

Full Length Research Paper

Assessment of the physicochemical qualities and microbiological profile of Idah River, Kogi State, Nigeria

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Received 11 May, 2021; Accepted 30 June, 2021

Analysis of water bodies, such as rivers and lakes can provide an insight into their intrinsic composition and potential impact on the environment. Water samples collected from four designated sites in Idah River, were assessed for their physicochemical parameters and microbial diversity using standard procedures. The temperature from all sites was 26.00°C and the pH ranged from 6.93 to 7.08. Turbidity values ranged between 32.00 and 38.00 NTU, while dissolved oxygen ranged between 6.28 and 9.28 ppm. Heavy metals, such as Selenium and Arsenic (with peak values of 0.10 and 0.09 ppm, respectively) were detected in the river. However, dissolved oxygen, arsenic and turbidity values across all sites exceeded the maximum limit set by World Health Organisation and the Standard Organisation of Nigeria. The total heterotrophic bacterial counts showed excessive bacterial load from all sample sites, while pathogenic bacteria, including *Escherichia coli*, *Klebsiella* and *Shigella* species, were isolated from regions with intense anthropogenic activities along the river, indicative of microbial pollution. Fungal studies identified the presence of *Fusarium*, *Aspergillus* and *Trichoderma* species as the most abundant in the river. Obtained results showed that Idah River is exposed to heavy metal seepage and subject to microbial contamination. Therefore, continuous monitoring and better management of the river body is recommended to prevent disease outbreak.

Key words: Aquatic ecosystems, Idah River, microbial diversity, physicochemical analysis.

INTRODUCTION

Water can be sourced from water bodies such as rivers, boreholes, lakes, springs and other large water bodies.

However, the quality of water bodies can be adversely affected by man-made activities. For example, pollution

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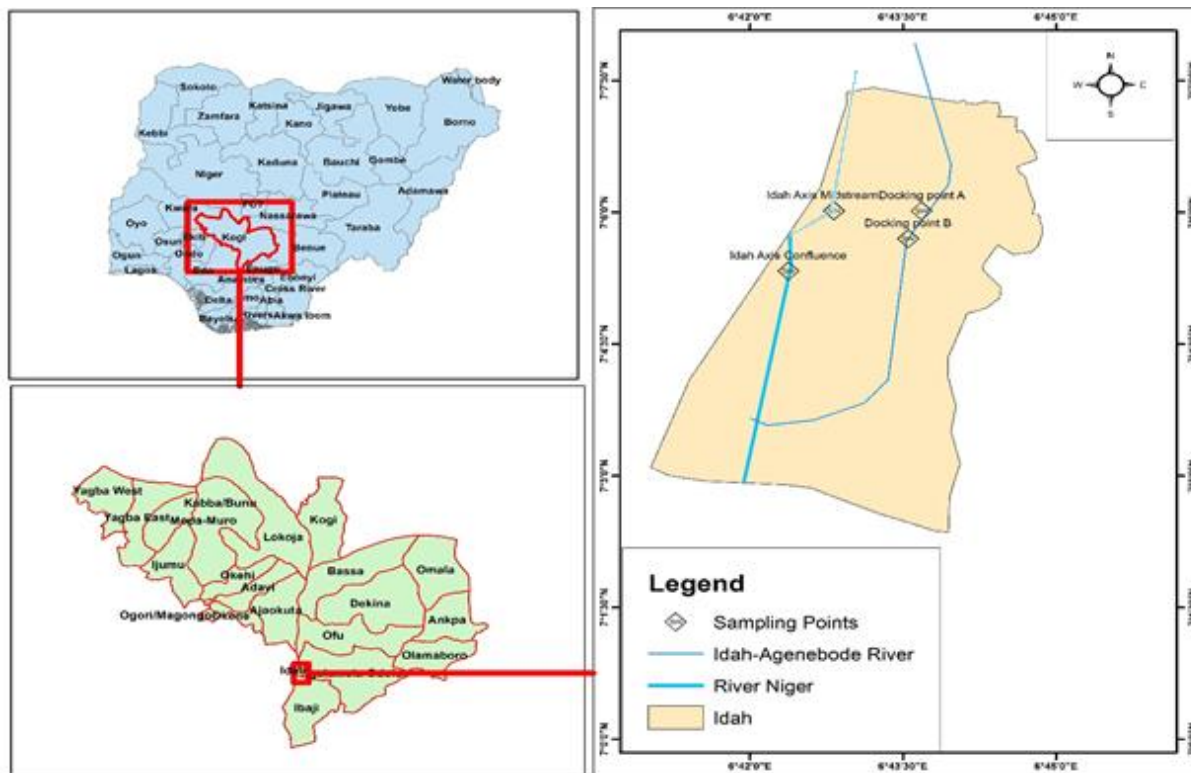


Figure 1. Map of the study area within Nigeria and its sampling points.

of freshwater bodies such as rivers (e.g. Idah River, Kogi State), streams, lakes and ponds are mostly experienced due to industrial discharge, municipal waste disposal and surface run-off (Akaniwor et al., 2007). Anthropogenic activities, such as discharges of domestic waste, untreated waste from sewage treatment plants, plastic materials, disposal of personal care products and household chemicals, improper disposal of car batteries, construction activities, mining activities, and pilgrim activities constantly deteriorate the water quality of rivers (Environmental Pollution Centers, 2018). Such deterioration in water bodies include an alteration in pH, increased turbidity, higher content of total dissolved solids and metals, as well as a higher risk of such water body hosting water-borne pathogens (Shaji et al., 2009; Ananthkrishnan et al., 2012). Water-borne pathogens pose a great health risk to humans, animals and plants, most especially, infants, young children under the age of five and immunocompromised individuals (EPA, 2016; WHO, 2014).

