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Research Article

Distribution and Antibiotic Resistance of Bacteria in Lobia Creek

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Abstract

A change in the distribution of species and diversity of aquatic population is a biological marker for measuring the stress on assimilative capacity or water quality. The impact of human activities on the population, distribution, diversity and antibiotic resistance of bacteria from Lobia creek was investigated. Water samples were collected from four different stations with human activities (Abattoir, toilet, jetty, and drinking water point) along Lobia creek and from a fifth station without any human activity which served as a control into separate sterile bottles. The sample bottles were transported in ice packed coolers to the laboratory for analyses. A total of 60 water samples were collected and analyzed during the six months sampling period (August 2020 to January 2021). The total heterotrophic bacteria, coliform and faecal coliforms were determined and identified using standard microbiological techniques. While the antibiotic susceptibility test was conducted using the Kirby-Bauer disk diffusion test. Results showed that counts (population) of total heterotrophic bacteria, coliform, and faecal coliforms ranged from 3.6×10^4 cfu/ml - 1.44×10^6 cfu/ml, 1.8×10^4- 7.6×10^4 cfu/ml and 7.0×10^2- 3.8×10^4 cfu/ml respectively. Generally, the decreasing order of the microbial population of total heterotrophic bacteria, coliform and faecal coliforms in the various locations was; Toilet > Abattoir > Jetty > Drinking water > Control. Statistical analysis showed that there were significant differences ($P < 0.05$) between the microbial counts recorded for the control and the other stations. A total of 320 bacteria were isolated and their percentage of occurrence were: *Bacillus sp (12.66%), Enterobacter* sp (14.6%), *Enterococcus sp (2.6%)*, *E. coli* (12%), *Klebsiella* (10.4%), *Micrococcus* sp (2%), *Proteus* sp (6.8%), *Pseudomonas* sp (7.8%), *Serratia* sp (2.27%), *Shewanella* sp (1.3%), *Shigella* sp (3.9%), *Staphylococcus* sp (18.8%), and *Vibrio* sp (4.87%). The antibiotic susceptibility showed a varying response of isolates to specific antibiotics. About 72 Gram-negative isolates were 100% sensitive to Ofloxacin, Ceftriaxone, and Nitrofurantoin while 72 isolates were resistant to Cloxacillin and 68 (94.4%) were resistant to Ceftazidime. Lower susceptibility of 22.2%, 5.6%, and 2.7% was recorded for Augmentin, Gentamycin, and Cefuroxime, respectively. A total of 46 Gram-positive isolates was completely sensitive to Ceftriaxone and ofloxacin with both species of *Staphylococcus* and *Micrococcus* showing a joint 86.9% and 67.4% resistance to Cloxacillin and gentamycin. The antibiotics, Ceftriaxone, Nitrofurantoin, and Ofloxacin are recommended for treatment of infections emanating from these locations. This study has shown that, Lobia creek is highly polluted and not fit for consumption without proper treatment. It is therefore advocated that the Government should provide potable water for the inhabitants of Lobia community as to mitigate the public health hazard that the consumption of the raw creek water poses to the inhabitants.

Keywords: Lobia Creek; Antibiotic Resistance; Cloxacillin; *Staphylococcus*; *E. coli*; *Shewanella*

Introduction

Clean, safe, and adequate freshwater is vital for the survival of all living organisms and the proper functioning of ecosystems, communities, and economies. Declining water quality has become a global issue of concern as human populations grow, industrial and agricultural activities expand, and climate change threatens to cause major alterations to the hydrologic cycle [1]. Freshwater quality in developing countries including Nigeria especially in the Southern Ijaw region of Bayelsa State, is declining, as a result of pollution from various kinds of human activities and other factors such as industrial and sewage outflows, agricultural run-off, leakage from septic tanks, flooding and saltwater intrusion [2]. Surface water quality status generally is deteriorating mainly due to human population growth, industrial and agricultural expansion and climate change [3]. Water has been an indispensable and multipurpose natural resource and exists in the three states of matter; gaseous, liquid and solid phases [4]. Although about 75% of the earth's surface is covered with water but freshwater accounts for only less than 2.7% [5]. The increasing human population, urbanization, rapid industrialization and expanding food production are all putting pressure on water resources, especially in developing countries as a source of provision for safe drinking and irrigation purposes. The challenge of water quality has become a global issue, in many developing countries. According to Obire and Aguda [6], in most developing countries including Nigeria, anthropogenic activities of different kinds such as bathing and washing, indiscriminate dumping of untreated waste including human feaces around the shoreline and into nearby rivers and streams, direct discharge of untreated or raw municipal and or industrial effluent into rivers and lakes, contaminate surface water directly and in turn contribute to increasing microbial pollution. Countries throughout the world are concerned with the effects of unclean drinking water because waterborne diseases are a major cause of morbidity and mortality [7]. Polluted surface waters can contain a large variety of pathogenic microorganisms including viruses, bacteria, and protozoa. These pathogens, often of faecal source, might be from point sources such as municipal wastewater treatment plants and drainage from areas where livestock are handled [8] or from non-point sources such as domestic and wild animal defecation, malfunctioning sewage and septic systems, storm-water drainage and urban runoff [9]. Fecal contamination of water is globally recognized as one of the leading causes of waterborne diseases. The potential of drinking water to transport microbial pathogens to great numbers of people, causing subsequent illness, is well documented in countries at all levels of economic development [9].

