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Microbiological evaluation and antimicrobial resistant pattern of bacteria isolated from surface drinking water sources in Ogbomoso, Oyo State, Nigeria

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Abstract

Water is vital for life, but in contrast, it might serves as the commonest route of transmission for many infectious diseases. This study was carried out to examine the quality of drinking water from two selected surface water within Ogbomoso. Water samples were collected from both water bodies at different points. Most Probable Number (MPN) techniques and pour plate method were used to estimate the bacteriological quality of water samples. The antibiotic sensitivity test was carried out on the isolated organisms, while heavy metals parameters were assessed with standard methods. Water samples were analyzed for faecal sterols. Results of MPN counts (49 to 1600 MPN per 100ml) and total heterotrophic counts (0.15×10^6 to 1.36×10^7 CFU/mL) revealed a high level of microbial pollution. Ten genera of bacteria; *Shigella, Corynebacterium, Streptococcus, Pseudomonas, Staphylococcus, Escherichia, Salmonella, Vibrio, Citrobacter* and *Klebsiella* were isolated and they all showed multiple antibiotic resistant (MAR) to all the antibiotics used. The multiple antibiotics resistant (MAR) index ranged from 0.63 to 0.75 and 0.63 to 0.88 for the isolates from Papa –Osiagoro and Oke- Baaki water works respectively. The heavy metals analyzed fell within the limits set by Nigerian Standards for potable waters with exception of Zn which had high concentrations across the sampling points. Water samples showed the presence of high concentrations of feacal sterols. The presence of coliforms and other pathogenic organisms present in these surface water bodies have shown that they are highly contaminated. Thus, the water is not fit for human consumption due to feacal contamination.

Keywords: Ogbomoso, Microbial pollution, Antibiotic resistance, Heavy metals, feacal sterols

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Introduction

Groundwater, surface water, atmospheric water, and springs are the main sources of water available to people; the portability being determined by its quality (Shittu et. al., 2008; Olatunde and Ayandele, 2018). The quality of any of these sources is an indicator of the attitude and socioeconomic condition of its users as well as the environmental conditions (Rajiv et. al., 2012).

Although water is vital for life, but it can serves as the commonest route of transmission for a number of infectious diseases. Therefore, maintaining a good quality surface water supply that is free of microbial and chemical pollution is rare (Johnson et. al., 2016). The major causes of water pollution are the waste generation, increased industrial development, and urbanization in the municipality. Most importantly, the problem of inadequate trained waste disposal personnel and equipment, poor waste collection, inadequate solid waste disposing methods, improper functioning septic tank systems contribute greatly to pollution (Adetunde et. al., 2011). Over two million deaths occurred annually due to waterborne diseases (WHO, 2000). Bacteria, protozoa and viruses are the major causative water-borne pathogenic organisms (Samy et. al., 2016), while typhoid fever, bacillary dysentery, salmonellosis,

Escherichia coli infections, campylobacteriosis, botulism, cholera, legionnaire's disease, leptospirosis and others are the most common water-borne bacterial diseases (Lee et. al., 2002).

The development of bacterial resistance to antibiotics is increasing daily and this is linked to anthropogenic activities (Knapp et. al., 2010; Bhullar et. al., 2012). The presence of antibiotic-resistant bacteria in the environment is becoming a global phenomenon and this poses a great threat to human health, and there is also a concern for the ecological fate and environmental pollution of these drugs in the aquatic environment (Ayandiran et. al., 2014). Multiple bacterial resistant to drugs has been reported in aqua-culture environments (Hatha et. al., 2005).

Researchers are also focusing on studies of heavy metals in rivers, lakes, fish and sediments in these last decades (Ali and Fishar, 2006). Because pollution of water bodies by trace metal ions is a major environmental problem. Heavy metals are of great concern because of their toxicity to living things and their persistence in the environment (Khali et. al., 2007). Metals ions in the environment can get into the food and water and bioaccumulation of heavy metals in the human bodies has been linked with many diseases like nervous system disorders, negative effects on reproductive systems and other body systems disorders (Khali et. al., 2007).