River Niger, at Idah, is an extension of the two major Nigerian rivers; River Niger- after which the country Nigeria is named, and River Benue, after their confluence in Lokoja. The Idah River is located between latitude $7^{\circ}6'1''N$ and longitude $6^{\circ}42'23''E$ (Figure 1) and it serves as a boundary between Kogi and Edo states. The temperature of the water ranges between 22 and $31^{\circ}C$

(which greatly depends on the season). It is relatively turbid and has a slightly alkaline pH between 7.5 and 7.8 (depending on the sampling location). The highest water levels are usually recorded between August and September, while the lowest water level is usually recorded between March and April (Adeyemi, 2010).

Although, microbial communities represent a fundamental part of aquatic ecosystems, and are of great importance for matter and energy flux (Kavka et al., 1996), little is known about the microbial biodiversity of River Niger (Idah Axis), despite its popularity in Nigeria and beyond. Local communities at the different axis of River Niger bank exploit the water for the fishery, aquatic medicinal plants, and domestic purposes, such as cooking, drinking, bathing, washing utensils and clothes, while the water is exposed to both human and animal waste, discharge of untreated industrial and domestic wastewater, runoff and dead organic plants and animals. Studying the unique diversity and functions of microbes in their ecological niche, as well as establishing the factors that affect them would aid in unraveling the role they play in animal, human, plant health, and in their environment (Marchesi, 2017).

This study is therefore aimed at evaluating the total microbial content of water at different points of River Niger at Idah axis, using a conventional approach. In addition, the study seeks to link the community present to

the physicochemical factors that characterize the river, in a bid to proffer necessary recommendations to avert infectious disease outbreaks.

MATERIALS AND METHODS

Study site

Idah is a town in Kogi State, in the middle belt region of Nigeria and situated on the east bank of Niger River. It has a land mass of 36 km² and located on latitude 7°06'48.42"N and longitude 6°44'19.18" E. Its human population was around 79,815 as at 2006 (National Population Commission, 2006). It has a tropical savannah climate with a wet season between late March and early November, and dry season between early November and late March. Idah River is exposed to water pollutants, such as chemical waste from farming activities, as well as discharge from gullies and streams, including the Inachalo River. The locals consume the water for domestic and dry farming activities. During rainy season, run-off washes domestic and municipal sewage, abattoir effluents and remnants of open defecation of both human and animals into the river.

Sample collection

Towards the end of the dry season in February 2020, a total of 20 water samples were aseptically collected in replicates from 4 selected sites in the river (designated Docking Point A, Docking Point B and the Idah Axis - Midstream and Confluence Area); all characterized by different levels of anthropogenic activities (Figure 1). Samples for bacteriological, mycological and physicochemical analyses were collected, at a depth of 20 cm below the water surface and against the water current into 250 mL sterile clean bottles (Ademorati, 1996). The temperature and water pH were monitored *in situ* using a mercury glass thermometer and a pH meter (ROHS Model), respectively before sampling (APHA, 2005). Collected samples were preserved in an icebox and transported immediately to the laboratory for microbiological and physicochemical analyses.

Physicochemical examination of water samples

Water samples placed on icepacks were transported to Soil Microbiology Laboratory at the International Institute of Tropical Agriculture, Ibadan, Oyo State, Nigeria within 24 to 48 h, for physicochemical analysis. In addition to pH and temperature (recorded *in situ*), a total of eighteen physicochemical parameters were evaluated. These included dissolved oxygen, specific ions (calcium, magnesium, potassium, sodium, iron, copper, nickel, arsenic, and selenium), turbidity, nitrates, sulphates, total dissolved solids, total nitrogen and electrical conductivity using titrimetric, colorimetric or spectrophotometric assays (Feng et al., 2009; Ologbosere et al., 2016; Adedire et al., 2021).

Isolation and identification of bacteria

Using aseptic techniques, four-fold serial dilution of each water sample was made, and isolation of bacteria from a serially diluted sample (1 mL) was done in Petri dish through the pour plate method on Nutrient Agar, prepared according to manufacturer's specification. The plates were incubated at 37°C for 24 h. The mean total viable count of the isolated bacterial colonies was enumerated and recorded. Colonies with distinct morphological differences were randomly picked from the nutrient agar plates and

repeatedly streaked on fresh, sterile agar plates (Nutrient Agar (Lifesave Biotech, USA), MacConkey Agar (Lifesave Biotech, USA), Eosin Methylene Blue Agar (Lifesave Biotech, USA), Salmonella-Shigella Agar (Lifesave Biotech, USA), and Centrimide Agar (Oxoid, UK) and subsequently incubated at 37°C for 24 h. Pure cultures were stored in the refrigerator at 4°C for further characterization and analysis. Pure cultures of isolates were characterized and identified using their macroscopic and microscopic characteristics, as well as biochemical tests (Catalase, Oxidase, Centrimide, Citrate Utilization, Methyl Red, Voges Proskauer, Urease, Gelatin Hydrolysis, Motility, Sugar Fermentation: Glucose, Lactose, Maltose, Sorbitol) as described by Cheesebrough (2000) and following the Bergey's Manual of Determinative Bacteriology (Genhardt et al., 1994).