According to the World Health Organization [10], diarrheal disease accounts for an estimated 4.1% of the total daily global burden of disease and is responsible for the deaths of 1.8 million people every year. In Nigeria, cases of water-related diseases abound. Agents of these diseases have been found to cut across various classes of organisms. However, most of these cases are not documented since the majority of the affected individual subscribes to self-medication rather than seek professional medical attention. The most common waterborne diseases in Nigeria include Cholera, Dracunculiasis, Hepatitis, and Typhoid [11]. Cases of water-borne diseases linked to contamination of drinking water with pathogens have also been reported in several towns [12]. Treatment of these diseases especially with antibiotics has become a burden as many of these pathogens responsible for this ailment have become resistant to antibiotics. Antibiotic resistance is a global problem, especially in developing countries; this condition increasingly compromises the outcome of various infections that were until recently, treatable and remain the common infections in Africa [13]. Due to the importance of Lobia creek to the indwellers especially as a source of drinking water and other domestic use including the source of the lively hood, it has become very important to investigate its water quality. A change in the distribution of species and diversity of aquatic population is a biological marker for measuring the stress on assimilative capacity or water quality. This has necessitated this present study of the impact of human activities on the population, distribution, diversity and antibiotic resistance of bacteria from Lobia creek. This study will also strengthen efforts by law enforcement agencies and community leaders to ensure strict compliance to policies, personal hygiene and waste management practices to avoid outbreak of epidemics from water pollution due to human activities.

Materials and Methods

Description of the Study Area

This research was carried out on surface water samples collected from Lobia Creek in Southern Ijaw region of Bayelsa State located in the central Niger Delta in Nigeria [14]. The Lobia Creek is about 85 km long with several communities located along its banks. The inhabitants are indigenous human population solely

engaged in the occupation of fishing activities and a few are traders who travel to larger cities to buy foodstuff and other commodities for sale in Lobia. The communities along the creek engage in similar economic activities and so they generate similar waste and adopted the same method of disposal.

The geographic coordinates of Lobia are Latitude (width): 4°39'23.8"N (4.6566100°) and Longitude (length) 5°48›38.9»E (5.8108100°). Distances from Lobia to equator (0° lat) is 516 km north of the equator to prime meridian (0° lon) is 645 km east of the prime meridian. The sampling stations were along the Lobia Creek area where Lobia communities are located.

Description of sample stations on lobia creek

The peculiar nature and sources of pollution from human activities along the study creek was the major factor that influenced the choice of sampled stations in this study. Five stations were chosen and designated as station 1, station 2, station 3, station 4, and station 5 respectively, for the purpose of this study. The choices of stations were based on sites where waste materials from human activities are channeled into or directly deposited into the creek. Station 1 is a toilet on wood planks where raw human feaces and urine are directly discharged by residents around the creek into the surface water without treatment, station 2 is a jetty where marine boats related and other anthropogenic activities are being carried out along the creek, station 3 is a fish abattoir dumpsite point where fishes are being slaughtered and many organic wastes are deposited, station 4 is the drinking water point where people around the creek use canoes to get water for domestic consumption. Station 5 is the last station and is located downstream to all other stations. It is located about 300 meters away from station 4 and is free of any human activities hence use as a control station. The sampled stations in the Lobia creek are captured in figure 1.

