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The Bacteriological Quality of Surface Water, Sediments and Selected Fish Species of Tagwai Lake, Minna, Niger State – Nigeria

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Abstract
The high contamination of aquatic systems with toxic heavy metals is of major concern since the elements are not biodegradable. The aim of this study was to investigate the level of bacteriological analysis in both surface water and sediment and in selected fish species of Tagwai Lake, Minna, Niger State - Nigeria. Standard methods were used in analyzing for bacteria load. The results showed that bacteria isolated from the surface water samples were as follows: Salmonella typhi, Bacillus subtilis, Escherichia coli, Staphylococcus aureus, Vibrio cholera, Pseudomonas aeruginosa, Streptococcus feacalis, Bacillus megaterim, Klebsiella pneumonia, Shigella dysentrea, Streptococcus pyogen and Staphylococcus epidermidis. Total bacteria counts (TBC) recorded ranged from 59.50 to 46.00 10^6 cfu/ml, while the total coliform, and total faecal coliform counts ranged from 40.00 to 31.50 MPN/100ml and 3.50 to 1.25 x 10^2 cfu/ml respectively. Also, the total bacteria counts (TBC) ranged from 18.88 to 22.88 10^6 cfu/ml, while the total coliform, and total fecal coliform counts ranged from 6.63 – 7.63 MPN/100ml and 0.13 – 0.50 x 10^2 cfu/ml respectively. Total bacteria counts fish species (TBC) ranged from 18.88 to 22.88 10^6 cfu/ml. There was significance different among the various fish species. The total coliform, and total fecal coliform counts ranged from 6.63 – 7.63 MPN/100ml and 0.13 – 0.50 x 10^2 cfu/ml respectively. Basically, there was no significance difference (P>0.05) among the various fish species for each of the parameters analyzed. This study therefore, suggested that the water from Tagwai Lake is not potable for human consumption based on high bacteriological quality except when treated using suitable treatment technology such as chlorination and boiling.

***Keywords**: Surface water, Sediments, Fish species, Tagwai Lake, Minna*

Introduction

Water is a finite resource that is very essential for human existence, agriculture and industry thus; inadequate quantity and quality of water have serious impact on sustainable development. Material pollution of rivers is caused by toxic pollutants (heavy metals, phenols and insecticides, among others) that have direct adverse effect on aquatic biota and by-pollutants (human and animal waste) that indirectly affect aquatic biota, which are not toxic but due to bacterial action on them, dissolved oxygen is used up which harms aquatic biota. Assessment of water is not only for suitability for human consumption but also in relation to its agricultural, industrial, recreational, commercial uses and for its ability to sustain aquatic life. Water quality monitoring is therefore a fundamental tool in the management of freshwater resources (Anake *et al*., 2013; Okomoda *et al*., 2014).

Microorganisms are found all throughout the world. They've also been linked to a variety of ailments. Microorganisms such as bacteria can be present in water and can cause disease in humans if they drink it. As a result, low-quality water is one of the mediums via which harmful microorganisms such as bacteria and viruses can spread. Poor water has been linked to a number of ailments, the most noteworthy of which are enteric fever and diarrhoea.

Disposal of sewage wastes into a big body of water may raise biological oxygen demands to the point where all available oxygen is depleted, resulting in the death of all aerobic species, such as fish (Sunday *et al*., 2014). Increasing numbers and quantities of industrial, agricultural, and commercial chemicals discharged into the aquatic environment have resulted in a variety of

negative consequences on aquatic creatures. Pollutants accumulate in aquatic organisms, including fish, both directly and indirectly through the food chain (Chukwuemeka *et al*., 2019). Technological advancements in recent years have resulted in an increase in the buildup of heavy metals in the environment; the toxicity of these heavy metals, which are not biodegradable, is a serious problem in the aquatic environment (Chukwuemeka *et al*., 2020).

Tagwai Lake, Minna is one of the primary sources of water in Niger state. In addition to fishing, irrigation, farming, and other anthropogenic activities, the lake hosts a variety of other activities (Chukwuemeka *et al*., 2019). As a result of all these anthropogenic activities taking place within and around the lake, it is necessary to identify and assess the presence of heavy metals, their status, and compare the results to regulatory standards such as to determine if the water is safe for drinking. This study was carried out to investigate heavy metals concentrations in water and sediment of the Lake and also to assess its presence in some selected fish species.