Water bodies are being polluted each day by feacal matter both from animals and humans. Different methods have been used for determination of feacal matter in water bodies but determination of sterols and its derivatives in water samples is the most reliable and acceptable human biomarkers for indication of feacal pollution (Gerardo et. al., 2000). Sterol derivatives, such as coprostanol mainly come from human feaces and it has been applied successfully to trace the degree of environmental stability in relation to feacal contamination (Farawati et. al., 2009). Due to an inappropriate discharge of human waste in dams, the detection of sewage pollution in water bodies is therefore of considerable importance for health, aesthetic and ecological reasons.

Provision of adequate and clean water supply to everyone by the government has necessitated the development of dams for rural water supply in developing countries. Reservoirs created by dams not only suppress floods but also provide water for activities such as irrigation, human consumption, industrial use, and navigability. However, human activities like indiscriminate disposal of waste and use of river banks for open defecation might lead to microbial pollution. Hence, it has become necessary to investigate the quality (microbial and chemical) of selected surface water in Ogbomoso Township to serve as baseline data for future research since people are using water collected from such directly without treatment for domestic and agricultural purposes due to water shortage.

Materials and Methods

Study area

The study was conducted on Oke-Baaki dam and Papa-Osiagoro waterworks located at Owode and Orisunbare communities in Ogbomoso, South West Nigeria respectively ($8^0$32'25"N to $4^0$16'18"E and 8^0 10'25" N to 4^0 11'55"E). Fig. 1 shows the map of the study area. The principal occupation of the population is farming, petty trading, artisans, and teaching.

Figure 1: Map of Nigeria showing Ogbomoso (Oyo State)
Source: http://www.nairaland.com (2014)

Sampling Sites

Water samples were taken from three different points designated by A1, A2, A3, B1, B2 and B3 from both Oke-Baaki dam and Papa-Osiagoro waterworks. Water sampling was carried out in July 2017. Samples were collected following the standard sampling procedures (WHO, 2011). The samples were taken into pre-sterilized bottles, kept in ice-boxes and transported immediately to the laboratory for heavy metal and bacteriological analyses. The two sampling sites were shown in Plates 1a and b.

Plate 1a: Oke–Baaki dam

Plate 1b: Papa-Osiagoro waterwork

Bacteriological analysis

Most Probable Number (MPN) technique was used to estimate microbial populations (Total Coliform) in water following presumptive test, confirmative test and completed test (APHA, 1998) while Total heterotrophic counts were carried out by standard plate count technique with the use of Salmonella-Shigella agar (SSA), Eosin Methylene Blue (EMB) agar and Mannitol Salt Agar (MSA). All media were prepared according to the manufacturer's instruction. Gram staining was used to check for morphology type of isolated bacteria. Characterization of isolates was determined by using biochemical tests which include; motility test, urease test, coagulase test, indole test, gelatin liquefaction, nitrate reduction, sugar fermentation test, MRVP, catalase, oxidation fermentation and citrate utilization for identification.

Antimicrobial susceptibility testing

Bacterial isolates were tested for their sensitivity to antibiotics using disc diffusion method on Mueller-Hinton agar plates and interpreted according to the recommendations of the Clinical and Laboratory Standards Institute (CLSI, 2014). Eight antibiotics were used, and these are Nitrofurantoin (10µg), Cefixime (5µg), Ofloxacin (5µg), Augmentin (30µg), Ciprofloxacin (5µg), Ceftazidime (30µg), Cefuroxime (30µg) and Gentamicin (10µg).

Heavy metal analysis

Heavy metals were analyzed according to the procedures outlined in the standard methods for the examination of water and wastewater for both the sediment and water samples (APHA, 1998; Elgobashy et. al., 2001; Franc et. al., 2005).

Extraction of Extractable Organic Matter (EOM) and faecal sterols

These were done following the methods of (Farawati et. al., 2009) with little modifications. Water samples for EOM estimation were collected in 250ml amber glass bottles. Glass vials were prepared accordingly. The sediment samples were first freeze and then dried before extracting with 25ml dichloromethane. The solvent was evaporated under vacuum on a rotary evaporator and the residue further dried under a stream of nitrogen to give the EOM.