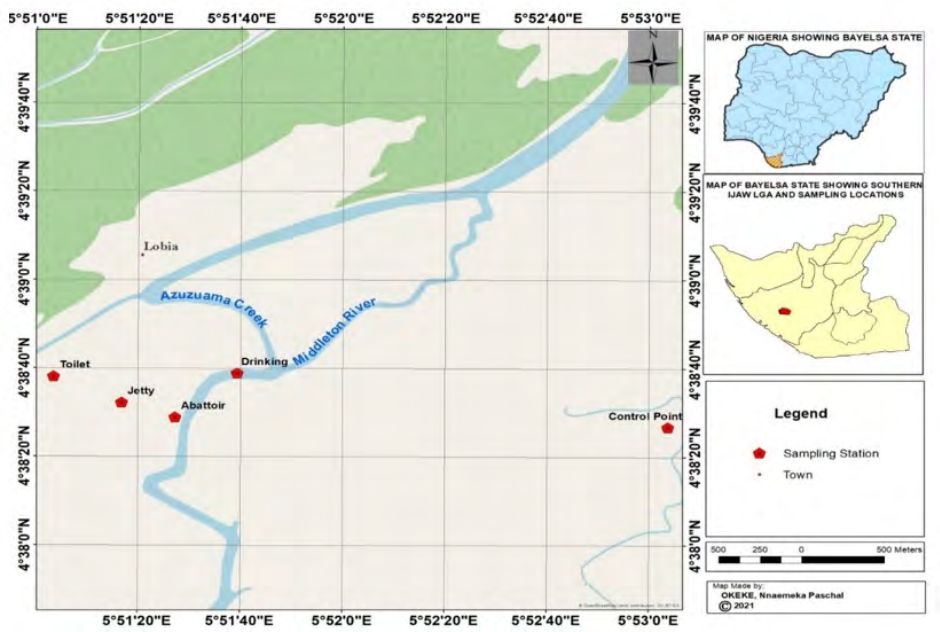

Figure 1: Map of the Study Area (Source: Research field survey, 2021).

Collection of water samples from stations

Prior to sample collection, sample bottles were sterilized by autoclaving at 121ºC for 15 minutes at 15psi. During the collection of the samples, the necks of the bottles were slightly tilted upwards towards the water current. The bottle was allowed to get filled and the cover was replaced while still underwater [15]. Methods adopted in the collection of water samples were in accordance with APHA [16]. Collected samples in sample bottles were appropriately labeled with the station code number immediately after collection at each station, and stored in a portable cooler box containing an

ice pack before transporting to the laboratory for analysis. Two (2) samples were collected from each station and a total of 10 samples were collected during each visit from the five stations. A total of 60 creek water samples were collected and analyzed during the six months sampling period from August 2020 to January 2021.

Microbiological analyses of water samples

Serial dilution

One millilitre each of the water samples was separately added to 9 ml of normal saline (diluents). After thorough shaking, further serial 10-fold (v/v) dilutions were made by transferring 1 ml of the diluted water sample to another tube of sterile normal saline (diluents) to a range of 10^{-3} dilutions [17].

Enumeration and isolation of microorganisms

The total heterotrophic bacteria, coliform, and faecal coliform were enumerated by inoculating aliquot (0.1ml) of 10^{-3} and 10^{-2} dilutions on Nutrient agar, MacConkey agar, and Eosin Methylene Blue agar in duplicates. The inoculated plates were incubated at 37^0C for the total heterotrophic bacteria and coliform while the plates for faecal coliforms were incubated at 45.5^0C. All bacterial plates were incubated for 24-48 hours [17]. After incubation, plates were observed for growth. The colonies which developed on the plates were counted and recorded so as to estimate the respective populations of the microorganisms [4] while discrete colonies on plates were also sub-cultured on nutrient agar plates.

The colony-forming unit per millilitre was calculated using the formula below;

CFU/ml = -------1

Purification of isolates

After incubation, pure isolates were obtained by picking (with a sterile inoculating loop) discrete culturally and morphologically different colonies from the various plates. These were subjected to streaking on sterile nutrient agar plates for bacterial isolates. Incubation at the required temperature and period was carried out as described above for the plates. This was done repeatedly until pure colonies void of contaminants and mixed cultures were obtained. Pure bacterial isolates were stored frozen in bijou bottles containing sterile 5 ml 10% glycerol. Stored isolates were subcultured and 24 hours old cultures were always used for further identification and antibiotic sensitivity test. Pure bacterial isolates were identified using biochemical and morphological characteristics. Tests such as oxidase test, Catalase test, Indole test, methyl red test, Voges Proskauer test, Starch hydrolysis test, Urease test, Citrate test, Sugar fermentation and Triple sugar iron agar test were carried out as described by Cheesbrough [15]. Gram staining and motility tests were also performed on the pure bacterial isolates to reveal their morphological characteristics.