Isolation and identification of fungi

Fungi were isolated through serial dilution (10⁻² and 10⁻⁴) method using sterile distilled water. One milliliter of each dilution was aseptically transferred into Potato Dextrose Agar (Lifesave Biotech, USA) media plates supplemented with Streptomycin (0.03 g/L) to inhibit bacterial growth (Hageskal et al., 2006). The plates were incubated at room temperature (25 ± 3.00°C) for 5 to 7 days. Using a flamed inoculating needle, the edge of each growing colony was picked and slides of the different colonies were made. A drop of Lactophenol cotton blue stain was added to the prepared slides, covered with a coverslip before microscopic examination using 10x and 40x magnifications to observe the microscopic features (hyphal characteristics, shape of sporangia, conidia and spores) of each isolate. Fungal colonies were also identified using cultural (macroscopic) characteristics (colony texture, elevation, chromogenesis/pigmentation, opacity and size) (Watanabe, 2002).

Statistical analysis

Data from physicochemical determinations and bacteriological plate counts were analyzed using Duncan's Multiple Range Test using SPSS (version 25.0). Mean occurrences of bacterial and fungal isolates were tested using Tukey Pairwise comparison of grouping at a 5% level of probability using SPSS (version 25.0).

RESULTS

Physicochemical characteristics of water samples from different sites of Idah River

The results of the physicochemical analyses of water samples collected from four different sites in Idah River are shown in Table 1. The observed water quality of the river was compared to acceptable standards reported by the World Health Organization (WHO, 2011) and Standard Organization of Nigeria (SON, 2007). The pH of water samples taken from different sampling points within Idah River was significantly different. However, the pH of Docking point A (DPA) and Idah Axis Confluence (IAC) water samples, as well as Docking point B (DPB) and Idah Axis Midstream (IAM) water samples, respectively were not significantly different. The pH ranges obtained also showed that IAM had the highest mean pH value of 7.08, which was quite similar to that obtained at Docking Point B (7.07). The lowest pH recorded was at the IAC

Table 1. Physicochemical quality of Idah River samples.

Parameter	Sample sites				Significance	WHO Limits (2011)	SON limits (2007)
	DPA	DPB	IAM	IAC			
pH	6.95 ^b	7.07 ^a	7.08 ^a	6.93 ^b	*	6.50 - 8.50	6.50 - 8.50
Temperature (°C)	26.00	26.00	26.00	26.00	NS	-	22.00 - 32.00
Ca (ppm)	5.98 ^c	6.93 ^a	7.01 ^a	6.37 ^b	*	200.00	-
Mg (ppm)	1.83 ^c	2.02 ^{bc}	2.30 ^a	2.12 ^{ab}	*	200.00	0.20
K (ppm)	2.96 ^{ba}	3.08 ^a	3.05 ^{ab}	2.89 ^c	*	30.00	-
Na (ppm)	3.98 ^b	4.24 ^a	4.12 ^{ab}	4.23 ^{ab}	*	200.00	200.00
Fe (ppm)	0.49 ^b	0.60 ^{ab}	0.56 ^b	0.78 ^a	*	0.50 - 50.00	0.30
Cu (ppm)	0.34 ^b	0.34 ^b	0.36 ^a	0.34 ^b	*	2.00	1.00
Ni (ppm)	0.01	0.01	0.01	0.01	NS	0.07	0.02
As (ppm)	0.04 ^b	0.04 ^b	0.09 ^a	0.04 ^b	*	0.01	0.01
Se (ppm)	0.05 ^b	0.06 ^b	0.10 ^a	0.05 ^b	*	0.04	-
Turbidity (NTU)	33.10	33.10	32.43	37.67	NS	5.00	5.00
NO ₃ (ppm)	3.73 ^a	3.20 ^b	1.22 ^c	1.19 ^c	*	<50.00	50.00
DO (ppm)	9.28 ^a	9.28 ^a	6.67 ^b	6.28 ^b	*	<5.00	3.00 - 5.00
SO ₄ (ppm)	1.89 ^a	1.84 ^a	0.60 ^c	0.84 ^b	*	250.00	100.00
TDS (ppm)	0.01 ^a	0.00 ^b	0.00 ^b	0.00 ^b	*	600.00	500.00
Total N (%)	0.00	0.00	0.00	0.00	NS	-	-
Electrical conductivity (S/m)	70.67 ^c	78.00 ^b	80.00 ^a	80.00 ^a	*	<1000.00	1000.00

DPA - Docking Point A, DPB – Docking Point B, IAM – Idah Axis Midstream, IAC – Idah Axis Confluence, Ca – Calcium, Mg – Magnesium, K – Potassium, Na – Sodium, Fe – Iron, Cu – Copper, Ni – Nickel, As – Arsenic, Se – Selenium, NO₃ – Nitrates, DO – Dissolved Oxygen, SO₄ – Sulphates, TDS – Total Dissolved Solids. Mean values with similar letter(s) across rows are not significantly different at 5% level of significance by Duncan's Multiple Range Test (DMRT). NS: Not significant; *: Significant.

site (6.93) ($p < 0.05$).

The recorded temperature was uniform across all sampled sites at 26.00°C. The mean values of calcium (7.01 ppm), magnesium (2.30 ppm), copper (0.36 ppm), arsenic (0.09 ppm) and selenium (0.10 ppm) were all found to be the highest in IAM. DPA had the lowest mean values for calcium (5.98 ppm), magnesium (1.83 ppm), sodium (3.98 ppm) and iron (0.49 ppm). The mean values of nickel, at 0.01 ppm, were uniform across all sampled sites. The highest potassium (3.08 ppm) and sodium (4.24 ppm) were recorded at DPB, and they were significantly higher than values recorded from other locations. Copper had a uniform value (0.34 ppm) at three sites: DPA, DPB and IAC areas. Turbidity mean values ranged from 33.10 NTU (at DPA and DPB) to 37.67 NTU (at IAC) and the values were not significantly different from one another. Nitrates, dissolved oxygen and sulphates were all found to be the highest in DPA with mean values of 3.73, 9.28 and 1.89 ppm, respectively.