The sterol derivatives were analyzed by gas chromatography using GC-Shimadzu 17-A (Radwan et. al., 2009). All the solvents used were of HPLC grade. Identification of the compounds was made by co-injection of the samples with authentic standards. Polycyclic aromatic hydrocarbons were estimated spectrofluorometrically and then finally analyzed by GC.

Statistical Analysis of the Results

Statistical analysis was carried out on the results obtained using standard deviation to determine values that are not significantly different according to according to Duncan's multiple range test ($p \leq 0.01$).

Results

Bacteria Count

The mean total heterotrophic (TH) bacteria and total coliform (TC) counts were shown in Table 1. For sampling sites A1 to A3 of Oke-Baaki dam, the bacterial population decreased from upstream to downstream on Nutrient agar but increased on other isolating media from upstream to downstream except in some cases. However, for sampling sites B1 to B3 of Papa-Osiagoro waterworks, bacterial count was between 4.9×10^{1} CFU/ml and 5.80×10^{6} CFU/ml. Results of MPN count showed the bacterial count of between 49 and 1600 MPN per 100ml. The results showed that Papa-Osiagoro is more polluted than the Oke-Baaki water work.

Table 1: Mean Total Heterotrophic and Total Coliform counts of the water samples.

Sampling Points	Total Heterotrophic Count (TH) (cfu/mL)				Total Coliform Count (TC) (MPN/100ml)
	Growth on Nutrient agar (cfu/ ml)	Growth on MSA (cfu/ ml)	Growth on EMB (cfu/ ml)	Growth on SSA (cfu/ ml)	
A1	$1.36 \times 10^{7} \pm 0.01^{a}$	$6.4 \times 10^{6} \pm 0.10^{e}$	$5.0 \times 10^{5} \pm 0.44^{c}$	$3.0 \times 10^{5} \pm 0.10^{d}$	160 ± 5.0^{f}
A2	$5.4 \times 10^{6} \pm 0.40^{c}$	$9.8 \times 10^{6} \pm 0.02^{f}$	$1.25 \times 10^{7} \pm 0.05^{a}$	$6.3 \times 10^{6} \pm 0.02^{f}$	180 ± 2.0^{c}
A3	$8.0 \times 10^{5} \pm 0.30^{d}$	$1.05 \times 10^{7} \pm 0.05^{a}$	$8.2 \times 10^{6} \pm 0.20^{d}$	$5.0 \times 10^{5} \pm 0.05^{e}$	350 ± 1.0^{d}
B1	$3.45 \times 10^{6} \pm 0.05^{b}$	$2.90 \times 10^{6} \pm 0.03^{d}$	$1.5 \times 10^{6} \pm 0.02^{ab}$	$2.85 \times 10^{6} \pm 0.02^{c}$	49 ± 2.0^{a}
B2	$5.80 \times 10^{6} \pm 0.01^{c}$	$2.0 \times 10^{5} \pm 0.03^{c}$	$1.95 \times 10^{6} \pm 0.01^{b}$	$1.95 \times 10^{6} \pm 0.01^{a}$	160 ± 4.0^{b}
B3	$3.60 \times 10^{6} \pm 0.04^{b}$	$1.80 \times 10^{6} \pm 0.01^{b}$	$1.5 \times 10^{5} \pm 0.02^{ab}$	$2.25 \times 10^{6} \pm 0.02^{b}$	920 ± 3.0^{e}

Value=Means ± standard deviation; values followed by the same superscript in the column are not significantly different according to Duncan's multiple range test ($p \leq 0.01$).

Bacteria isolation and Identification

Twenty four isolates within 10 genera were identified and characterized using both microscopic and morphological growth characteristics as well as biochemical tests.