This present study was designed to determined the bacteriological quality of surface water and sediment of some selected fish species in Tagwai Lake, Minna, Niger State, with a view to establishing a basic data on the current pollution status of the lake. The results obtained from this study would also provide information on current levels of bacteriological quality of water and sediments of the lake, contributing to the effective monitoring of both environmental quality and health of the organisms inhabiting the lake.

MATERIALS AND METHODS

Study Area

The study was carried out in Tagwai Lake, Minna, Niger State, located within longitude 6°33'E and latitude 9°37'N, covering a land area of 88 km2 (Fig 1). The area has a tropical climate with mean annual temperature, relative humidity and rainfall of 30°C, 61.00% and 1334.00 mm, respectively. The climate presents two distinct seasons, a rainy season (between January to August), and a dry season (between November and March). The vegetation in the area is typically grass-dominated savannah with scattered tree species. Tagwai Lake is about 10 km away from Minna town. Mean maximum temperature remains high throughout the year having about 30°C, particularly in March and June. The vegetative cover is characterized by woodland and tall grasses inter spread with tall, dense species. In some areas, traces of rain forest species can be seen of Sudan Savannah alongside the plain of the River. The secondary benefits from this dam include fishing, recreation and wildlife (NSPC, 2011).

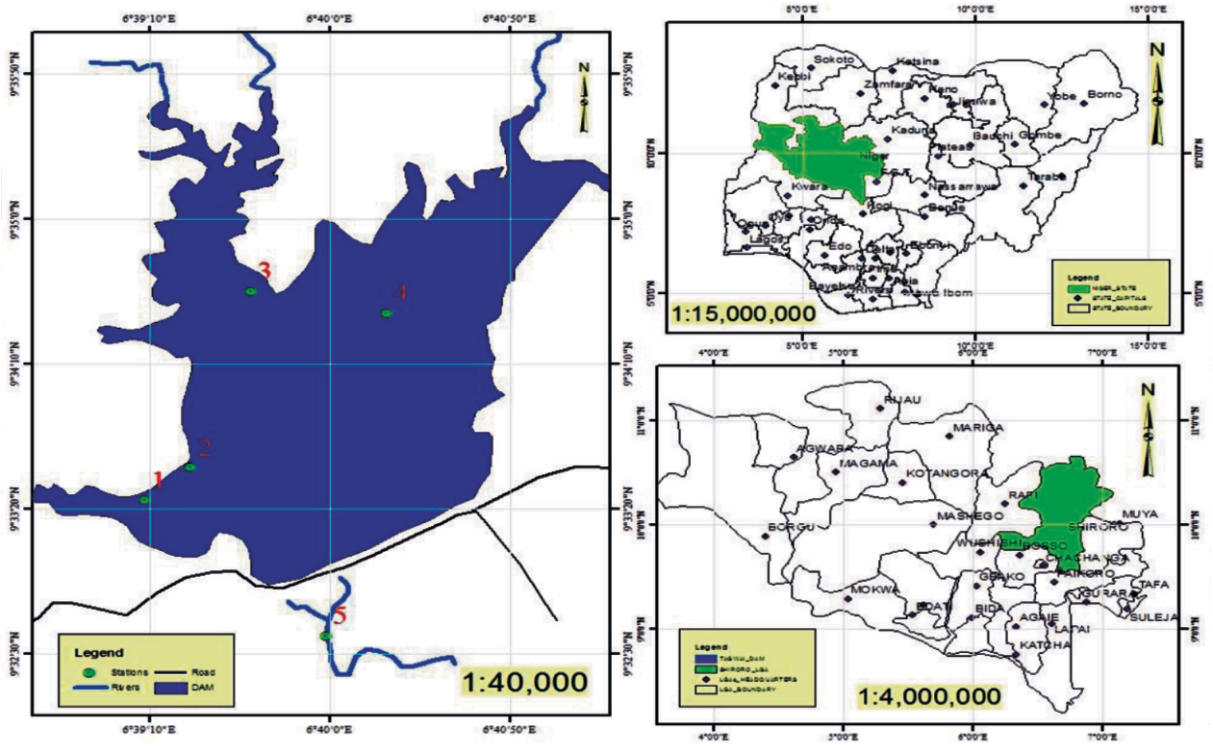

Figure 1: Map of the study site (Tagwai Lake) in Niger State, Nigeria (Source: The Department of Geography, FUT, Minna. Centre for Remote Sensing (2018).