Bacteria distribution and frequency

The total heterotrophic bacteria counts (THBC) of bacteria are seen in the four sites shown in Table 1. The highest microbial load was recorded at both DPA and

DPB with mean values of 1.55×10^4 and 2.52×10^4 CFU/mL, respectively. The lowest microbial load was recorded at IAM with a mean population of 1.27×10^2 CFU/mL. Ten genera of bacteria were identified from a total of 97 isolates. These genera included *Acinetobacter* species, *Staphylococcus* species, *Bacillus* species, *Pseudomonas* species, *Escherichia coli*, *Klebsiella* species, *Bacillus subtilis*, *Aeromonas hydrophilia*, *Shigella* species and *Streptococci* species. Out of these ten species, *Acinetobacter* spp. had the highest percentage frequency of occurrence (50.52%), followed by *Staphylococcus* (18.56%) and *Bacillus* spp. (10.31%) (Figure 2). Across all sampled sites, *Acinetobacter*, *Staphylococcus* and *Bacillus* spp. were the most predominant. The least dominant microbes from each sample site were *B. subtilis* (in DPA and IAM), *A. hydrophilia* (in DPB and IAM), *Shigella* spp. (DPB and IAC) and lastly, *Streptococcus* spp. (in IAM only). Cumulatively, *Acinetobacter* spp. had a mean microbial prevalence of 12.25 and was the most predominant bacteria ($P < 0.05$), while *Streptococcus* spp. was the least with a cumulative mean value of 0.25. Also, the two docking points A and B had the highest number of bacterial isolates with 30.00 and 39.00, respectively, while the least number of bacterial isolate (10) was observed at the Idah midstream area (Table 2). Concerning the total viable THBC observed in water

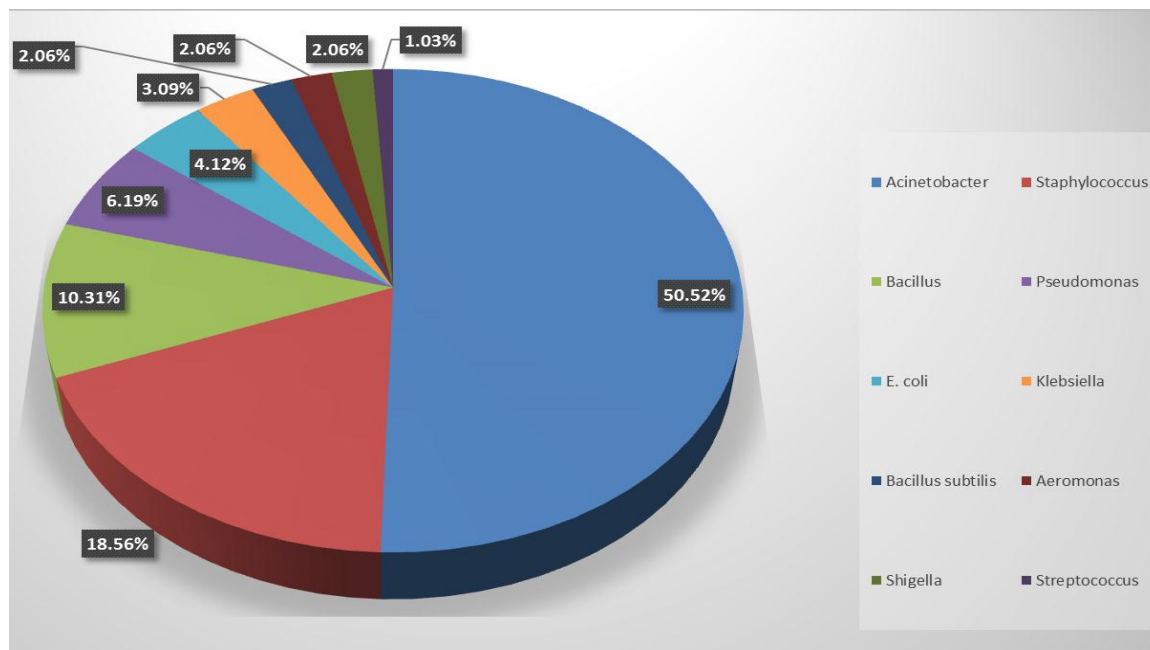


Figure 2. Percentage frequency of total bacteria isolates found in sites of study at Idah River.

Table 2. Number and types of bacteria species isolated from different sites in Idah River.

Genus or species	Docking point A	Docking point B	Idah Axis Midstream	Idah axis confluence	Mean values (Tukey's test)
<i>Acinetobacter</i> spp.	12.00	24.00	5.00	8.00	12.25 ^a
<i>Staphylococcus aureus</i>	5.00	9.00	2.00	2.00	4.50 ^{ab}
<i>Bacillus</i> spp.	4.00	2.00	0.00	4.00	2.50 ^b
<i>Pseudomonas aeruginosa</i>	5.00	0.00	0.00	1.00	1.50 ^b
<i>Escherichia coli</i>	2.00	1.00	0.00	1.00	1.00 ^b
<i>Klebsiella</i> sp.	1.00	1.00	0.00	1.00	0.75 ^b
<i>Bacillus subtilis</i>	1.00	0.00	1.00	0.00	0.50 ^b
<i>Aeromonas hydrophilia</i>	0.00	1.00	1.00	0.00	0.50 ^b
<i>Shigella</i> spp.	0.00	1.00	0.00	1.00	0.50 ^b
<i>Streptococcus</i> spp.	0.00	0.00	1.00	0.00	0.25 ^b
THBC (CFU/mL)	1.55×10^4	2.52×10^4	1.27×10^2	4.50×10^3	11.33×10^{4ab}
Total	30.00	39.00	10.00	18.00	-

Means values (across the row) with same letters are not significantly different ($P < 0.05$) using Tukey's test at 95% confidence interval. THBC: Total Heterotrophic Bacteria Count.

samples collected from the four sample sites, bacteria colonies ranged from 1.27×10^2 CFU/mL (IAM) to 2.52×10^4 CFU/mL (DPB).

