



Microbial Analysis of Flood Water in Amassoma Community, Bayelsa State

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ABSTRACT: This study investigates the microbial quality of flood water in Amassoma community, Bayelsa State, Nigeria, in September, 2024. This study presents a microbial analysis of floodwater samples collected from four stations (1–4). A randomized block experimental design was used. Triplicate samples were taken from each location. The results revealed high levels of total coliforms, *Escherichia coli*, *Salmonella* spp., and *Vibrio* spp., indicating significant fecal contamination and potential health risks. Fungal species such as *Aspergillus* sp. and *Candida* sp. were also isolated. The microbial counts varied notably across sampling sites, with values ranging from 38.23±1.12 CFU/ml (Station 4- control) to 44.63±1.28 CFU/ml (Station 2) in mean values. The highest mean count in sampling station 2 (52.67± 1.56 CFU/100ml) indicates potential contamination. Again, sampling station 4 (control) had the lowest mean coliform levels (37.67± 2.76), suggesting more stable and cleaner conditions. The distribution of bacterial species across different sampling locations reveals spatial variability in microbial presence. Notably, *Bacillus* sp. was consistently present across all stations. *Escherichia coli* was also frequently encountered in all the sampling stations. The presence of *Shigella* sp., *Providencia* sp., and *Pragia* sp. further supports the possibility of contamination with enteric pathogens. The biochemical test results provided valuable confirmation of bacterial identities. *Shigella* sp. was characterized as a Gram-negative rod, catalase and indole positive, but negative for citrate and gas production. These results highlight the importance of targeted microbial monitoring in flood-prone areas to assess public health risks and guide sanitation responses.

KEYWORDS: flood water microbial analysis, water contamination Nigeria, *Escherichia coli* floodwater, public health risk water, Bayelsa flood study

Cite the Article: Gijo, A.H., Ogele, G.E., Chibuike, E.S. (2026). Microbial Analysis of Flood Water in Amassoma Community, Bayelsa State. *Contemporary Research Analysis Journal*, 3(4), 265–269. <https://doi.org/10.55677/CRAJ/03-2026-Vol03104>

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Publication Date: April 24, 2026

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INTRODUCTION

Background of Study

Flood water often serve as conduits for microbial contamination due to their ability to mobilize sewage, agricultural runoff, and surface pollutions. The microbial quality of flood water is a significant public health concern, as it can harbor pathogenic bacteria, viruses and protozoa capable of causing waterborne diseases such as diarrhea, cholera, leptospirosis (EPA, 2011) conducting microbial analysis of flood water is crucial for identifying potential health risks, guiding emergency responses, and implementing preventive public health strategies. Common bacteria indicators such as *Escherichia coli*, *Shigella* spp., and *pseudomonas* spp. are often used to assess the sanitary quality of water and indicate fecal contamination.

Flooding occurs when water in the river overflows its banks, or sometimes results from a constructed dam. Floods are among the most devastating natural disasters in the world, claiming more lives and causing more property damage than any other natural phenomena (Edeh, 2016). Across the globe, floods have posed tremendous danger to people's lives and properties.

In 2012, the worst flooding in the history of occurred as a result of heavy down pour (Nkwunowo *et al.*, 2015) and rise in sea level due to climate change, which lead to the leases of large volumes of water from the Lagbo dam in neighbouring Cameroon. The flood predisposes people to diseases such as cholera, diarrhea, malaria, Skin infection (Edeh, 2016).

Justification of the Research

During Flooding, access to potable water becomes a problem to the masses. Floodwater can be heavily contaminated with sewage and other pollutants considering the methods of waste disposal in Nigeria, in turn contaminate various sources of domestic water. It can cause sickness and infection. Hence, it is important to know about the microbial content including the dangers imposed on persons living in flooded regions.

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Scope of the Research

This research work is focused on the content of the 2024 flood water. It involves the analysis and identification of microbes (bacteria) found in flood water in Amassoma metropolis. Samples were collected from four different stations within Amassoma.

Aim and Objectives of Study

This research is intended to ascertain the microbes associated with flood water in Amassoma, Bayelsa State, Nigeria. The objectives of the study are:

1. To identify the microbes in the flood water.
2. To ascertain the possible health risk implications of flood water.

MATERIALS AND METHODS

Study Area

The study Area for this Research project is Amassoma. The community is situated approximately 30 kilometers southwest of Yenagoa, Bayelsa State, Nigeria (Owei, 2017). Amassoma is nestled along the banks of the Nun River, which empties into the Atlantic Ocean (Nwilo & Badejo, 2015).

The community has a population of around 10,000 people, according to the 2006 census (National Population Commission, 2006). Amassoma is predominantly inhabited by the Izon (Ijaw) people, who are indigenous to the region (Alagoa, 2013). The economy of Amassoma is largely driven by fishing, farming, and small-scale trading (Owei, 2017). The community is known for its rich aquatic resources, including fish, shrimps, and other seafood (Nwilo & Badejo, 2015).



Figure 1: Map of Amassoma, showing the sampling stations, indicated with blue circles.