Antibiotic susceptibility testing

The antibiotic susceptibility patterns of the isolates to common antibiotics were evaluated using the Kirby Bauer disc diffusion technique and 0.5 MacFarland's (1.5×10^8/ml) was employed in the standardization of inoculum according to the recommendations of the CLSI [18]. Peptone water (0.1%) diluent was prepared. Five discrete colonies of the different identified isolates were inoculated into 5 ml of the broths and incubated at 35°C for 4 - 6 hours. The inoculum for primary sensitivity testing was prepared from a broth that has been incubated for 4 - 6 hours. The density of the suspension was adjusted by adding the bacterial suspension to a 4ml sterile saline tube to match the density of the desired 0.5 McFarland standard. Each of the isolates was uniformly and aseptically inoculated into a different labeled Mueller-Hinton agar by swabbing the surface of the dried Mueller-Hinton agar plates with the respective inoculum suspension. Inoculated plates were allowed to dry for 3minutes before appropriate antibiotic discs (abtek commercial antibiotics) were aseptically placed on the agar using sterile forceps. The plates were then incubated at 37^0C for 24 hours. Interpretation of results was done using the zones of inhibition sizes as recommended by CLSI [18].

Statistical analyses

Statistical analyses were carried out using one-way ANOVA and mean separation was done using Tukey-Kram. The mean and standard deviation of the microbial counts including the percentages of occurrence and percentage susceptibility to antibiotics were obtained through descriptive statistics. All analysis was done on SPSS (version 25).

Results

Bacterial load of sampling stations along lobia creek

Results of the counts of total heterotrophic bacterial (THB), total coliform and feacal coliform obtained from the five (5)

sampled stations within Lobia Creek are as presented in table 1. Results showed that the THB bacteria count from the Creek water samples ranged from 3.6 ± 4.24×10^5 CFU/ml to 1.44 ± 2.28×10^6 CFU/ml. The toilet station had the highest count while the control had the least THB counts. The Total coliform count ranged from 1.8×10^4 to 7.6×10^4 CFU/ml while the feacal coliform count ranged from 7.0×10^2 to 3.8×10^4 CFU/ml. Similarly, the coliform and faecal coliform were highest in the water samples obtained from the toilet station while the least coliform and faecal coliform count was recorded in the control and drinking water samples, respectively.

Parameter	Microbial Load (CFU/ml) Sampling Station				
	Toilet	Jetty	Abattoir	Drinking	Control
Total Heterotrophic Bacteria	1.44 ± 2.28×10^{6a}	7.9 ± 0.02×10 ^{4abc}	1.10 ± 0.49×10 ^{6cd}	3.9 ± 0.9×10 ^{4a}	3.6 ± 0.04×10 ^{4a}
Total Coliform	7.6 ± 0.28×10^{4d}	3.1 ± 0.99 ×10 ^{4abc}	5.0 ± 0.57×10 ^{4cd}	2.7 ± 0.14×10 ^{4a}	1.8 ± 0.28×10 ^{4a}
Feacal Coliform	3.8 ± 0.57 ×10 ^{4b}	1.5 ± 0.42×10 ^{4a}	2.1 ± 0.42×10 ^{4a}	9.0 ± 0.14×10 ^{2a}	7.0 ± 0.21×10 ^{2a}

Table 1: Bacterial Load (Population) Variation in Stations along Lobia Creek.

Mean with different superscript (^{abcd}) shows significant difference along columns (P ≤ 0.05).

The distribution and frequency of occurrence of the bacterial isolates from the water samples of stations along Lobia Creek are presented in table 2. A total of 320 bacteria were isolated during the study and their percentage of occurrence were: *Bacillus* sp (12.66%), *Enterobacter* sp (14.6%), *Enterococcus* sp (2.6%), *E. coli* (12%), *Klebsiella* (10.4%), *Micrococcus* sp (2%), *Proteus* sp (6.8%), *Pseudomonas* sp (7.8%), *Serratia* sp (2.27%), *Shewanella* sp (1.3%), *Shigella* sp (3.9%), *Staphylococcus* sp (18.8%), and *Vibrio* sp (4.87%) as shown in figure 2. *Staphylococcus* species had the highest frequency while *Shewanella* sp had the lowest frequency across the five sampled stations of Lobia Creek. However, *E. coli* was the most dominant bacterial isolate in the toilet station. *Bacillus* sp was dominant in both the Drinking water station and Abattoir station while *Staphylococcus* sp was the dominant bacterial isolate in the jetty and control station.

