream flow direction to avoid contamination (Leong *et al*., 2018). Thereafter, samples were placed on ice pack and immediately transported to the microbiology unit in the Department of Food Science and Technology, Rivers State University, Port Harcourt for analysis. To maintain integrity, samples were analysed microbiologically within 24 hours for Total bacteria count (THBC), total coliform count, *Salmonella* and *Shigella* counts and *Escherichia coli* count.

Media preparation and Sterilization

Microbial media were prepared and sterilized according to manufacturer's instruction. Nutrient agar (NA) was employed for total bacterial count; *Salmonella Shigella* Agar (SSA) for *Salmonella and Shigella* count; MacConkey agar (MCA) for total coliform count; and Eosin-methylene blue agar (EMB) for *Escherichia coli* count as well as diluent (peptone water) were sterilized in an autoclave (High Pressure Electric Heating Portable Autoclave, DW-280A 18L Chongqing Drawell Instrument Co., Ltd) for 15 mins at 15psi (121ºC) (Lal and Cheeptham, 2007; Suzan *et al*., 2019).

All glass wares were sterilized by autoclaving; plastics and workspace were sterilized with 95% ethanol. Thereafter materials were removed and placed on a properly disinfected laboratory work bench.

Sterile media were allowed to cool to about 45ºC before aseptically dispensing into the sterile Petri dishes to set (Obinna-Echem and Thomas, 2023).

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Serial dilution, spread plating and enumeration of microorganisms

Microorganisms were detected and enumerated following the procedure as described by Sanders (2012) and Blaize *et al.* (2016). Surface water (1ml) and sediment (1g) samples were aseptically prepared in a 10-fold dilution with sterile peptone water (9 ml) in triplicate design for serial dilution to 10^{10}. Spread plating was done by pipetting aliquots (0.1ml) of the inoculum into sterile Petri dishes containing the different sterile media for each microorganism, spread one directionally with a sterile spender to enable equal distribution within the Petri dish and incubated at 37ºC for 24-48 hours. Thereafter, the total number of the microorganism colony forming units on each plate were enumerated, results calculated and expressed in CFU/ml. Identification and Characterization of microorganisms was based on their observed characteristics on the medium employed for their cultivation and with reference to previous reports.

Statistical Analysis

Statistical analysis was carried out on all data using the Minitab version 16 for Microsoft windows. Data were presented as mean ± standard deviation (SD) and analysed by one-way analysis of variance (ANOVA). Microbiological quality data were transformed into natural log before statistical analysis. The Tukey's post-hoc test at 95% confidence limit to provide specific information on which means are significantly different from each other.

Results

The results for the Identification and Characterization of microorganisms are as described below. Total heterotrophic bacteria: are present when white to creamy colonies were observed on nutrient agar, suggesting the presence of a diverse range of heterotrophic microorganisms capable of growing under standard laboratory conditions. These colonies represent a mixture of potential bacterial species from the sample (Obinna-Echem and Thomas, 2023). *Escherichia coli* was present when dark green colonies were observed on eosin methylene blue agar and fermented lactose producing acidic byproducts that resulted in the characteristic green sheen (Obinna-Echem and Thomas, 2023). Total coliform: was present when pink and white colonies were observed on MacConkey agar. Pink colonies indicated the presence of lactose-fermenting coliforms, while the white colonies were non-lactose fermenters, possibly indicating enteric pathogens or other non-coliform bacteria (Edberg *et al*., 2000). *Salmonella* and *Shigella* sp: was present when black and colourless colonies were observed on *Salmonella* and *Shigella* agar. Colourless colonies with black centers were indicative of *Salmonella* sp, due to hydrogen sulfide (H_2S) gas production but do not ferment lactose. Colourless colonies without black centres were likely *Shigella* sp, as it does not produce H_2S gas nor ferment lactose. Pink colonies were likely *Escherichia coli* spp., which do not produce H_2S but ferment lactose in the medium, leading to acid production and a pink coloration due to the neutral red pH indicator. The white colonies represent other non-Salmonella and non-Shigella enteric bacteria (WHO 2010; Aryal, 2011). The results of the microbiological analysis of surface water and sediment samples collected from Amadi creek are presented in Table 1. It revealed the presence of microbial species (*E. coli*, *Salmonella* and *Shigella*; coliform and heterotrophic bacteria) as identified using selective and differential media.