Bacteriological Analysis

Collection of Water Samples: All water analyses were carried out aseptically, and this followed the standard methods as described in American Public Health Association 2012). The bacteriological analysis of the water samples from the lake and streams was performed for the presence of coliform bacteria, total and faecal coliform, *E. coli*, *Aeromonas sp, Ente*roc*occus* sp. (these bacteria can survive longer in adverse environmental conditions due to their bacterial membrane. A membrane filtration and pour plate technique was employed in analyzing the water samples. Aliquots of 100 ml each of the water samples was separately filtered through 0.45-µm-pore-size membrane filters. Determination of total coliform, *E. coli*, and fecal coliform will be undertaken by placing the filter on Hicrome (Difco) Media in Petri dishes and incubated at 37 ± 0.5 °C and 44 °C for 16–24 h, respectively. *Salmonella sp., Pseudomonas sp. and Aeromonas sp*. were determined by placing the filter on SS agar, Cetrimide and *Aeromonas* media, respectively, in Petri dishes and incubating at 37 ± 0.5 °C, for 16–24 h. Slanetz and Bartley medium will be used for the determination of *Enterococcus* spp. Furthermore, it will be incubated at 44 °C ± 0.5 °C for 48 h. Total heterotrophic bacteria was determined by the pour plate technique using an aliquot of 1 ml of water sample on nutrient agar and incubating at 37 ± 0.5 °C for 48 h. Colonies will be counted with the aid of the colony counter, and numbers was expressed as coliform forming units (CFU) per 100 ml for membrane filtration and CFU per 1 ml for pour plate technique (APHA 2012).

Water Sample for Microbiological Analysis: Samples were collected monthly from January to August, 2020. Water samples were collected in five (5) different collection points. Water samples for microbiological analysis were collected in a sterile amber coloured glass bottle. At each sampling point, the bottle was opened and immersed in the river to a depth of about 30cm with its mouth facing the water current, filled to three quarters its capacity and quickly stoppered to avoid contamination. The water was then transported on ice to the Laboratory of the Department of Microbiology, Federal University of Technology (FUT), Minna. Bacteriological analyses of the samples commenced within three hours of collection. This process and methods were repeated for each sample.

Collection of Fish Samples: Four samples of the selected fish species namely: *Tilapia sarotherodon, Auchenoglanis occidentalis, Claria gariepinus*, and *Mormyrus hasselquistii* caught from Tagwai Lake were obtained from vendors monthly, for six months. The fish samples were transported in a Jerry cans (25litres rubber) containing the river water (the reason is to get the fishes acclimatize and avoid casualties), to the Laboratory of the Department of Microbiology, Federal University of Technology (FUT), Minna, where they were cleaned with sterile distilled water. One gram of muscle was cut aseptically and labeled appropriately for microbiological analysis. The remaining portions of the fish were taken to the Department of Fishery, Federal University of Technology (FUT), Minna, for digestion (Cheesbrough, 2010).

The following (*Tilapia sarotherodon, Clarias gariepinus, Auchenoglanis occidentalis* and *Mormyrus hasselquistii***)** were the fish species used.

Plate I: ***Tilapia sarotherodon*** **(Source: Field work, 2020)**

Plate II: ***Mormyrus hasselquistii*** **(Source: Field work, 2020)**

Plate III: ***Auchenoglanis occidentalis*** **(Source: Field work, 2020)**

The bacterial counts on the external surfaces, intestines, and tissue were estimated as follows:

Skin surfaces: Sample from different stations of the skin of fish samples was taken by rubbing the sterilized cotton swab over the skin and then inoculated into 9ml of Nutrient broth, which is dispensed in separate tubes. The most appropriate serial dilution of the bacterial suspension already inoculated in peptone water was prepared in duplicate, and viable aerobic bacterial counts were enumerated using 0.1ml and 1ml inoculums in standard plate count agar as described by Cheebrough (2010), and then incubated at 37oC for 48 hrs.