Fungi distribution and frequency

Seven fungal genera were identified from a total of 23 fungal isolates. These included *Aspergillus flavus*, *Aspergillus niger*, *Penicillium* species, *Fusarium* species,

Cladosporium species, *Trichoderma* species and *Curvularia* species. Table 3 shows their distinct morphological differences and microscopic characteristics with 2 of the fungi species belonging to *Aspergillus* genus. *Fusarium* spp. had the highest percentage occurrence (39.13%), followed by *Trichoderma* spp., *A. flavus* and *Penicillium* spp. (all at 13.04%) (Figure 3). *Fusarium* spp. had the highest microbial incidence across all sites with a mean value of 2.25 ($P < 0.05$), and the least occurring isolate being *Curvularia* spp. with a cumulative

Table 3. Fungi isolates and their probable identification.

Isolate	Morphological observations						Microscopic characteristics	Probable fungal identity
	Form	Elevation	Surface	Opacity	Chromogenesis	Size		
1	Irregular	Flat	Glistening	Opaque	White edge, yellowish green in the center	Large	Septate hyphae with long and erect conidiophores	<i>Aspergillus flavus</i>
2	Irregular	Raised	Rough	Opaque	Initially white, then changes to dark brown/black	Covers entire surface	Long smooth conidiophores with very rough conidia	<i>Aspergillus niger</i>
3	Irregular	Flat	Rough	Opaque	Green and black edge with a velvety look	Large	Broom-like conidiophores with septate hyphae	<i>Penicillium</i> spp.
4	Circular	Flat	Smooth	Opaque	White cottony look	Medium	Hyaline and abundant microconidia with one or two septa, short conidiophores	<i>Fusarium</i> spp.
5	Irregular	Umbrate	Smooth	Opaque	Suede-like and black	Medium	Erect conidiophores, conidia in branched chains	<i>Cladosporium</i> spp.
6	Circular	Raised	Rough	Translucent	Yellowish green and white in the center	Medium	Repeatedly branched conidiophores with clusters of bent phialides	<i>Trichoderma</i> spp.
7	Irregular	Flat	Rough	Opaque	Black, spiky and fluffy	Medium	Curved conidia	<i>Curvularia</i> spp.

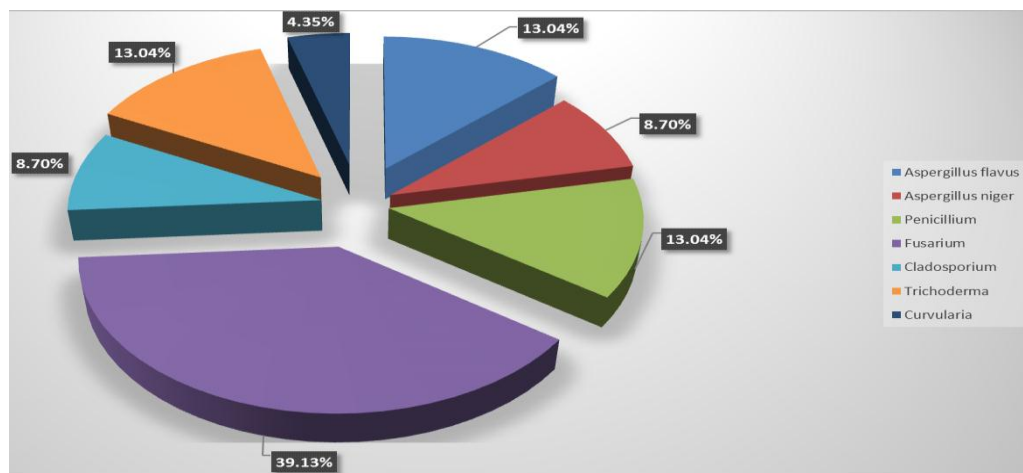


Figure 3. Percentage frequency of total fungi isolates found in sites of study at Idah River.

mean of 0.25. Also, DPA had the highest number of fungi isolates (9.00), followed by DPB (7.00) while the IAM area had the lowest number of fungi isolates 2 (Table 4).

DISCUSSION

From the analysis of the physicochemical features of water samples, recorded pH values were within

a narrow range of 6.93 to 7.08. This fell within the acceptable range according to the standards set by WHO (2011) and SON (2007), thus making it suitable for aquatic life. This observation was in

Table 4. Number and types of fungi species isolated from different sites in Idah River.

