



RESEARCH PAPER

Bacteriological Analysis of Water from Emu-Stream, Kusotachin, Nigeria

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ABSTRACT

Clean and quality water is of public health importance especially in developing countries like Nigeria where access to clean water is lacking in rural areas. The presence and abundance of some bacteria species are known indicators of unhealthy nature of water bodies that are subjected to environmental pollution (especially anthropogenic activities). Therefore, this study was conducted to evaluate the bacteria diversity of surface water in Emu stream in North-central Nigeria for a period of Eight (8) months using standard methods and procedure. Water samples were collected from four different sampling stations. The highest mean bacterial colony count of 5.4×10^3 CFU/ml was recorded in station 2, while the least value of 4.3×10^3 CFU/ml was recorded in station 4. A total of Ten (10) species of bacteria comprising nine (9) Gram-negative (*Escherichia coli*, *Proteus* spp., *Campylobacter* spp., *Citrobacter* spp., *Shigella* spp., *Klebsiella* spp., *Salmonella* spp., *Pseudomonas* spp. and *Aeromonas* spp.) bacteria and one (1) Gram-positive (*Staphylococcus aureus*) bacterium were isolated and identified. *Staphylococcus aureus* and *Escherichia coli* were the commonest isolates. Station 2 and 3 recorded the highest number (8) of bacteria diversity, whereas station 4 recorded the least number of 4 isolates. The presence of these isolate is an indication that the water is polluted and people consuming the water are at risk of water borne bacterial infectious diseases. Therefore, proper water treatment mechanisms are encouraged to be put in place before its consumption.

Keywords: Bacteria, Water-Quality, Emu-stream, Anthropogenic activities,

INTRODUCTION

Water is one of the most essential natural resources required by living organisms for their sustainability. Its uses (drinking, bathing, food production or recreational purposes) are crucial for public health (Eboh *et al.*, 2017, Adeiza *et al.*, 2018). According to the reports of world health organization WHO (2018) an estimated 2.6 billion persons lack access to clean water and adequate sanitation, with more than 2 million persons, mostly children, dying of diarrhea disease (Fardami *et al.*, 2020). Therefore, an adequate, safe and accessible water supply must be available to all (Agbabiaka and Sule, 2010; Fardami *et al.*, 2020). Lack of safe drinking water poses threat to public health thereby exposing man to various water borne diseases (diarrhea, cholera, typhoid, dysentery, gastroenteritis) as well as chemical intoxication (Agbabiaka and Sule, 2010; WHO 2011; Gambo *et al.*, 2015; WHO 2018). According to WHO (2018), the diseases contracted through drinking water kill about 5 million children annually and make 1^{6th} of the world population sick (WHO 2018).

Therefore, there is an urgent need to have water that is free from disease producing microorganisms and chemical substances that are dangerous to health (Adamu *et al.*, 2018; Shittu *et al.*, 2008).

In the developing world, assessing the quality of surface and groundwater remains a key public concern (Kpiagou *et al.*, 2022; Boukari *et al.*, 2022). Monitoring water quality is in great demand, and establishing the presence of hazardous bacteria in water is a critical challenge for human and animal health protection (Maishanu *et al.*, 2022). Consumers and public health officials are worried about the microbiological quality of water because some microorganisms, such as bacteria, viruses, fungi, and parasites, are well-known water pollutants that can cause waterborne illness and epidemics (Mohammed and Adamu, 2019). Some Coliform bacteria in water have been shown to predict the presence of other potentially harmful germs such

Received 3 March, 2023

Accepted 03 July, 2023

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as *Salmonella typhi*, *Escherichia coli*, *Pseudomonas* spp., *Vibrio* species, *Shigella* species and *Aeromonas hydrophilia* among others (Nicholson *et al.*, 2017).