Table 2 present the results of the monthly variations of the microbiological qualities of the surface water and sediment while the result of the spatial variation in the microbiological qualities of surface water and sediment are presented in Table 3.

Table 1: Morphological Characteristics of Isolated Organisms

Isolated organisms	Morphological characteristics	Media
Total heterotrophic bacteria	Small, round white to creamy colonies	Nutrient agar
E. coli	Greenish to black colonies	Eosin-methylene blue agar
Salmonella spp.	Colourless colonies with black centres	Salmonella Shigella agar
Shigella spp.	Colourless colonies without black centres	Salmonella Shigella agar
Coliform	Smooth pink colonies with shiny texture	MacConkey agar

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Table 2. Monthly Variation of Microbial Counts (load) in the Surface Water and Sediment along Amadi Creek from June-August 2023

A. *Escherichia coli* Count

MATRIX		**Surface water**			**Sediment**	
Month	Mean (CFU/ml)	Mean (log_{10} CFU/ml)	P-value	Mean (CFU/g)	Mean (log_{10} CFU/g)	P-value
June	1.32 x 10^7	5.45 ± 1.68**a**	0.23	3.51 x 10^6	5.90 ± 1.15**a**	0.44
July	2.73 x 10^6	6.32 ± 0.36**a**		1.19 x10^6	5.72 ± 0.71**a**	
August	2.68x 10^5	5.27 ± 0.49**a**		3.90 x 10^5	5.19 ± 1.01**a**	

B. Total *Salmonella* and *Shigella* sp Count

MATRIX		**Surface water**			**Sediment**	
Month	Mean (CFU/ml)	Mean (log_{10} CFU/ml)	P-value	Mean (CFU/g)	Mean (log_{10} CFU/g)	P-value
June	1.00 x 10^4	4.00 ± 0.00**c**	0.00	1.33 x 10^4	4.08 ± 0.19**c**	0.00
July	6.33 x 10^5	5.76 ± 0.20**a**		2.00 x 10^5	5.30 ± 0.00**b**	
August	1.42 x 10^5	4.88 ± 0.58**b**		7.62 x 10^5	5.87 ± 0.11**a**	

C. Total Heterotrophic Bacteria Count

MATRIX		**Surface water**			**Sediment**	
Month	Mean (CFU/ml)	Mean (log_{10} CFU/ml)	P value	Mean (CFU/g)	Mean (log_{10} CFU/g)	P-value
June	7.55 x 10^6	6.74 ± 0.37**a**	0.00	4.50 x 10^8	8.51± 1.42**a**	0.02
July	7.67 x 10^5	5.69± 0.54**b**		1.40 x 10^8	8.12 ± 0.15**ab**	
August	4.08 x 10^7	7.31 ± 0.66**a**		1.02 x 10^7	7.96 ± 0.25**b**	

D. Total Coliform Count

MATRIX		**Surface water**			**Sediment**	
Month	Mean (CFU/ml)	Mean (log_{10} CFU/ml)	P-value	Mean (CFU/g)	Mean (log_{10} CFU/g)	P-value
June	1.57 x 10^7	5.38 ± 1.78**b**	0.02	2.67 x 10^6	6.39 ± 0.21**b**	0.00
July	5.37 x 10^6	6.35± 0.81**ab**		1.32 x 10^6	6.04 ± 0.30**c**	
August	1.89 x 10^8	7.74 ± 0.84**a**		1.72 x 10^8	8.20 ± 0.17**a**	

Data are means (SD) of *n*=6/station. Different letter across columns indicates significant difference at (ANOVA, $p<0.05$) for each matrix