From Oke-Baaki dam, the identified bacteria include *Corynebacterium kutscheri, Streptococcus pyogenes, Shigella flexneri* and *Pseudomonas aeruginosa*, at the upstream, *Staphylococcus aureus, Escherichia coli, Corynebacterium kutscheri* and *Shigella sonnei* the middle stream, *Corynebacterium kutscheri, Staphylococcus aureus, Escherichia coli* and *Klebsiella oxytoca* at the downstream.

From Papa-Osiagoro, the identified bacteria include *Staphylococcus epidermidis, Pseudomonas aeruginosa* and *E. coli* in the upstream, *Streptococcus pyogenes* and *Staphylococcus epidermis* in the middle stream, *Citrobacter freundii, Salmonella typhosa* and *Shigella dysentariae* in the downstream.

As shown in Fig. 2, E coli species were the most predominant (16.7%) bacteria found in the water samples followed by *Streptococcus pyogenes* and *Corynebacterium kutscheri* each with a frequency of 12.5%.

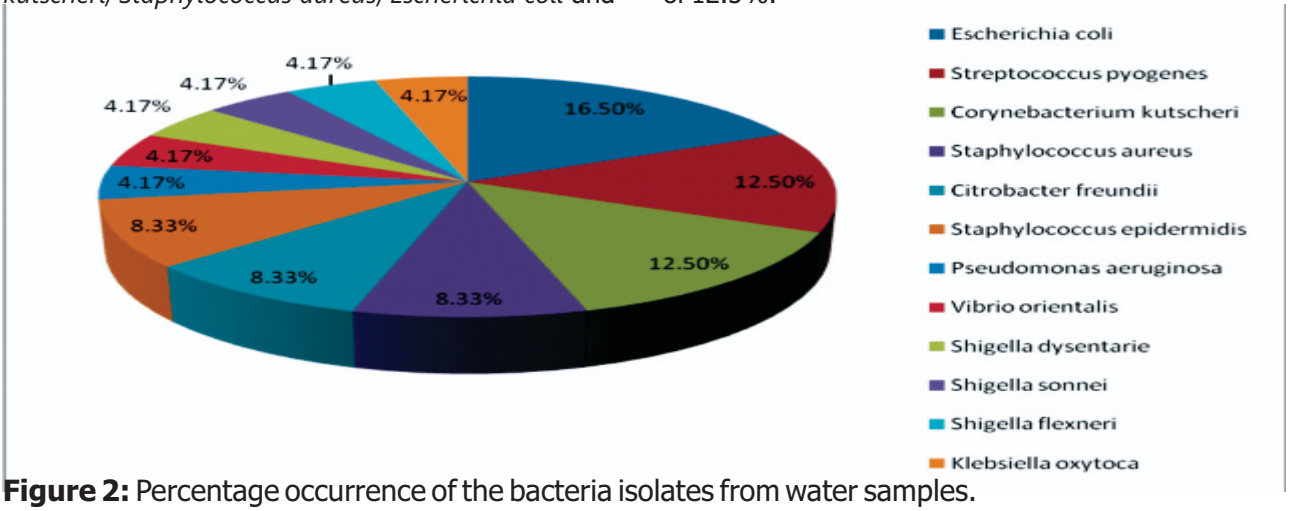


Figure 2: Percentage occurrence of the bacteria isolates from water samples.

Antimicrobial Testing

For Oke-Baaki dam, all the isolated bacteria showed 100% resistance to Cefixime, Augmentin, Ceftazidine, Cefuroxime, and Gentamicin. The same resistant pattern was found in the bacteria isolated from Papa-Osiagoro water works as shown in Tables 2 and 3. Also for Oke-Baaki dam, all the isolated bacteria in the downstream showed 100% resistance to ciprofloxacin (Table 2), however, all the bacteria were sensitive to ciprofloxacin in Papa-Osiagoro waterworks (Table 3). The results showed that all bacterial isolates showed multiple resistant of $\geq$ 5 to all the antibiotics used in this study. The multiple antibiotics resistant (MAR) index ranged from 0.63 to 0.75 and 0.63 to 0.88 for the isolates from Papa –Osiagoro and Oke-Baaki water works respectively. The percentage of antibiotics resistant ranged from 62.5 to 87.5% in Oke Baki dam, while that of Papa – Osiagoro ranged from 62.5 – 75.0 %.