Genus or Species	Docking point A	Docking point B	Idah Axis Midstream	Idah Axis Confluence	Mean values (Tukey's test)
<i>Aspergillus flavus</i>	2.00	0.00	1.00	0.00	0.75 ^{ab}
<i>Aspergillus niger</i>	1.00	0.00	0.00	1.00	0.50 ^{ab}
<i>Penicillium</i> spp.	1.00	2.00	0.00	0.00	0.75 ^{ab}
<i>Fusarium</i> spp.	2.00	2.00	1.00	4.00	2.25 ^a
<i>Cladosporium</i> spp.	1.00	1.00	0.00	0.00	0.50 ^{ab}
<i>Trichoderma</i> spp.	2.00	1.00	0.00	0.00	0.75 ^{ab}
<i>Curvularia</i> spp.	0.00	1.00	0.00	0.00	0.25 ^b
Total	9.00	7.00	2.00	5.00	-

Mean values (across the row) with same letters are not significantly different ($P < 0.05$) using Tukey's test at 95% confidence interval

agreement with the findings of Adesakin et al. (2020) who reported a similar pH range for domestic water sources in Zaria, Nigeria. The pH values observed in this study could be attributed to the major soil type in the area or the buildup of organic materials from runoff, as described by Taiwo et al. (2020).

The pH in water bodies is among the major physiological factors that play a critical role in shaping microbial structures and other biological activities in water (Adesakin et al., 2020). There appears to be a correlation between the microbial population observed across all sample sites and the pH of Idah River. All isolated microbes were neutrophilic in nature and this may be related to the near-neutral pH of the river body, encouraging the proliferation and prevalence of neutrophils.

The temperature of any water body determines the proliferation and survival rate of microorganisms (Bouzid, 2016). In this study, the temperature value of 26.00°C in water samples could be regarded as optimal for the growth of heterotrophic mesophilic bacteria and fungi. However, this was within the standard permissible temperature limit of SON (2007) set for aquatic water life. Igbinosa et al. (2012) also observed a similar temperature range of 26 to 27.2°C in Shanomi creek, in the Niger Delta region. In addition, Nwoko et al. (2015) in their report on the assessment of seasonal physicochemical parameters of Oguta Lake in Nigeria, observed a similar temperature range.

The calcium (Ca) levels in water samples collected from different points along the river, was significantly different from each other and ranged from 5.98 ppm (DPA) to 7.01 ppm (IAM); however, these levels were below the permissible limit (200.00 mg/L) recommended by WHO (2011). As such, there might be no detrimental effect on aquatic life and on humans who ingest foods harvested from the river. Magnesium is generally associated with calcium in water bodies and with a concentration usually lower than that of calcium (Venkatasubramani and Meenambal, 2007). Magnesium values observed in this study support this statement as

they ranged from 1.83 ppm (DPA) to 2.30 ppm (IAM).

The potassium and sodium values ranged from 2.89 ppm (IAC) to 3.08 ppm (DPB) and 3.96 ppm (DPA) to 4.23 ppm (IAC), respectively. Many water bodies have sodium concentrations well below 50.00 mg/L (Ikhuorah et al., 2016). Copper levels ranged narrowly from 0.34 to 0.36 ppm and they were notably lower than what Kuz'mina and Ushakova (2007) reported in their metal assessment of fishponds (10.6 ppm). The heavy metal, Nickel is known to be associated with gastrointestinal irritation without inherent toxicity (Hammer and Hammer, 2003). In this study, Nickel value was recorded as 0.01 ppm across the four different samples, which was within the acceptable limit in WHO (2011) recommendations, hence, the river appeared devoid of the heavy metal. These values were contrary to the much higher values reported by Okereke (2014), who assessed the physicochemical properties of the Ihuku River (0.07 - 0.082 mg/L).

Arsenic is a metalloid widely distributed in the earth and usually found in natural groundwater (Thi et al., 2009) but its concentrations vary based on the geological formations, weathering processes of rocks, microbial activities, leaching or other anthropogenic activities such as mining and application of pesticides (Katsoyiannis et al., 2004; Oremland and Stolz, 2003). The metal has no known biological function and is extremely toxic in high concentrations. The arsenic mean values in this study were slightly above the WHO permissible limit, with the highest being 0.09 ppm in the IAM area. This can pose certain risks to consumers of water from the river, as this metal has been characterized as a carcinogen. Regular consumers of contaminated water and contaminated aquatic foods may be at risk of arsenic buildup in the body. Selenium is an essential micronutrient found in groundwater as well but toxic at elevated levels. Its concentration levels usually rise when there is an occurrence of industrial emissions or mining activities (Fernandez-Martinez and Charlet, 2009). Selenium recorded for the different water samples were relatively close to recommended WHO limit (0.05 mg/L) except for

the IAM sample, which showed a high value of 0.10 ppm.

Turbidity is the degree of clarity or cloudiness of water and it is evaluated by the presence of suspended solids in the water (Health Canada, 2012). The mean turbidity values obtained from all water samples ranged from 32.43 to 37.67 NTU. This raises another concern, as the values obtained exceeded recommended limits by WHO and SON, thereby rendering it unfit for drinking. Suspended solids in water promote the growth of microorganisms and as such, high turbidity is often correlated with a high presence of disease-causing microorganisms (Shittu et al., 2008). The high turbidity values obtained are clear indicators of Idah River pollution. The concentrations of the nutrients (nitrates and sulphates) were within the acceptable limits for both WHO and SON standards. Therefore, they did not pose a serious water quality issue.

Dissolved oxygen (DO) is a measure of oxygen levels dissolved in an aqueous solution, which plays a major role in the biological activities of cultured organisms (Murphy, 2005). It is an important criterion for assessing quality, as it provides details on pollution levels, metabolic activities of microorganisms and nutrient availability (Premlata, 2009). The DO concentration range for the four sites: DPA (9.28 ppm), DPB (9.28 ppm), IAM (6.67 ppm) and IAC (6.27 ppm) were all higher than the statutory permissible limit (5 mg/L) necessary for aquatic life. Although, slightly above the permitted threshold, there have been higher concentrations of DO reportedly used for agricultural purposes in brackish aquaculture (Ayedun et al., 2011). Also, microorganisms use DO for the decomposition of organic materials at the bottom of water bodies. Low DO may lead to an anaerobic environment, resulting in a bad odour of water (Adekunle et al., 2007).