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Table 3: Spatial variation of microbial load in the sediment along Amadi creek from June-August 2023

A. *Escherichia coli* Count

MATRIX	Surface water			Sediment		
Station	Mean (CFU/ml)	Mean (log10 CFU/ml)	P-value	Mean (CFU/g)	Mean (log10 CFU/g)	P-value
Marine base jetty	1.35×10^7	6.26 ±1.08**a**	0.32	2.43×10^6	5.84 ± 0.87**ab**	0.04
NDDC water front	1.82×10^6	5.38 ± 1.13**a**		3.27×10^5	4.83 ± 1.02**b**	
Eastern bye-pass bridge	1.12×10^6	5.42 ± 1.05**a**		2.34×10^6	6.14 ± 0.50**a**	

B. Total *Salmonella* and *Shigella* sp Count

MATRIX	Surface water			Sediment		
Station	Mean (CFU/ml)	Mean (log10 CFU/ml)	P-value	Mean (CFU/g)	Mean (log10 CFU/g)	P-value
Marine base jetty	4.60×10^5	5.40 ± 0.74**a**	0.52	2.92×10^5	4.88 ± 1.02**a**	0.94
NDDC water front	3.28×10^5	4.80 ± 0.98**a**		3.23×10^5	5.06 ±0.86**a**	
Eastern bye-pass bridge	1.78×10^5	4.89 ± 0.73**a**		4.85×10^5	5.11 ± 1.02**a**	

C. Total Heterotrophic Bacteria Count

MATRIX	Surface water			Sediment		
Station	Mean (CFU/ml)	Mean (log10 CFU/ml)	P-value	Mean (CFU/g)	Mean (log10 CFU/g)	P-value
Marine base jetty	1.44×10^7	6.47 ± 1.18**a**	0.68	3.39×10^8	8.22 ± 0.59**a**	0.66
NDDC water front	3.00×10^7	6.84 ± 0.88**a**		2.27×10^8	8.28 ± 0.27**a**	
Eastern bye-pass bridge	4.78×10^6	6.43 ± 0.44**a**		1.27×10^8	8.09 ± 0.13**a**	

D. Total Coliform Count

MATRIX	Surface water			Sediment		
Station	Mean (CFU/ml)	Mean (log10 CFU/ml)	P-value	Mean (CFU/g)	Mean (log10 CFU/g)	P-value
Marine base jetty	2.41×10^7	6.80 ± 1.15**a**	0.84	8.68×10^7	7.07 ± 1.05**a**	0.81
NDDC water front	1.36×10^8	6.39 ± 1.70**a**		4.57×10^7	6.67 ± 1.15**a**	
Eastern bye-pass bridge	4.99×10^7	6.28 ± 1.88**a**		4.32×10^7	6.90 ± 0.96**a**	

Data are means (SD) of *n*=6/station. Different letter across columns indicates significant difference at (ANOVA, $p<0.05$) for each matrix

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Table 2 shows that, for surface water, there was no monthly variation for *E. coli* and total coliform count. However, total *Salmonella* and *Shigella* counts were significantly higher in the order July > August > June while, Total heterotrophic bacteria count decreased in July (7.67×10^5) compared to June (7.55×10^6) and August (4.08×10^7) which were not significantly different from each other. For total coliform count in the surface water, August was higher (1.89×10^8) than June (1.57×10^7), but July (5.37×10^6) was not significantly different from either June or August. Also, for the sediment, there was no monthly variations for *E. coli* ($p=0.44$). However, there was significant monthly variations for total *Salmonella* and *Shigella* count ($p=0.00$), Total heterotrophic bacteria count ($p=0.02$) and total coliform count ($p=0.00$), with *Salmonella* and *Shigella* (7.62×10^5) and total coliform (1.72×10^8) recording highest counts in August while Total heterotrophic bacteria count (4.50×10^8) was highest in June.

The results of the spatial variation in the microbiological qualities of surface water and sediment are presented in Table 3. There were no spatial variations in the surface water for all microbiological quality counts.