In Nigeria, majority of the rural populace do not have access to potable water, thus, depends on well, stream and river as water sources for domestic use and many studies have shown that the presences of coliform counts in water sources in Nigeria, exceeds the recommended value of World Health Organization (Iloba *et al.*, 2022). According to the World Health Organization standards, drinking water should not contain any microorganism known to be pathogenic or any bacteria indicative of faecal pollution (Ukpong and Okon, 2013). The understanding of the microbiological quality of water sources should be a cause of concern to consumers, water suppliers, regulators and public health authorities (Ukpong and Okon, 2013). The paucity information on the bacteriological properties of

Emus-Stream has propelled the study with the increasing human activities around the water body thus, the study was designed to evaluate the bacteriological status of Emu-stream Kusotachin Niger State, Nigeria.

METHODOLOGY

Study Area

The study was carried out in Emu-Stream in Kusotachin area of Lavun Local Government Area in the outskirt of Bida town a socio-economic town in the region located between latitudes 090 03' 8N and 09006'40"N, and longitudes 06001'0"E and 06002'42"E in Niger State, Nigeria. The research site is located in Kusotachin community of Lavun Local Government Area Niger State, North central Nigeria which falls within the savannah region (Figure 1). The study area has 2 distinguished climatic seasons (rainy and dry season).

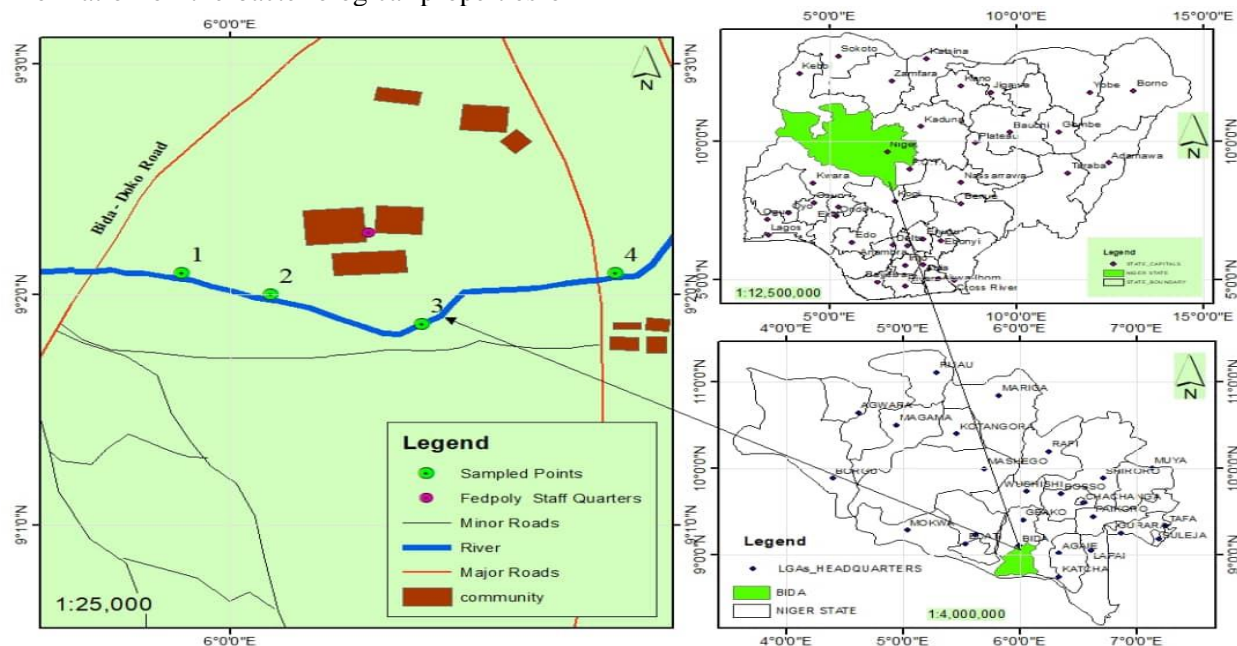


Figure 1: Map of the study area

Sampling stations

Station 1

Sampling station 1 is located close to staff quarters of the Federal Polytechnic Bida. It is close to the headwater that serves as the reference site with relatively no or low anthropogenic activities along the sampling site. The vegetation is mixed with different plant and tree species, prominent among them are mango (*Mangifera indica*), shea tree (*Vitellaria paradoxa*), oil palm (*Elais guineensis*), and different species of grasses.