Table 2: Antibiotics sensitivity pattern of bacteria isolated from Oke-Baaki Water-body

Sampling point	Probable organism	NIT	CXM	OFL	AUG	CPR	CAZ	CRX	GEN	% Of Resistance
A1	Corynebacterium kutscheri	I	R	S	R	S	R	R	R	62.5
	Streptococcus pyogenes	I	R	S	R	S	R	R	R	62.5
	Shigella flexneri	S	R	I	R	S	R	R	R	62.5
	Pseudomonas aeruginosa	R	R	S	R	S	R	R	R	75.0
A2	Staphylococcus aureus	I	R	S	R	S	R	R	R	62.5
	Escherichia coli	R	R	I	R	S	R	R	R	75.0
	Corynebacterium kutscheri	I	R	S	R	S	R	R	R	62.5
	Shigella sonnei	I	R	S	R	S	R	R	R	62.5
A3	Vibrio orientalis	R	R	I	R	R	R	R	R	87.5
	Corynebacterium kutscheri	S	R	S	R	R	R	R	R	75.0
	Staphylococcus aureus	I	R	S	R	R	R	R	R	75.0
	Escherichia coli	R	R	I	R	R	R	R	R	87.5
	Klebsiella oxytoca	S	R	S	R	R	R	R	R	75.0

Legend: R-Resistant, S-susceptible, I- intermediate Resistant, NIT- Nitrofurantoin, CXM-Cefixime, OFL-Ofloxacin, AUG-Augmentin, CPR-Ciprofloxacin, CAZ-Ceftazidine, CRX-Cefuroxime, GEN-Gentamicin.

Table 3: Antibiotics sensitivity pattern of bacterial isolated from Papa-Osiagoro Water body

Sampling point	Probable organism	NIT	CXM	OFL	AUG	CPR	CAZ	CRX	GEN	% of Resistance
B1	Staphylococcus aureus	S	R	S	R	S	R	R	R	62.5
	Pseudomonas a eruginosa	R	R	S	R	S	R	R	R	75.0
	Escherichia coli	R	R	I	R	S	R	R	R	75.0
B2	Streptococcus p yogenes	I	R	S	R	S	R	R	R	62.5
	Staphylococcus epidermidis	I	R	S	R	S	R	R	R	62.5
B3	Citrobacter freu ndii	I	R	I	R	S	R	R	R	62.5
	Salmonella typ hosa	S	R	S	R	S	R	R	R	62.5
	Citrobacter freu ndii	I	R	I	R	S	R	R	R	62.5
	Shigella dysent eriae	S	R	S	R	S	R	R	R	62.5

Legend: R-Resistant, S-susceptible, I- intermediate Resistant, NIT-Nitrofurantoin, CXM-Cefixime, OFL-Ofloxacin, AUG-Augmentin, CPR-Ciprofloxacin, CAZ-Ceftazidine, CRX-Cefuroxime, GEN-

Metal Analysis

The mean concentrations of the heavy metal (mg/L) from the sampling sites are presented in Table 4.The concentrations ranged from 0.01mg/L for Iron to 4.84mg/L for Zinc across the two sampling sites. But Nickel and Boron are not detected in any of the sampling sites.