Bacterial Isolate	Occurrence of Bacteria in the sampling Stations						
	Toilet	Jetty	Abattoir	Drinking	Control	Total Frequency	(%)
Bacillus sp.	8	3	13	12	3	39	12.66
Enterobacter sp	23	8	10	3	1	45	14.6
Enterococcus sp.	8	0	0	0	0	8	2.6
Escherichia coli	25	0	12	0	0	37	12
Klebsiella sp.	15	7	10	0	0	32	10.4
Micrococcus sp.	0	6	0	0	0	6	2
Proteus sp.	6	0	10	2	3	21	6.8
Pseudomonas sp	8	4	12	0	0	24	7.8
Serratia sp	7	0	0	0	0	7	2.27
Shewanella sp.	0	0	0	4	0	4	1.3
Shigella sp.	8	4	0	0	0	12	3.9
Staphylococcus sp	20	7	15	6	10	58	18.8
Vibrio sp.	5	2	8	0	0	15	4.87
Total	133	41	90	27	17	308	

Table 2: Distribution, Diversity and Frequency of Bacteria in Stations of Lobia Creek.

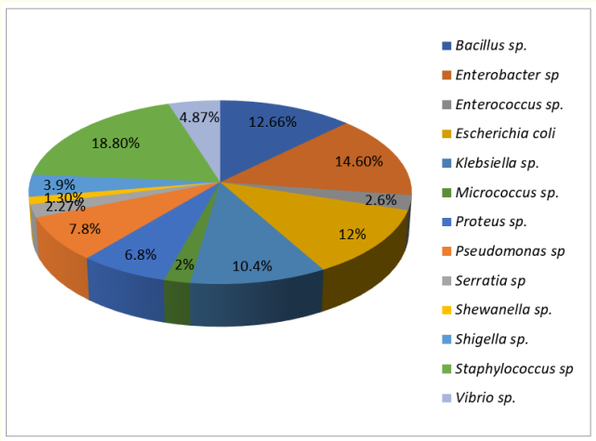

Figure 2: Percentage occurrence (%) of the bacterial isolates from Lobia Creek.

Antibiotic sensitivity of bacterial isolates from the five sampled stations of lobia creek

The susceptibility pattern of the Gram-positive bacteria isolates to Ceftazidime (30 µg), Cefuroxime (30 µg), Gentamycin (10 µg), Ceftriaxone (30 µg), Erythromycin (5 µg), Cloxacillin (5 µg), Ofloxacin (5 µg), and Augmentin (30 µg), respectively is as shown in table 3. While table 4 shows the results of antibiotic sensitivity pattern of Gram-negative bacteria isolates to Ceftazidime (30 µg), Cefuroxime (30 µg), Gentamycin (10 µg), Cefixime (5 µg), Ofloxacin (5 µg), Augmentin (30 µg), Nitrofurantoin (300 µg), and Ciprofloxacin (5 µg). Results showed the varied responses of the isolates to the antibiotics used in this study.

Antibiotic	***Staphylococcus* species N = 30**			***Micrococcus* species N = 16**			**Overall sensitivity report for the Gram positive bacteria (N = 46)**		
	S	I	R	S	I	R	S	I	R
Ofloxacin (OFL)	30(100)	0(0)	0(0)	16(100)	0(0)	0(0)	46(100)	0(0)	0(0)
Augmentin (AUG)	15(50)	15(50)	0(0)	0(0)	0(0)	16(100)	15(32.6)	15(32.6)	16(34.8)
Cetazidime (CAZ)	15(50)	15(50)	0(0)	6(37.5)	10(62.5)	0(0)	21(45.6)	25(54.3)	0(0)
Gentamicin (GEN)	15(50)	0(0)	15(50)	0(0)	0(0)	16(100)	15(32.6)	0(0)	31(67.4)
Erythromycin (ERY)	0(0)	15(50)	15(50)	16(100)	0(0)	0(0)	16(34.8)	15(32.6)	15(32.6)
Cloxacillin (CXC)	0(0)	0(0)	30(100)	4(25)	2(12.5)	10(62.5)	4(8.7)	2(4.4)	40(86.9)
Cefuroxi (CRX)	0(0)	0(0)	30(100)	0(0)	0(0)	16(100)	0(0)	0(0)	46(100)
Ceftriaxone (CTR)	30(100)	0(0)	0(0)	16(100)	0(0)	0(0)	46(100)	0(0)	0(0)

Table 3: Antibiotics sensitivity profile of the Gram's Positive isolates.