Intestines, Gills & Tissues: 1g of the fish sample will be dissected out, blended, and appropriately mixed in a mortar. It was aseptically transferred to a sample bottle containing 9mls of 0.1% sterile peptone water. The bottle was closed and shaken thoroughly and allowed to stand for 20mins, after which a ten-fold serial dilution will be carried out in duplicates and viable aerobic bacterial counts will be enumerated in standard plate count agar after incubation at 37^{o}C for 48 hrs as described by Cheebrough (2010). Coliform organism and gram-negative enteric bacteria counts will be determined using the pour plate method with MacConkey agar, EMB Agar, respectively. Mueller-Hinton Agar for Pseudomonas *sp. Salmonella sp*.

Shigella spp. was enumerated using *Salmonella Shigella Agar* (SSA) and *Thiosulphate Citrate Bile Salt* Sucrose (TCBS) agar for pathogenic Vibrio *spp*. The plates were then incubated at 35+2^{o}C for 24h. The observed colony growth was counted using the Coulter™ Colony counter according to the plate count method. The identification of the organisms was made using the phenotypic and biochemical characteristics, as described by Cheesbrough (2010).

Preparation of Fish Samples for Microbiological Analysis

One gram (1.0g) each of the fish samples were weighed aseptically, and macerated in 9.0mls of 0.1% peptone water and serially diluted three fold and labelled appropriately (Cheesbrough, 2010). This was used for the microbiological analysis.

A 1.0 ml from the 10-3 dilution was used for heterotrophic bacterial count while 1.0 ml from the 10-2 dilution was used for faecal coliform count.

1. Preparation of Bacteriological Media

The dehydrated media were reconstituted with freshly prepared distilled water and distributed into containers as specified by the manufacturers. Except those not required to be sterilized, sterilization of these media was achieved by autoclaving at 121°C for 15 minutes. Prepared media were stored in refrigerators at 4°C until needed (Cheesbrough, 2006).

2. Tentative identification of the microbial isolates

The different isolates found in the water samples were subjected to biochemical tests following the scheme of Cheesbrough (2006) and Benson (2002). Thereafter, the resultant appearances were compared with those of known taxa using scheme of Cheesbrough (2006) and Bergey's Manual of Determinative Bacteriology by Holt *et al*. (1994) Based on gram reaction, the gram positive organisms were streaked in Mannitol Salt Agar plate and incubated inverted at 37°C for 24 hours. The presence of yellowish pigments in Mannitol Salt Agar indicates *Staphylococcus aureus* (Kigigha and Baraseibai, 2017). Tubes with colour change and gas production were shaked and streaked in Levine's eosin Methylene Blue (EMB) Agar and incubated at 37º C for 24 hours. The presence of small nucleated colonies with greenish metallic sheen indicates *E. coli* (Pepper and Gerba, 2005). The colonies were streaked in blood agar, the presence of swarming growth and haemolytic properties on medium after incubation indicates *Proteus* species and *Streptococcus* species respectively (Kigigha and Baraseibai, 2017). A Triple Sugar Iron Agar was prepared into slants and the colonies were aseptically transferred into the slants (Odu and Adeniji, 2013). A positive tube was confirmed by presence of cracks and blackening of the medium (Izah *et al*., 2015).

3. Enumeration of Total Bacteria Counts

Two media was used to enumerate the bacteria population. Nutrient Agar was used for total bacteria count and Salmonella-Shigella Agar was used for Salmonella-Shigella counts). Both media were prepared and used according to the manufacturers' instruction following pour plate method previously described by Pepper and Gerba (2005) and Benson (2002). 1.0 ml of serially diluted sample was aseptically plates in both media and incubated inverted at 37ºC for 24-48 hours. The resultant colonies were counted and expressed as colony forming units per the water sample. The different colonies were isolated into nutrient Agar.

4. Examination of total and feacal coliform counts

The total and fecal coliform test (presumptive, confirmatory and completed test) of the water was carried out using three tubes most probable number previously described by Pepper and Gerba (Pepper and Gerba, 2005), Benson (2002) Akubunenyi *et al*. (2013). The result based on gas production and colour change was compared with table presented by Pepper and Gerba (2005).