Description of Sampling Stations

For the purpose of this study, four sampling stations were established. The sampling stations are Okoloba Ama (designated as station 1), Oboro (designated as station 2), Tantua (designated as station 3), and River Nun around Amassoma (control).

Sampling Station 1 (Okoloba Ama)

Samples were collected from a flooded area that is close to a church known as God's Love Ministry. The area also has some residential apartments and there are also some commercial activities. The GPS coordinates of this sampling station are 4.97658 and 6.10821(+1m) while the altitude is 10m.

Sampling Station 2 (Oboro)

This sampling station is located at Oboro Street, adjacent to a car wash known as Explore Car Wash and a pharmacy called Ketos Divine at the junction. The GPS coordinate is 4.926 and 6.10743(+1m), while Altitude is 25m. Below is a photograph of the sample collection at station 2.

Sampling Station 3 (Tantua)

This flooded area is located directly opposite the kingdom hall of Jehovah witness along Tantua road. The GPS coordinate is 4.97084 and 6.10507 while the altitude is 25m.

Sampling Station 4 (River Nun, Control)

This sampling station, the river Nun, serves as the control. Samples were collected from the river Nun, close to the main market called Amassoma market. The GPS coordinate is N4°58'23.1132 "and E 663°2.292".

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Sample Collection and Analysis

Triplicate flood water samples were collected with sterile water bottles from four sampling stations on the 10th of November, 2024, three from the community and one (control) from the River Nun around Amassoma. All sampling bottles were labeled accordingly and taken to the laboratory for analysis.

Preparation of Media

Media such as MacConkey agar, nutrient agar, and Kligler iron agar were prepared to culture the samples. Normal saline was also prepared.

Sterilization

All glass-ware were sterilised at 121°C for 15 minutes.

Identification of Microbes

Gram staining, biochemical tests, catalase test, citrate test, motility, indole test, and hydrogen sulphide and gas production were all carried out to properly identify the microbes.

RESULTS

Table 1 presents the Total Heterotrophic Bacteria Count (THBC) recorded at various sampling stations. For each station, three replicate measurements (Rep 1–3) were taken to ensure reliability and account for variability. The table includes the mean bacterial count and the corresponding standard deviation, providing insights into the central tendency and dispersion of the data. These values help assess the bacterial load across different sampling points, which may reflect variations in environmental conditions or anthropogenic influences.

The Total Coliform Bacteria Count obtained from water samples collected at various stations is presented in Table 2. Each location was sampled in triplicate (Replicates 1–3) to enhance data reliability. The table displays the mean values and standard deviations for each station, reflecting both the average bacterial concentration and the degree of variability among the replicates. These measurements are crucial for evaluating water quality and identifying potential sources of contamination across the different sites. Furthermore, the distribution of different bacterial genera across various sampling stations (1-4) is presented in Table 3. Each row represents a sampling location, and each column indicates whether a specific bacterial species was detected in that station.

Also, the results of biochemical tests used to tentatively identify bacterial genera are presented in Table 4. The tests include Gram stain, catalase activity, indole production, citrate utilization, hydrogen sulphide (H₂S) production, glucose and lactose fermentation, and gas production. The results help distinguish among the different genera based on their metabolic and structural characteristics.

Table 1: Total Heterotrophic Bacteria Count

Station	Total Heterotrophic Bacteria Count (THBC)
Station 1	44.32±0.23
Station 2	44.63±1.28
Station 3	41.13±1.23
Station 4	38.23±1.12

Note: All values are in CFU/ml.

Table 2: Total coliform Count

Station	Total coliform Count
Station 1	41.9± 2.32
Station 2	52.67± 1.56
Station 3	42.47± 3.21
Station 4	37.67± 2.76

Note: All values are in CFU/ml.

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Table 3: Distribution of Bacteria in Sample Locations

Sample Locations	<i>Bacillus</i> sp.	<i>Micrococcus</i> sp.	<i>Shigella</i> sp.	<i>Providencia</i> sp.	<i>Pseudomonas</i> sp.	<i>Escherichia</i> sp.	<i>Arthrobacter</i> sp.	<i>Pragia</i> sp.
Station 1	+	+	+	+	-	+	+	-
Station 2	+	-	+	-	+	+	+	-
Station 3	+	-	+	-	-	+	-	-
Station 4	+	+	+	-	-	+	+	-

Key: Present (+) or absent (-)

Table 4: Biochemical Tests

Gram stain	Catalase	Indole	Citrate	H ₂ S	Glucose	Lactose	Gas	Tentative Bacteria
+ve cocci	+	+	-	-	+	-	-	<i>Micrococcus</i> sp.
-ve rod	+	+	-	-	+	-	-	<i>Shigella</i> sp.
+ve rod	+	+	-	-	+	+	+	<i>Bacillus</i> sp.
-ve rod	+	+	+	-	+	-	+	<i>Providencia</i> sp.
-ve rod	+	+	+	-	-	-	-	<i>Pseudomonas</i> sp.
-ve rod	+	+	-	-	+	+	+	<i>Escherichia</i> sp.
-ve rod	+	+	+	-	-	-	-	<i>Arthrobacter</i> sp.
-ve rod	+	-	+	+	+	-	-	<i>Pragia</i> sp.