Likewise, for the sediment, all microbiological quality counts did not indicate any spatial variation apart from *E. coli*. *Escherichia coli* count was significantly increased in Eastern bye-pass bridge (station 3; 2.34×10^6) compared to NDDC water front (station 2, 3.27×10^5). However, *E. coil* count in Marine base jetty (Station 1; 2.43×10^6) was not significantly different from the other 2 stations.

Table 4 presents the microbiological quality counts recorded in the surface water and sediment in comparison to set standards. The results showed that all counts except Total heterotrophic bacteria count exceeded with several magnitude the standards set by EU estuary and harbour basin water (Table 4).

Microbiological quality in the sediment and surface water for the different stations were compared. There was no statistical difference between the microbiological quality counts in the surface water compared to the sediment except for Total heterotrophic bacterial count (THBC). Total bacterial count was significantly higher in the sediment compared to the surface water across the station (Student, *t*-test, $p<0.05$).

Table 4: Comparative Analysis of the Present Study Range of Microbiological Quality Counts (CFU/ml or CFU/100ml in bracket) of Surface Water with EU Estuary and Harbour Basin Water Standard* (CFU/100 ml)

Microbiological quality	Present study range CFU/ml (CFU/100 ml)	EU Estuary and Harbour Basin Water Standard (CFU/100 ml)	Magnitude of increase compared to EU Estuary and Harbour Basin Water Standard (CFU/100 ml)
E. coli count	1.00×10^4-4.10×10^7 (1.00×10^6-4.10×10^9)	2000 (2.00×10^3)	500-2050000 (5.00×10^2-2.05×10^6) fold
Total *Salmonella* & *Shigella* count	1.00×10^4-7.00×10^5 (1.00×10^6-7.00×10^7)	0	1000000-70000000 (1.00×10^6-7.00×10^7) fold
Total heterotrophic Bacteria count	1.00×10^5-9.70×10^7 (1.00×10^7-9.70×10^9)	-	-
Total coliform Count	1.00×10^4-7.90×10^8 (1.00×10^6-7.90×10^{10})	10000 (1.00×10^4)	100-7900000 (1.00×10^2-7.90×10^6) fold

* Sciortino and Ravikumar (1999).

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Discussion

Microbiological Analysis of Surface Water and sediment from Amadi Creek

Microbiological analysis of surface water and sediment samples from Amadi Creek revealed the presence of key microbial indicators, including *Escherichia coli*, total *Salmonella* and *Shigella* spp., total coliforms, and total heterotrophic bacteria, identified using selective and differential media. The results showed significant temporal but not spatial variations in microbial quality in both the surface water and sediment, with most values exceeding with several magnitude the EU estuary and harbour basin water standard (Sciortino; and Ravikumar, 1999). The observed variations pose potential risks to aquatic life and human health and can be attributed to several anthropogenic activities prevalent in Amadi creek. According to Lackey (2001), ecosystem health and human health are strongly interconnected. Microbiological risks to humans may occur directly or indirectly. Indirect risks include the consumption of contaminated seafoods, crops irrigated with polluted water, as well as exposure during recreational activities or algal bloom events (Tauxe, 1997; UNEP, 1997, 1998). The degree of contamination is often indicated by the presence of microbial communities, which thrive in the presence of specific compounds. For example, faecal bacterial indicators such as *E. coli* and Enterococci thrive well where there is sewage pollution (EU, 2006; Tyagi *et al.*, 2006).

In the present study, the detection of *Escherichia coli*, *Salmonella* spp., *Shigella* spp., coliform, and heterotrophic bacteria in the surface water and sediment, suggested contamination from faecal sources. These microorganisms are indicators of anthropogenic influences, primarily from sewage discharge, agricultural runoff, and industrial effluents, and are known to cause gastrointestinal diseases in humans (Kpikpi, 2023). The presence of total coliforms also confirms the water quality in Amadi creek. High levels of coliform bacteria are often associated with the potential presence of pathogenic microorganism (Abdullahi and Suleiman, 2023). *E. coli* is a reliable indicator of faecal contamination and the potential risk of zoonotic pathogens (Tortorello, 2003; EU 2006; Tyagi *et al.* 2006; Marcheggiani and Mancini, 2011; Saxena *et al*., 2015).