Preliminary Identification of the Isolates

1. *Isolation and Identification of selected Bacteria*

One milliliter (1 ml) of stock culture were mixed with 9.0 ml of peptone water as pre-enrichment and incubated at 37°C for 24 hours. The 24 hours culture was then streaked on to several selective media: MacConkey Agar, Salmonella-Shigella Agar, E.M.B Agar and Mannitol Salt Agar (Cheesbrough, 2010).

2. *Gram staining*

Colony of bacteria was smeared on slide and fixed. It was then smeared with crystal violet stain for 60 seconds. The stain was washed off with clean water. Lugol's iodine was used to cover the smear for 60 seconds and washed off with clean water. This was followed by decolourization of the stain using alcohol and washed immediately with clean water. The smear was there after counter stained with neutral red stain for 2 minutes and washed off with clean water. The smear was then placed in a draining rack to air-dry and examined microscopically with oil immersion objective to report the bacteria and cells (Cheesbrough, 2010).

3. *Growth on Selective Media*

The isolates were incubated for 24 hour at 37°C on the following selective media. The colour and morphology of the colonies were observed and noted. MacConkey agar was used to differentiate the lactose fermenters from the non-lactose fermenters, while Mannitol salt agar was used to presumptively identify *S. aureus*. *Staphylococcus aureus* appears as golden yellow colonies (Izah *et al*., 2015).

On Eosin methylene blue agar, *an E. coli colony appears* greenish with metallic sheen. Salmonella-Shigella agar presumptively identifies *Salmonella* spp. by the appearance of black centred colony. The isolates were further identified biochemically.

Data Analysis

Data generated were analyzed to get the mean and standard error. The data were then subjected to statistical analysis using SPSS software version 22.0 to carry out the statistical analysis of the heavy metals and bacteria density. One-way analysis of variance was carried out at $P = 0.05$.

RESULTS

Distribution of bacteria present in the surface water

The bacteria isolates from the surface water samples from Tagwai Lake is presented in Table 1. The bacteria isolated from the surface water samples were denoted using a positive (+) sign while those bacteria not found in some surface water samples were shown using a negative (-) sign. The tentative bacteria isolates identified include *Salmonella typhi, Bacillus subtilis, Escherichia coli, Staphylococcus aureus, Vibrio cholera, Pseudomonas aeruginosa, Streptococcus feacalis, Bacillus megaterim, Klebsiella pneumonia, Shigella dysentrea, Streptococcus pyogen and Staphylococcus epidermidis.*

Bacteriological concentration in sediment

The bacteriological concentration in sediments obtained from Tagwai Lake, Minna is presented in Table 2. Total bacteria

counts (TBC) ranged from 59.50 to 46.00 10^6 cfu/ml. There was significance difference in TBC concentration in the various sampling stations. The total coliform, and total fecal coliform counts ranged from 40.00 to 31.50 MPN/100ml and 3.50 to 1.25 x 10^2 cfu/ml respectively. Basically, there was significance difference ($P<0.05$) in TCC in the various sampling stations and no significance difference ($p>0.05$) TFCC concentration among the various sampling stations.

Bacteriological characteristics of the different fish species

The bacteria population of fish species obtained from Tagwai Lake, Minna is presented in Table 3. Total bacteria counts (TBC) ranged from 18.88 to 22.88 10^6 cfu/ml. There was significance different among the various fish species. The total coliform, and total fecal coliform counts ranged from 6.63 – 7.63 MPN/100ml and 0.13 – 0.50 x 10^2 cfu/ml respectively. Basically, there was no significance difference ($P>0.05$) among the various fish species for each of the parameters analyzed.