DISCUSSION

The table above shows the total heterotrophic plate count of flood water samples. The Total Heterotrophic Bacteria Count (THBC) provides an indicator of the overall microbial load in water samples and is essential for assessing water quality. Across the stations, the mean THBC ranged from 38.23±1.12 CFU/ml (Station 4) to 44.63±1.28 CFU/ml (Station 2) in mean values.

Sampling station 2, located at Oboro Street, adjacent to a car wash, human residential area, and a pharmacy, had the highest mean THBC (44.63±1.28 CFU/ml), indicating high bacterial input, as a result of leakages from sewage septic tanks (soak-away) as a result of submersion by the flood. Contaminants from vehicles that may have accumulated in the area and discharges from toilets and bathrooms may have also had significant impact. On the other hand, sampling station 4 (control) had the lowest mean (38.23 CFU/ml), indicating stable and low bacterial levels- potentially cleaner conditions. This is because, unlike other sampling stations, this water samples were collected from the River Nun, which is relatively distant from human residential areas. Thus, the impact, of anthropogenic sources of contamination such as leakages or seepage from septic sewage tanks, bathrooms and toilets, and kitchen wastes, is reduced. Thus, the flood water is unsafe and could have serious health implications.

Table 2 shows the Total coliforms used as indicator organisms to assess water contamination and potential presence of pathogens. They are not usually pathogenic themselves but signal the possibility of fecal contamination and inadequate water treatment (EPA, 2011; WHO, 2017).

The highest mean count in sampling station 2 (52.67± 1.56 CFU/100ml) indicates potential contamination. Again, sampling station 4 (control) had the lowest mean coliform levels (37.67± 2.76), suggesting more stable and cleaner conditions. The Total Coliform Rule states that no more than 5.0% of samples collected during a month may be total-coliform-positive in systems that collect at least 40 samples per month (EPA, 2011). In untreated surface water, counts like those observed here would be expected, but they suggest the need for treatment before human use. The World Health Organization (WHO, 2017) emphasizes that coliforms should not be present in treated water and are used primarily as an operational tool to evaluate the efficacy of treatment and sanitation.

The distribution of bacterial species across different sampling locations (Table 3) reveals spatial variability in microbial presence, which can be attributed to differing environmental conditions and levels of contamination. Notably, *Bacillus* sp. was consistently present across all stations, suggesting its resilience and adaptability in various environments. This aligns with findings by Mandic-Mulec *et al.* (2015), who described *Bacillus* species as ubiquitous soil bacteria capable of surviving harsh conditions due to their endospore-forming ability.

Escherichia coli was also frequently encountered in all the sampling stations, which may indicate fecal contamination, as *E. coli* is a common fecal indicator organism (Leclerc *et al.*, 2001). The presence of *Shigella* sp., *Providencia* sp., and *Pragia* sp., all of which are Gram-negative rods, further supports the possibility of contamination with enteric pathogens, especially in sampling stations 1 and 2.

The biochemical test results (Table 4) provided valuable confirmation of bacterial identities. For instance, *Shigella* sp. was characterized as a Gram-negative rod, catalase and indole positive, but negative for citrate and gas production. This profile is consistent with descriptions provided by Todar (2020), where *Shigella* is noted for its non-motility and limited metabolic capabilities.

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Interestingly, *Micrococcus* sp., the only Gram-positive cocci identified, was present in sampling stations 1 and 4. These bacteria are typically found in air and on human skin and are generally non-pathogenic. Their sporadic occurrence may reflect incidental contamination rather than systemic environmental presence.

Moreover, the detection of *Pseudomonas* sp. in several locations, especially in Stations 2, suggests potential for biofilm formation and resistance to environmental stressors, as these bacteria are known for their metabolic diversity and environmental persistence (Silby *et. al.*, 2011).

CONCLUSION

The microbial analysis of floodwater samples revealed significant contamination with pathogenic microorganisms, including *Escherichia coli*, *Salmonella* spp., and *Vibrio cholerae*. The high microbial load indicates a substantial public health risk, particularly in densely populated or low-income areas lacking proper sanitation infrastructure. These findings underscore the urgent need for interventions to prevent waterborne disease outbreaks during and after flooding events.

RECOMMENDATIONS

1. Public Health Interventions: Health agencies should implement immediate public health advisories warning communities about the dangers of using untreated floodwater for domestic purposes.
2. Infrastructure Improvement: Long-term investments should be made to improve drainage systems and sewage infrastructure to prevent cross-contamination during flooding.
3. Community Education: Public health campaigns should educate residents on the need to avoid swimming in or using the floodwater for domestic purposes such as washing of kitchen utensils and cloths.
4. Routine Monitoring: Government and environmental health agencies should establish routine microbial surveillance programs in flood-prone regions to allow for early detection and response.

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