The lack of significant monthly variation in *E. coli* and total coliform counts suggested a continuous and steady source of microbial contamination, likely emanating from persistent sewage discharge. The consistent levels of *E. coli* and total coliforms confirms the ongoing inputs of faecal material into the creek like direct discharges from septic tanks, open defecation and inadequate sewage treatment facilities which consequently led to the proliferation of these pathogens. This finding is in agreement with reports from other rivers with residential areas built near it (Adibe *et al*., 2020; Amadi *et al*., 2020; Kpikpi, 2023). Common practices in such areas include waste dumping, discharge of domestic effluents, open defecation, and direct sewage discharge.

The observed seasonal increase in *Salmonella* and *Shigella* counts in July, compared to June and August, may be attributable to increased rainfall in the region, leading to runoff that introduced these microorganisms from various sources into surface waters. The runoff may carry faecal contaminants and other anthropogenic input from agricultural fields, urban areas, and sewage systems, further elevating the microbial load (Pachepsky and Shelton 2011; Onwuka *et al*., 2023). Such conditions create a conducive environment for the resurgence of these microorganisms. In contrast, fluctuations in heterotrophic bacteria counts, with lower values in July and a peak in August, could be influenced by nutrient availability. These results are consistent with reports by Adibe *et al.* (2020), who reported the highest microbial counts in August, attributing the increase to rainfall patterns in the tropics. According to their study, the first heavy rains wash substantial amounts of faecal matter and market waste accumulated in drainage channels and surrounding land during the dry season into nearby water bodies, leading to a surge in bacterial counts. Also, the present study supports and confirms the widely accepted perception that seasonal variation in faecal contamination is real and significant, with the wet season recording greater contamination (WHO/ UNICEF, 2010; Wu *et al*., 2011).

The absence of significant spatial variation in microbial counts suggests a uniform distribution of contamination sources along the creek, likely due to widespread sewage discharge and surface runoff. This pattern, observed across the study stations, is a common occurrence in many coastal communities.

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Residential houses and businesses are often built along creek banks, where the water body is frequently used as an informal waste disposal site, including the direct release of sewage. As we know, increased population density, intensifies waste generation which consequently exacerbates microbial contamination especially in regions without adequate or no control of waste disposal (Elliot and Colwell, 1985). Sewage discharge introduces various nutrients into aquatic ecosystems, altering microbial community composition and reducing bacterial diversity and richness. When raw sewage contaminates water bodies, pathogenic microorganisms can spread, posing health risks to individuals engaging in activities such as swimming, boating, and fishing (Xie *et al*., 2022).

The microbial counts in Amadi Creek exceeded with several magnitude the EU estuary and harbour basins water standard (Sciortino; and Ravikumar, 1999). This indicated severe microbial pollution that poses risks to aquatic life and human health. High microbial loads can lead to oxygen depletion (Guo *et al.*, 2022) due to increased biological oxygen demand (BOD), impairing fish health and survival (Adibe *et al.*, 2020). Pathogenic bacteria may also infect fish, affecting their growth and reproduction. Consumption of contaminated seafood from Amadi creek poses a significant health risk due to microorganisms bioaccumulation. In general, the creek surface water is unsafe for any intended use without treatment.

Conclusion

This study has shown that Amadi creek is highly contaminated with microorganisms that is influenced by the various anthropogenic activities in the study stations. The values of microbial counts which exceeded with several magnitude the EU estuarine and habour basin water standard indicated the extent of the contamination. Consuming seafood or using water from Amadi Creek without adequate treatment is an evolving public health risk. Hence, there is need for immediate intervention that will safeguard the ecological integrity and safety of the creek.

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