Electrical conductivity is defined as a measure of the degree of ions in an aqueous solution or the capacity of water to pass electrical flow. The source of these conductive ions could be from dissolved salts and inorganic materials such as chlorides, carbonate compounds or sulfides (Miller et al., 1988). The range of electrical conductivity values recorded from all sample sites was within the acceptable limit reported by WHO (2011). This may imply that the river receives low amounts of dissolved salts and inorganic substances (Kidu et al., 2015).

Results also showed that lesser concentrations of calcium, magnesium, potassium, nitrates and sulphates were recorded in IAM and IAC sample sites. This might be connected to the continuous movement of water, thereby diluting the concentrations of organic and inorganic wastes that might have been introduced at the docking sites of the river.

The total heterotrophic bacteria counts of bacteria exceeded the WHO's stipulated standards for water bodies. Notably, the high population of bacteria seen at the two docking points could be due to the fishing and other observed anthropogenic activities occurring around

the Idah riverbank. The high abundance of bacteria isolated from these two areas could also be linked to the bathing activities, washing and sewage run-offs, which was noticed at the riverbank, and is most likely to transmit an array of infectious diseases (Anyanwu and Okoli, 2012).

In the IAM area, the highest arsenic and selenium values were recorded, which were above the WHO limit. This might be indicative of toxicity, and could be the reason for the low heterotrophic bacterial plate count and the low number of bacteria and fungi isolated (Leon et al., 2018).

The bacteriological analysis showed that Gram-negative bacteria were predominant amongst the bacterial isolates from Idah River. The microorganisms isolated in order of prevalence were *Acinetobacter* spp., *Staphylococcus aureus*, *Bacillus* spp., *Pseudomonas aeruginosa*, *E. coli*, *Klebsiella* spp., *B. subtilis*, *Aeromonas hydrophilia*, *Shigella* spp. and *Streptococcus* spp. The bacterial diversity reported in this study had some similarities to previous reports by Anyanwu and Okoli (2012) who reported the presence of *Enterobacter* species, *Alcaligenes* species, *E. coli*, *Proteus* species, *Klebsiella* spp., *P. aeruginosa*, *Acinetobacter* spp., *S. aureus* and *Bacillus* spp. in different water supplies at Nsukka, Nigeria. Also, Umeh et al. (2020) reported the prevalence of *Klebsiella pneumoniae*, *Acinetobacter calcoaceticus*, *E. coli*, *S. aureus*, *Vibrio* species, *Pseudomonas* spp., *B. subtilis*, *Shigella flexneri*, *Salmonella* Typhi in selected fish ponds in Anambra State, Nigeria.

Based on the frequency rate of isolated bacteria, *Acinetobacter* spp. was found to be the most predominant across the four sites, constituting 50.52% of the total bacterial community. The high prevalence of this species is most likely linked to the observed discharge of abattoir effluents into the Idah River, which was also reported in the study of Tsai et al. (2018). This is also in agreement with the report of Okechi et al. (2020) who found that *Acinetobacter* was the most predominant bacteria in the sediment area of Otamiri River, constituting about 42.10%. In Northeastern China, Zhao et al. (2014) found that the genus *Acinetobacter* was also the most prominent group of isolates in zinc and arsenic polluted rivers. Species of the genera *Acinetobacter* are ubiquitous in a wide range of ecological areas like water, soil, sludge, and wastewater (Hamouda et al., 2011). However, some scientific reports argued that the *Acinetobacter* genus is a nosocomial pathogen and the possibility of it thriving in natural environments is low (Peleg et al., 2008). It would also seem that they are resilient, as documented by few reports, which showed that they can survive in various environments containing low amounts of nutritious components, as well as their resistance to adverse environmental conditions (Gospodarek and Ziolkowski, 2000). Strains of this organism are commonly known to harbor antibiotic resistance genes and they are regarded as emerging opportunistic pathogens of fish farmed in Poland

(Kozłńska et al., 2014). There might be a possibility of this occurring in Idah River, if precautionary measures are not taken.

The isolated Gram-positive bacteria, *S. aureus*, were also widespread across the river with a total percentage of 18.56%. The daily routine of washing, sand packing and fishing activities observed at the riverbank might account for its abundance at the docking sites. At the midstream and confluence areas of the river, its prevalence was relatively low. *S. aureus* is known to be commensal in the mucosa of mammals and birds. However, they can also be opportunistic pathogens (Quinn et al., 2004). The risk of *S. aureus* infections is premised on the possibility of its resistance to beta-lactamase antibiotics, including penicillin and thus, its presence in water calls for public health concern. *Streptococcus* spp. was found only in the midstream area of the river. This organism has been associated with illnesses such as pneumonia and upper respiratory tract infections. *Bacillus* spp. were identified across all sample sites. *Bacillus* spp. can occupy a wide range of ecological niches and its spores are quite ubiquitous (Nicholson, 2004). In particular, *B. subtilis* found in the docking and midstream area could have the potential to be used as probiotic additives in aquaculture, as reported by Guo et al. (2016).