Station 2

Sampling station 2 is located along Ndarubu road, its 1 km away from station 1 and it is among the impacted areas with various degrees of human activities such as farming throughout both seasons. The vegetation is mixed with different and scattered trees like the African locust beans (*Parkia biglobosa*), Mango (*Mangifera indica*), Malaina (*Gmeilana arborea*) and few grass species.

Station 3

Sampling station 3 is 2 km away from station 2 and it is located along Busu-Gaba road Close to Kusotachin settlement. This station is impacted with various degree of human activities such as laundry, washing house hold utensil, car wash, and agricultural activities throughout the season. The vegetation is mixed with different scattered trees like mango (*Mangifera indica*), shea tree (*Vitellaria paradoxa*), african locust beans (*Parkia biglobosa*), malaina (*Gmeilana arborea*) and few grass species.

Station 4

Sampling station 4 is 1 km away from station 3. This station is predominantly characterized by sand dredging and farming activities. The vegetation is mixed with scattered trees like mango (*Mangifera indica*), shea tree (*Vitellaria paradoxa*), locust beans (*Parkia biglobosa*), malaina (*Gmeilana arborea*) and few grass species.

Sample collection

At the point of sample collection, the sample bottle (1L plastic bottles) was washed with distilled water and rinsed three times with sampling water before collecting the water for the study. The water sample were collected once in a month for a period of Eight (8) months (July 2021 to February 2022). Vertical column method of water sampling was adopted. The samples were labeled with the date, time and location before taking to the laboratory for bacteriological analyses.

Isolation and identification of Bacteria

In the laboratory, the water samples collected from each sampling station of the stream was subjected to serial dilution and 1 ml of the water sampled was poured into test tube containing 9 ml of distilled water, and 1 ml of the water was aseptically transferred from the first test tube to the next test tube containing distilled water up to the ninth test tube.

The media (Nutrient agar) was prepared according to manufacturer's instruction and pour plate technique was employed in which 1 ml of water sample was delivered into a sterile Petri dish using sterile pipette and 20 ml of nutrient agar that was melted and cooled to 45 °C was poured into the dish. The content (water sample and nutrient agar) of the dish were carefully mixed together. The mixture was allowed to set

(solidify) and the Petri dish was incubated at 35°C for 24 hours and the number of colonies of bacteria formed were counted using colony counter (Model R250000614 manufactured by Stuart Scientific Co. Ltd., Great Britain).

Standard bacteriological methods (Macroscopic morphology, Gram stain, and other biochemical assays) were used to identify the bacterial isolates (Cheesbrough, 2000).

RESULTS

The mean bacterial count recorded in this study was 4.30×10^3 CFU/ml in station 4 and 5.40×10^3 CFU/ml in station 2. There was no significant difference ($p > 0.05$) in mean colony count among the sampling stations (Table 1). There were nine (9) Gram negative bacteria and one (1) Gram positive bacteria (Table 2) isolated and identified in this study. The Gram-negative bacteria were *Escherichia coli*, *Proteus* sp; *Campylobacter* sp; *Citrobacter* sp; *Shigella* sp; *Klebsiella* sp; *Salmonella* sp; *Pseudomonas* sp; and *Aeromonas* sp. The only Gram-positive bacterial species isolated was *Staphylococcus aureus*. Table 3 showed bacteria distribution per stations; where stations 2 and 3 recorded the highest number of bacterial species.

Table 1: Mean colony of bacteria count in Emu-Stream Emu-Stream Kusotachin Niger state.

Station	Mean colony	CFU/ml
1	50	5.00×10^3
2	54	5.40×10^3
3	47	4.70×10^3
4	43	4.30×10^3

Table 2. Biochemical characteristics of bacteria isolated in water of Emu-Stream Kusotachin Niger state.