Key: Numbers in parenthesis are the percentage of Response by the Respective organisms to various antibiotics, Numbers in the Table are the frequency of the respective organism's response to various antibiotics, S = Susceptibility, I = Intermediate and R = Resistant

Antibiotic	***Vibrio* sp. N = 21**			***E. coli* N = 13**			***Pseudomonas* sp. N = 20**			***Proteus* sp. N = 18**			**Overall sensitivity report for the Gram-negative bacteria (N = 72)**		
	S	I	R	S	I	R	S	I	R	S	I	R	S	I	R
Ceftazidime	0(0)	0(0)	21(100)	0(0)	0(0)	13(100)	0(0)	4(20)	16(80)	0(0)	0(0)	18(100)	0(0)	4(5.6)	68(94.4)
Cefuroxime	0(0)	0(0)	21(100)	0(0)	0(0)	13(100)	2(10)	4(20)	14(70)	0(0)	0(0)	18(100)	2(2.7)	4(5.6)	66(91.7)
Gentamicin	0(0)	6(28.6)	5(71.4)	1(7.7)	5(38.5)	11(46.2)	3(15)	5(25)	12(60)	2(11.1)	4(22.2)	12(66.7)	6(5.6)	20(27.8)	46(63.9)

Cloxacillin	0(0)	0(0)	21(100)	0(0)	0(0)	13(100)	0(0)	0(0)	20(100)	0(0)	0(0)	18(100)	0(0)	0(0)	72(100)
Ofloxacin	21(100)	0(0)	0(0)	13(100)	0(0)	0(0)	20(100)	0(0)	0(0)	18(100)	0(0)	0(0)	72(100)	0(0)	0(0)
Augmentin	5(23.8)	0(0)	16(76.2)	4(30.8)	2(15.4)	7(53.8)	2(10)	0(0)	18(80)	5(27.8)	3(16.7)	10(55.5)	16(22.2)	5(6.94)	51(70.8)
Ceftriaxone	21(100)	0(0)	0(0)	13(100)	0(0)	0(0)	16(80)	2(10)	2(10)	18(100)	0(0)	0(0)	72(100)	2(0)	2(0)
Nitrofurantoin	21(100)	0(0)	0(0)	13(100)	0(0)	0(0)	20(100)	0(0)	0(0)	18(100)	0(0)	0(0)	72(100)	0(0)	0(0)

Table 4: Antibiotics sensitivity profile of the Gram's Negative isolates.

Key: Numbers in parenthesis are the percentage of Response by the Respective organisms to various antibiotics, Numbers in the Table are the frequency of the respectorganism's response to various antibiotics, S = Susceptibility, I = Intermediate and R = Resistant.

Discussion

The present study has revealed the population and diversity of bacteria in Lobia creek water. From the results obtained reliance on this surface water source by the rural communities without water treatment facilities and basic hygienic practices therefore could pose a serious public health risk, especially where there are no other alternative water sources for most rural communities of Lobia in Bayelsa State, Nigeria. The health of the aquatic ecosystem especially the Lobia Creek can be negatively affected by the presence of toxic substances due to various activities around the creek. Generally, for measuring water quality, the microbiological analyses (fecal coliform, total coliform, and enterococci count) are usually performed [19]. The most significant contaminant when it comes to human health are microorganisms that come into the water from human and animal excreta, mainly due to the unhygienic disposition of wastewater. Despite that it is an essential commodity. Access to safe drinking water in many parts of the world has been threatened basically due to the contamination of water by human activities [10,19].

Results of the present study showed that counts (population) of total heterotrophic bacteria, coliform, and faecal coliforms ranged from 3.6×10^4 cfu/ml - 1.44×10^6 cfu/ml, 1.8×10^4 - 7.6×10^4 cfu/ml and 7.0×10^2 - 3.8×10^4 cfu/ml respectively. Generally, the decreasing order of the microbial population of total heterotrophic bacteria, coliform and faecal coliforms in the various locations was; Toilet > Abattoir > Jetty > Drinking water > Control. Statistical analysis showed that there were significant differences ($P < 0.05$) between the microbial counts recorded for the control and the other stations. The highest microbial populations of total heterotrophic bacteria, coliform, and faecal coliforms were recorded in toilet station where the residents around the Creek used for defecation. Here, raw human feaces are discharged directly into the creek. The fish abattoir has a waste dump and other decomposable organic wastes are present, compared to stations 4 and 5 which are free of any noticeable activities. The variation in bacterial load or population depends on the source of discharge and its constituents which have the ability to influence the microbial load. The result of this study is in accordance with the work reported by Mandri and Lin [20] and Khan and Rizvi [21] who worked on surface water at different stations where various anthropogenic activities are carried out [22].