Table 1: Distribution of bacteria in the surface water

Bacteria isolates	Station 1	Station 2	Station 3	Station 4	Station 5
Salmonella typhi	+	+	+	+	+
Bacillus subtilis	+	-	+	+	-
Escherichia coli	+	+	+	+	+
Staphylococcus aureus	+	+	-	+	-
Vibrio cholera	-	-	+	+	+
Pseudomonas aeruginosa	+	+	+	-	+
Streptococcus feacalis	+	+	+	+	+
Bacillus megaterim	-	+	+	-	-
Klebsiella pneumonia	+	+	+	+	+
Shigella dysentrea	+	+	-	+	+
Streptococcus pyogen	-	-	+	.	-
Staphylococcus epidermidis	+	+	-	-	+

Table 2: Bacteriological concentration in sediment

Stations	TBC	TCC	TFCC
1	48.25±2.39a	31.50±3.01a	3.00±1.08a
2	50.25±7.99b	39.00±3.14b	1.25±0.63a
3	46.00±5.61a	40.00±1.08b	2.25±0.63a
4	59.50±2.59b	39.00±10.59b	2.50±0.65a
5	54.00±2.16b	54.00±3.03c	3.50±0.96a

Data is expressed as mean ± Standard Error; Different alphabets along the column indicate significance difference (P>0.05) using Duncan Multiple Range Test (DMRT).

Table 3: Bacteriological characteristics of the different fish species

Fish Species	TBC	TCC	TFCC
Tilapia sarotherodon	$22.88±1.82^b$	$6.63±1.85^a$	$0.13±0.13^a$
Clarias gariepinus	$18.88±1.75^a$	$7.50±1.21^a$	$0.13±0.13^a$
Auchenoglanis occidentalis	$20.34±1.34^b$	$7.25±1.72^a$	$0.50±0.19^a$
Mormyrus hasselquistii	$18.88±1.93^a$	$7.63±1.32^a$	$0.50±0.19^a$

Data is expressed as mean ± Standard Error; Different alphabets along the column indicate significance difference (P>0.05) using Duncan Multiple Range Test (DMRT).

Keys: TBC = Total Bacteria Count, **TCC** = Total Coliform Count, **TFCC** = Total Feacal Coliform Count

Discussion

Assessment of bacteriological analysis of surface water, sediments and some selected fish species in Tagwai Lake Minna are discussed in relation to World Health Organization (WHO) and Standard Organization of Nigeria (SON) guidelines for drinking water quality. Variations in the total bacteria count (TBC) could be due to difference in the anthropogenic activities in the water prior to sampling. However, lack of significant difference for total coliform and total feacal coliform counts could be due to similarity in activities leading to their presence in the water at various stations sampled. However, the occurrence of coliforms (total and fecal coliform) could be due to the fact that wastes (municipal and sewage) are discharge into the water body directly. Researchers have variously reported that sewage is discharge into most surface water by communities aligning rivers (Agedah *et al*., 2015; Ogamba *et al*., 2015; Izah and Angaye, 2016a; Izah and Angaye, 2016b).

The bacteria population exceeded World Health Organization/Food and Agricultural Organization allowable limit of 1.0 x 10^2cfu/ml (Eze and Madumere, 2012; Oludare and Sikiru, 2012; Sunday *et al*., 2014; Angaye *et al*., 2015; Izah *et al*., 2015). While the total coliform and fecal coliform often exceeded the limit of 10cfu/ml and 0cfu/100ml for total coliforms and Thermo tolerant Coliform/*E. coli*/faecal streptococcus respectively as specified by Standard Organization of Nigeria (Standard organization of Nigeria, 2007; Izah *et al*., 2015).

The bacteria population recorded in this study is higher than the ones previously reported in surface water in Bayelsa state. Agedah *et al*. (2015) reported total bacteria count in the range of 6.389 – 6.434Log cfu/ml from surface water around Wilberforce Island. Angaye and Mieyepa (2015) reported total, total coliform and total feacal coliforms in the range of 0.44 - 1.159 X 106 cfu/ml, 76.72 - 260.23 MPN/100 ml and 53.67-157.02 MPN/100 ml respectively from Efi lake.