Sample	Gram Reaction	Gram shape	Indole	Methyl red	Vogel Proskauer	Citrate	Lactose	Glucose	Sucrose	Isolates
1	-	Rod	+	+	-	-	+	+	-	<i>Escherichia coli</i>
2	-	Rod	+	+	+	-	+	+	+	<i>Proteus spp</i>
3	-	Rod	+	+	-	-	+	+	+	<i>Campylobacter spp</i>
4	-	Rod	+	+	-	-	+	+	-	<i>Citrobacter spp</i>
5	-	Rod	+	+	-	+	+	+	+	<i>Shigella spp</i>
6	-	Rod	+	+	-	+	+	+	+	<i>Klebsiella spp</i>
7	-	Rod	+	+	-	-	+	+	+	<i>Salmonella spp</i>
8	-	Rod	-	+	-	+	+	+	+	<i>Pseudomonas spp</i>
9	-	Rod	+	-	-	-	+	+	+	<i>Aeromonas spp</i>
10	+	Cocci	-	+	+	+	+	+	+	<i>Staphylococcus aureus</i>

Note; +=positive, -=Negative

Table 3: Distribution of Bacteria isolate of water in sampling stations of Emu-Stream Kusotachin Niger state.

Bacteria Species	Station 1	Station 2	Station 3	Station 4	Frequency
<i>Escherichia coli</i>	+	+	+	+	4
<i>Proteus spp</i>	-	+	+	-	2
<i>Campylobacter spp</i>	+	-	+	-	2
<i>Citrobacter spp</i>	+	-	-	+	2
<i>Shigella spp</i>	-	+	+	+	3
<i>Klebsiella spp</i>	-	+	+	-	2
<i>Salmonella spp</i>	-	+	+	-	2
<i>Pseudomonas spp</i>	-	+	+	-	2
<i>Aeromonas spp</i>	+	+	-	-	2
<i>Staphylococcus aureus</i>	+	+	+	+	4
Total	5	8	8	4	25

Note: += Present -= Absent

DISCUSSION

The report of Malhotra *et al.*, (2015) showed that safe water is a basic human right that is still denied to hundreds of millions of people throughout the developing world. Water-related diseases caused by insufficient safe water supplies, coupled with poor sanitation and hygiene, cause 3.4 million deaths a year, mostly in children (Malhotra *et al.*, 2015). The mean bacterial counts encountered in this study exceeds 1.0×10^2 CFU/ml which is the standard limit of heterotrophic count for drinking water (Shittu *et al.*, 2008) in all the sampling station of Emu-Stream. The high bacteria colony count

observed in this study is an indication of the presence of organic waste in the water (EPA 2002; Shittu *et al.*, 2008) and may be attributed to the anthropogenic activities.

The presence of primarily Gram-negative bacteria isolates in the stream indicates substantial anthropogenic influence, as they are associated with pollution (Panneerselvam and Arumugam 2012; Adamu *et al.*, 2018). These groups of bacteria identified in this study are part of the frequently isolated bacteria species in Nigeria freshwater (Shittu *et al.*, 2008; Adamu *et*

al., 2018; Abu *et al.*, 2020, Fardami *et al.*, 2020; Maishanu *et al.*, 2022) Several of these bacteria species are causal agents of food poisoning, and food poisoning is one of the leading causes of disease and mortality in underdeveloped nations (Sapkota *et al.*, 2012; Mostafa *et al.*, 2018). The presence of certain isolates, such as *Escherichia coli*, at all of the stream's sample stations is linked to feces from warm-blooded animals. This might indicate a higher risk of additional pathogenic isolates which could be dangerous to humans if ingested (Maishanu *et al.*, 2022).