The health of the aquatic ecosystem can be negatively affected by the presence of toxic substances. This is further exacerbated by the high population of potential pathogens in the water. The use of microbiologically contaminated water for domestic and other purposes is detrimental to human health and society at large [23]. The results of microbial count (population) of surface water samples from the five sampling stations of Lobia Creek revealed that the mean values of total heterotrophic bacterial, total coliform and Feacal coliform counts obtained from the five (5) sampled stations within Lobia Creek were significantly higher across the five stations. Station 1 recorded the highest microbial load followed by the fish abattoir waste dump point, Jetty, and drinking stations while the control point which is free of any noticeable anthropogenic activities recorded the lowest counts. Mean separation using all pairs Turkey Kramer showed that there were significant differences ($P < 0.05$) in the microbial counts between the control and other stations. This indicated that the various human activities in all the other stations actually had a significant effect on the microbial quality and hence on water quality. Hence, the high microbial load recorded in this study could be attributed to the various human activities taking place in all the stations. The microbial counts recorded in this present study were far above interim standards for drinking water [10]. WHO [10] stipulated that total heterotrophic bacterial counts for drinking water must not be above 100 CFU/ml which total and faecal coliform must be 0 respectively.

According to the report of Obire., *et al.* [4], low DO values from sampling zone and stations as a result of high organic matter and nutrients can also enhance the increase in microbial populations that degrade organic matter. Obire and Aguda [6] reported high bacteria counts from leachate and an adjacent stream due to the high content of organic matter. High microbial counts (population) reported in this study for the different stations could be a reflection of the high level of pollution

influenced by the various anthropogenic activities on the banks of Lobia creek. High microbial counts are associated with the presence of a high nutrient load. Microorganisms of enteric origin are one of the most common pathogens encountered in the aquatic environments, including discharged municipal wastewater effluents as well as surface water. In this study, three hundred and eight (308) bacterial species belonging to thirteen (13) genera were isolated. The decreasing order of the number of bacterial general (diversity) isolated from the various locations was Toilet (11) > Abattoir and Jetty (8) > Drinking water (5) > Control (4). This change in the population, distribution of species and diversity of the bacteria is attributed to the stress on assimilative capacity or water quality by the human activity which occurred in each station. The bacteria isolated and their percentage of occurrence in parenthesis are as follows; *Bacillus* sp (12.66%), *Enterobacter* sp (14.6%), *Enterococcus* sp (2.6%), *E. coli* (12%), *Klebsiella* (10.4%), *Micrococcus* sp (2%), *Proteus* sp (6.8%), *Pseudomonas* sp (7.8%), *Serratia* sp (2.27%), *Shewanella* sp (1.3%), *Shigella* sp (3.9%), *Staphylococcus* sp (18.8%), and *Vibrio* sp (4.87%). These bacteria isolates are potential pathogens capable of causing various diseases. The presence of faecal coliforms especially *E. coli* which is used as an indicator of fecal contamination of water is universally accepted to indicate faecal contamination and possible presence of other pathogenic organisms [17]. Although the vast majority of *E. coli* are completely harmless, some strains of the bacteria have acquired genetic capabilities which enable them to encode virulence factors [24]. Pathogenic *E. coli* strains cause diverse forms of bacterial-induced illnesses with symptoms ranging from mild diarrhoea to severe complications and even death [25]. The presence of total and faecal coliform in the drinking water and Control stations indicated that Lobia creek is highly polluted with potential pathogens which suggested that the water is not potable. Thus, not fit for drinking without prior treatment.

The microorganisms isolated from the Lobia Creek may have entered the water through the waste dump during run-off and leaching, and direct discharges at station 1 (toilet). This supports the findings of Obire and Aguda [6] that the organisms isolated in their study may have found their way into the water through leachate from an open waste dump. Most of these bacteria are potential pathogens that can be acquired through the drinking of water polluted by these organisms. Most waterborne diseases that can result from drinking water polluted by these organisms ranged from gastro-intestinal tract infections that can be caused by *E. coli, Vibrio* sp., *Enterobacter* sp., *Enterococcus* sp., *Proteus, Pseudomonas* sp., *Serratia* spp., and *Shewanella* species which are known to cause urinary tract infections in the young and elderly. Other diseases they cause include wound and skin infections, respiratory infections, food poisoning, and others.