The bacteria isolates from the water samples from Tagwai Lake, Minna is presented in Table 2. The tentative bacteria isolates identified include *Salmonella typhi, Bacillus subtilis, Escherichia coli, Staphylococcus aureus, Vibrio cholera, Pseudomonas aeruginosa, Streptococcus feacalis, Bacillus megaterim, Klebsiella pneumonia, Shigella dysentrea, Streptococcus pyogen and Staphylococcus epidermidis*. Various bacteria species tentatively isolated have been reported from potable water sources (surface water i.e. fresh water, groundwater i.e. borehole and rainwater) in Nigeria. In a recent review study, Izah and Ineyougha (2015) reported *Staphylococcus aureus, E. coli, Pseudomonas, Enterobacter, Yersia, Shigella, Bacillus, Micrococcus, Serratia, Proteus, Salmonella, Klesbsiella, Streptococcus* species as bacteria isolates frequently found in potable water sources. These bacterial are microbes of public health importance. Some of the isolates have been linked to several disease conditions such as diarrhoea (*E. coli, Enterobacter, Salmonella* species etc). Other bacteria are also associated with infectious diseases including gastroenteritis, typhoid fever, dysentery, cholera (Nwidu *et al*., 2008), and urinary tract infections etc. The presence of these bacteria isolates is an indication that such water sources are not potable (Akubuenyi *et al*., 2013).

Ogeneogaga and Solomon (2017) reported a total of eight bacteria species isolated from the fish ponds with the following percentage occurrence; *Escherichia coli* (25%), *Flavobacterium* spp. (16.7%), *Psuedomonas* spp. (8%), *Samonella* spp. (8%), *Bacillus* spp. (16.7%), *Staphylococcus* spp. (16.7%), and *Bacillus cereus* (8%). Torimiro *et al*. (2014) revealed the presence of *Escherichia coli, Aeromonas sp. Klebsiella sp., Staphylococcus aureus* and *Shigella spp* in the fish pond water samples stocked with

Clarias gariepinus in Ile-Ife. He stated that this may pose a threat to the health of the fishes and consumers.

Njoku *et al*. (2015) isolated *Escherichia coli, Salmonella sp. Shigella sp. Pseudomonas sp. Proteus sp. Klebsiella sp. Vibrio sp. Enterobacter sp, Serratia sp, Aeromonas sp, Staphylococcus sp,* and *Streptococcus sp* from some fish pond water samples within the Niger Delta region of Nigeria. The coliforms isolated were an indication of the contamination of the Tagwai Lake with fecal materials. Adedayo and Anthony (2014) revealed the presence of *Staphyloccocus sp, Streptococcus sp, Bacillus sp, Pseudomonas sp, Escherichia coli, Enterobacter sp, Proteus sp, Citrobacter sp, Salmonella sp,* and *Klebsiella sp* in the selected fish pond water samples from Akungba Akoko, Ondo Sta**te.**

Conclusion

This study assessed bacteriological quality of surface water and sediments of some selected fish species in Tagwai Lake, Minna, Niger State.

Tagwai Lake water quality did not compare well with stipulated standards of WHO, 2015. The Tagwai Lake water samples examined in Minna, Niger State were of poor quality with regards to bacteriological parameters. The detection of total bacteria, total coliforms, and faecal coliforms in significant numbers indicated that the water samples are not potable and safe for consumption and this may be attributed to bad sanitary practices by fish farmers and villagers living around the Lake area.

The study found that the bacteria counts exceeded 10^2 cfu/ml allowable limits recommended by World Health Organization and Standard Organization of Nigeria. While the total coliform and fecal coliform often exceeded the limit of 10cfu/ml for total coliforms specified by Standard Organization of Nigeria. As such the water is unfit for human consumption based on bacteriological quality.

Recommendations

We recommend that:

1. The water should be treated according via chlorination and boiling prior to consumption.
2. Proper sanitary practices should be employed. Samples of the fish (fingerlings) should be taken and examined in the laboratory for its microbiological quality before stocking.
3. More studies should be carried out on the fish surface and body organs to determine the microbial load and heavy metal contamination.
4. Water treatment campaigns should be organized in the studied area to enlighten the residents and fish farmers on the safety of potable water thereby enhancing economic growth, food security and maintenance of natural systems hence; there is need for treated water in fish farming. Environmental education should be incorporated in school curricula at all levels.

Authors' contributions

Authors CVI and ELN conceived and designed the experiments. Author ELN performed the experiments. Authors CVI and AFO review and edit the manuscript. Author ELN wrote the first draft of the manuscript. Authors ESS and OVU analyzed the data. All authors agreed to the final state of the manuscript.

Competing interests

The authors declared that they have no competing interests in the submission and publication of this research.

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