The presence of *Escherichia coli* and other total coliform bacteria in volumes beyond the permissible levels, 0 and 10CFU/ml respectively, in all sampling points, make these water sources unsuitable for drinking purposes (Olasoji *et al.*, 2019). The presence of *Salmonella typhi* and *Shigella* species in the river might be linked to the aquatic ecosystem being used as a feces route and micturition activities. *Salmonella* sp. has been identified as a significant cause of enteritis and systemic illnesses (Adamu *et al.*, 2020). Fecal contamination is seen as a major danger to human health (Elamary, 2022; Maishanu *et al.*, 2022). *Shigella* spp., *Salmonella* sp., *Pseudomonas aeruginosa*, multicellular parasites enteroviruses, *Vibrio parahaemolyticus*, and *Aeromonas hydrophila* are only a few of the bacteria or pathogens that may be transmitted to humans through contaminated water (Maishanu *et al.*, 2022). *Staphylococcus aureus* is generally recognized as the causative agent of streptococcal infections in a number of freshwater fishes and is also thought to be a normal component of human skin microflora (Adamu *et al.*, 2018).

The presence of some bacteria in surface water makes it unsafe for drinking and unsafe water is a global public health threat, placing individuals at risk for a host of diarrhea and other diseases as well as chemical intoxication (Adeiza *et al.*, 2018). Contaminated water sources are vehicles for the transmission of waterborne diseases such as cholera, shigellosis, and Campylobacteriosis (Burgess and Pletschke 2010) The most frequently implicated microorganisms in waterborne diseases are the enteric bacteria such as *Escherichia coli*, *Shigella* spp, *Salmonella* spp, among others, which according to WHO/UNICEF have been associated with the estimated 80% diseases affecting developing countries. Unsanitary water particularly has

devastating effects on young children in the developing world (WHO 2004; Adeiza *et al.*, 2018)

The bacteriological quality observed in Emu-stream Kusotachin during the sampling period indicates that water from the stream should not be used for drinking purposes without proper treatment to prevent water-borne diseases and other health challenges associated with the utilization of poor-quality water. This study aligns with the findings of Iloba *et al.*, (2022) who ascertained the bacteriological quality of some drinking water source in Eku and it environ in the Niger Delta region of Nigeria and reported poor water quality. Most contamination of water by bacteria such as the coliforms and other enteric pathogens in water which result to poor water quality status has been pointed to poor sewage disposal and surface run off around the water bodies (Iloba *et al.*, 2018; Ondieki *et al.*, 2021)

Other bacteria isolated from the water samples such as *Staphylococcus aureus*, *Pseudomonas* spp and *Proteus* spp. *Proteus* spp are also of public health significance. *Staphylococcus aureus* is known to produce enterotoxin (Shittu *et al.*, 2008; Abu *et al.*, 2020). *Proteus* spp belongs to the intestinal flora but is also widely distributed in soil and water (Schlegel, 2002). *Enterobacter aerogenes* isolated from the water samples are examples of non-fecal coliforms and can be found in vegetation and soil which serves as sources by which the pathogens enter the water (Schlegel, 2002). The presence of total coliforms and fecal coliform, *E. coli*, *Salmonella* spp, *Shigella* spp, and *Vibrio* spp have been documented as National Primary Drinking Water Regulations (NPDWRs) or primary standards which protect public health by limiting the levels of contaminants in drinking water (EPA, 2002; Shittu *et al.*, 2008).

Conclusion

Bacteriological analysis of water sample from Emu-stream shows the presence of *Escherichia coli*, *Proteus* spp, *Campylobacter* spp, *Citrobacter* spp, *Shigella* spp, *Klebsiella* spp, *Salmonella* spp, *Pseudomonas* spp, *Aeromonas* spp and *Staphylococcus aureus*. The nearby settlement utilizing or consuming such water are at risk of several clinical symptoms of certain diseases such as gastro-intestinal disorders, diarrhea and typhoid fever. It has been evident that water borne diseases are due to improper

disposal of refuse, contamination of water by sewage, surface runoff, therefore programmes must be organized to educate the general populace on the proper disposal of refuse, treatment of sewage and the need to purify water to make it fit for drinking because the associable organisms are of public health significance being implicated in one form of infection or the other. In areas lacking in tap water as in rural dwelling, educative programmes must be organized by researchers, and government agencies to enlighten the villagers on the proper use of surface water.

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