In this study, the overall antibiotics susceptibility analysis done on the Gram's negative and positive isolate showed varying patterns to specific antibiotics. The Gram's negative organisms tested showed high susceptibility to Ceftriaxone (CTR), Nitrofurantoin (NIT), and Ofloxacin (OFL). A total of 72 Gram-negative isolates showed 100% sensitivity to Ofloxacin, Ceftriaxone, and Nitrofurantoin. A total of 72 (100%) isolates were resistant to Cloxacillin while 68 (94.4%) were resistant to Ceftazidime. However, Lower susceptibility of 22.2%, 5.6% and 2.7% were recorded for Augmentin, Gentamycin, and Cefuroxime, respectively. All Gram's negative organisms isolated in this study were completely (100%) resistant to Cloxacillin. Likewise, non was sensitive to Ceftazidime (CAZ) but an intermediate of 5.6% and 94.4% resistance profile was recorded for the antibiotic. Differing Gram's negative bacterial resistance profiles of 94.4%, 91.7%, 70.8%, and 91.7% were recorded for Ceftazidime, Cefuroxime, Augmentin, and Gentamycin, respectively. In terms of an individual response, the Grams negative isolates such as *Vibrio* spp*., Escherichia coli,* and *Proteus* spp*.* were totally resistant to at least three (3) of the antibiotics used while *Pseudomonas* spp*.* was most susceptible showing total resistance 72(100%) to only Cloxacillin and over 50% susceptibility to at least three (3) other antibiotics tested. Likewise, the overall antibiotics resistance analysis done on the two Gram's positive isolates showed a more varying susceptibility and resistance profile compared to the Gram's negative isolates. A total susceptibility of 46(100%) was recorded for Ceftriaxone and ofloxacin with both species showing a joint 86.9% and 67.4% resistance to cloxacillin and gentamycin. However, sixteen *Micrococcus* sp*.* showed 100% resistance to Gentamycin and Augmentin with an alternate susceptibility of 100% to Erythromycin. *Staphylococcus* sp*.* and *Micrococcus* sp showed a 50:50 resistance to susceptibility ratio to gentamycin and a 50:50 sensitivity and intermediate sensitivity to Augmentin. This resulted to the overall Gram's positive bacterial 32.6% susceptibility to gentamycin and Augmentin with a corresponding 67.4% and 34.8% resistance pattern.

Antibiotics have over the decades been used for both human and animal disease treatment. They are however continuously found in the environment due to poor metabolism in the body. Several studies have reported a lack of tangible relationship between anthropogenic activities and antibiotic resistance in bacteria and many believe that the elements that select for resistance are naturally present within the microbial genome [26]. On the other hand, evidence abounds that increased bacterial resistance to antibiotics and the transfer of resistant elements is a modern phenomenon having a strong link with anthropogenic activities [27-29]. Besides the human health risks posed by the presence of antibiotic-resistant bacteria in the environment, and the unwanted presence of antibiotics in water bodies, concern for the ecological fate and environmental threat of these drugs in the aquatic milieu is becoming a global phenomenon [29]. Bacterial resistance to antibiotics has been considered a global public health menace. Different kinds of antibiotic-resistant bacteria (ARB) are continuously detected in various environments ranging from aquatic to terrestrial ones. There is a high possibility of resistance being spread by ARB from the environment to related human pathogenic microorganisms through numerous routes thereby suppressing the effectiveness of antibiotics [30].

Conclusion

The microbial parameters determined for the Lobia creek water have helped to ascertain the microbiology of the water quality and hence the potability. The dynamic nature of the creek water and human activities along the bank of the creek, irrespective of the stations considered account for the uneven distribution and fluctuations in the microbial counts examined. The results obtained in this study showed that human activities around and within Lobia creek could have a significant effect on the microbiological characteristics of the creek and the potability of the water. The presence of coliforms especially faecal coliforms across all the five stations including the drinking and control point indicated a high level of faecal contamination of the water body. Most of the microorganisms isolated are known potential pathogens of various diseases affecting man and other animals. Moreover, the presence of *Escherichia coli* which is an indicator of faecal pollution and other coliform organisms is sufficient to conclude that the water is highly polluted with pathogenic organisms able to initiate different enteric diseases. Lobia creek water is therefore microbiologically unsafe for drinking. Thus, there should be protection of the bank and creek water. Outreach and enlightenment campaigns should therefore be carried out to educate the inhabitants on proper sanitary or hygiene practices and proper disposal of wastes. More so, proper treatment measures that are capable of eliminating bacteria from the water should be done before the water from Lobia creek can be used for drinking and any domestic purpose for which it is currently being used. Ceftriaxone, Nitrofurantoin, and Ofloxacin which were the most active antibiotics are therefore the drug of choice and recommended for the treatment of infections or diseases caused by bacterial isolates from these stations. This study has shown that, Lobia creek is highly polluted and not fit for consumption without proper treatment. It is therefore advocated that the Government should provide potable water for the inhabitants of Lobia community as to mitigate the public health hazard that the consumption of the raw creek water poses to the inhabitants.

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