The main indicator of faecal pollution, *E. coli*, was found in all sites, except for the midstream area of the water. These bacterial isolates were discovered from both docking areas, which is suggestive of sewage pollution and abattoir effluents observed at the Idah riverbank. Contamination of the river by other members of the Enterobacteriaceae family seen in this study – *Shigella* spp., *A. hydrophilia*, *P. aeruginosa* and *Klebsiella* spp. could be related to a combination of direct faecal contamination and agricultural run-off at the docking sites. These Gram-negative bacteria are typically responsible for some waterborne diseases, including Shigellosis, typhoid, dysentery, diarrhea, as well as urinary tract infections, and they have been implicated in high mortality rate across the world (WHO, 2011). *Pseudomonas* spp. has been isolated from fishes in contaminated rivers. When consumed raw or insufficiently processed, such fishes could serve as a vector for the transmission of pathogens to humans (Jeyasekaran et al., 2006). Generally, the prevalence of Gram-negative bacteria in this river could be as a result of faecal contamination and other human interference, which could result in the proliferation of pathogenic organisms in fish, affecting human consumers (Kay et al., 2008). Their presence is most likely linked to the washing activities in the area, as well as the agricultural/seepage runoffs entering the river (Abulreesh, 2012). This implies a significant health risk for humans consuming this water (Franciska et al., 2005).

The mycological analysis in this study showed the presence of *A. niger*, *A. flavus*, *Penicillium* spp., *Fusarium*

spp., *Cladosporium* spp., *Trichoderma* spp. and *Curvularia* spp. in Idah River. This agrees with the observations of Ili et al. (2019), who reported *Candida* species, *Fusarium* spp., *A. flavus*, *Penicillium* spp., *A. niger* and *Mucor* species in Okokpon River, Edo State. Furthermore, Agbabiaka and Oyeyiola (2012) documented the presence of *Curvularia*, *Aspergillus*, *Penicillium*, *Saccharomyces*, *Cladosporium*, *Geotrichum*, *Trichoderma*, *Mucor*, *Rhizopus*, *Fusarium* and *Mortierella* (fungi) as sediment contaminants of Foma River, Ita-Nmo, Ilorin.

The abundance of fungi, in the docking areas of Idah River, is likely linked to its high sulphate concentration, thus constituting an indicator of water pollution from anthropogenic and agricultural origins. Pietryczuk et al. (2018) reported a similar observation in their study of fungi diversity in selected rivers. Fungal population increases with pollution and this might be connected to the high number of fungal contaminants observed at the docking areas of the river.

Amongst the various fungi species isolated in this river samples, *Fusarium* spp. was the most predominant, constituting about 39.13%. *Fusarium* spp. are plant pathogens or rhizosphere fungi, and their presence in Idah River could be attributed to agricultural activities occurring around this river. This is quite similar to the observation of Sharma and Tiwari (2015) who reported *Fusarium* spp. as one of the most abundant soil fungi isolated from the Shivnath River and it is known to cause several superficial infections. *A. niger* and *A. flavus* found in this river are known to be among the main agents of food spoilage but it is co-related to a range of infections such as Aspergillosis, leading to respiratory infections. Refai et al. (2010) also confirmed *Aspergillus* as pathogenic fungi of freshwater fishes. *Trichoderma* spp. was found only in DPA and DPB, which had the most observed anthropogenic activities. It is one of the beneficial fungi in the environment that can serve as a bio-fungicide against various fungal pathogens (Schuster and Schmoll, 2010). It was suggested that it might have the potential to also control infectious diseases in aquaculture (Citarasu et al., 2012). *Penicillium* spp. was prevalent only in the two docking points, and the genus was reported to produce mycotoxins (Pohland and Wood, 1997). Contamination of fish with these mycotoxins could accumulate in their tissues, which could invariably affect humans when consumed. The processing of fish does not necessarily eliminate the presence of mycotoxins in their tissues. *Cladosporium* and *Curvularia* spp. isolated from the docking points in the river are predominantly saprophytic in nature, and they are known to colonize and parasitize aquatic plants.

Conclusion

In this study, physicochemical and microbial

(bacteriological and mycological) profiling of Idah River were assessed from four designated sampling points. Although, thirteen physicochemical parameters were within the safe limits as indicated by the WHO (2011) and SON (2007) standards, parameters indicative of pollution were obtained. They included high total heterotrophic bacterial counts, presence of pathogenic microbes and toxic levels of certain physicochemical factors, such as arsenic, selenium, turbidity and nickel, when compared with standards. Such extreme values derived from physicochemical analysis might be connected to anthropogenic activities of locals of the community, resulting in inorganic pollution. In addition, the various fungi and bacterial species found in the river raises health concerns, with regards to direct consumption of water and ingestion of food (such as fishes and aquatic plants) sourced from the water body. It is therefore recommended that programs and policies, such as continuous monitoring and public health awareness programs are set in place to enlighten locals of the community, about the dangers of unsuitable discharge of animal, human and inorganic wastes into the river. This could in turn, prevent the river from being an environmental reservoir of antibiotic-resistant pathogens, hence preventing public disease outbreaks.

This study provides the first report about physicochemical properties and microbial diversity (using culture-based techniques) inherent in the Idah River. However, additional microbial analysis, such as metagenomic studies, could be used to reveal a deeper microbial structure inherent in the river, which culture-dependent methodology might not have captured.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENT

We would like to thank Mrs. Roseline Ideh of Bio entrepreneurship and Extension Services Department, National Biotechnology Development Agency (NABDA), Abuja, for her technical support. We also appreciate Ms. Halima Idris of the National Space Research and Development Agency (NASRDA), Abuja, for assisting with the GIS map of the sample sites in Idah River.

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