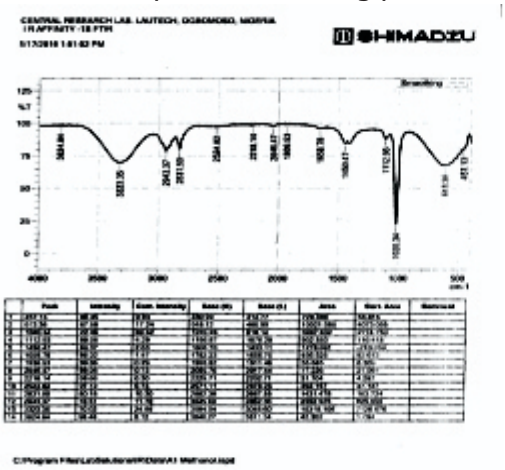
Table 4: Heavy metals analysis of the water samples

Heavy metals	WHO Standard (mg/L)	Nigeria Standard (mg/L)	Sample A1 (mg/L)	Sample A2 (mg/L)	Sample A3 (mg/L)	Sample B1 (mg/L)	Sample B2 (mg/L)	Sample B3 (mg/L)
Iron (Fe)	0.10	0.30	0.10 ± 0.01^{a}	0.12 ± 0.01^{ab}	0.11 ± 0.02^{a}	0.14 ± 0.01^{b}	0.14 ± 0.01^{b}	0.12 ± 0.01^{ab}
Zinc (Zn)	5.0	3.0	3.50 ± 0.04^{a}	3.44 ± 0.04^{a}	3.48 ± 0.02^{a}	4.80 ± 0.03^{b}	4.84 ± 0.02^{b}	4.82 ± 0.01^{b}
Lead (Pb)	0.10	0.01	0.01 ± 0.001^{a}	0.01 ± 0.002^{a}	0.02 ± 0.002^{b}	0.04 ± 0.001^{d}	0.03 ± 0.001^{c}	0.05 ± 0.002^{e}
Cadmium (Cd)	0.01	0.003	0.01 ± 0.002^{a}	0.01 ± 0.001^{a}	0.01 ± 0.002^{a}	0.03 ± 0.001^{b}	0.03 ± 0.002^{b}	0.03 ± 0.001^{b}
Copper (Cu)	0.05	1.0	0.03 ± 0.001^{b}	0.03 ± 0.002^{b}	0.025 ± 0.001^{a}	0.08 ± 0.002^{d}	0.08 ± 0.003^{d}	0.07 ± 0.001^{c}
Manganese(Mn	0.05	0.2	0.01 ± 0.001^{a}	0.01 ± 0.002^{a}	0.01 ± 0.001^{a}	0.03 ± 0.001^{b}	0.03 ± 0.002^{b}	0.03 ± 0.001^{b}
Chromium (Cr)	0.05	0.05	0.00 ± 0.0	0.00 ± 0.0	0.00 ± 0.0	0.001 ± 0.0	0.001 ± 0.0	0.001 ± 0.0
Boron (B)	0.00	0.00	0.00 ± 0.0	0.00 ± 0.0	0.00 ± 0.0	0.00 ± 0.0	0.00 ± 0.0	0.00 ± 0.0

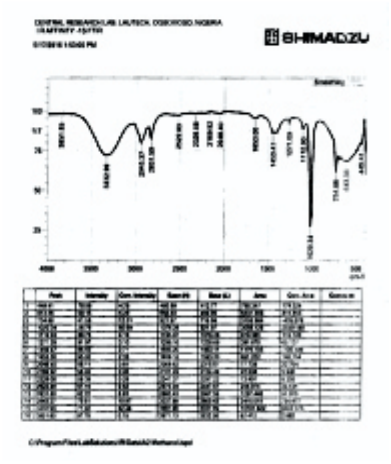
Value=Means ± standard deviation; values followed by the same superscript in the row are not significantly different according to Duncan's multiple range test ($p\leq0.01$).

Fourier Transform Infra-Red Spectroscopy (FTIR)

The FTIR results for Sample A1showed strong peaks at 3323.55, 2943.37,2831.50, 1470.47, 1020.34, 613.36 cm^{-1} as shown in Supplement 1 which shows that the biogenically synthesized methanol was capped and stabilized by proteins. For Sample A2 the strong peak was observed at 3332.99, 2943.37, 1450.47, 1020.34, 1271.09, 734.88cm^{-1} as shown in Supplement 2 which shows that the biogenically synthesized methanol was capped and stabilized by proteins. The band at 3332.99$cm^{-1}$is indicative of N-H stretch of 1°,2°amines..



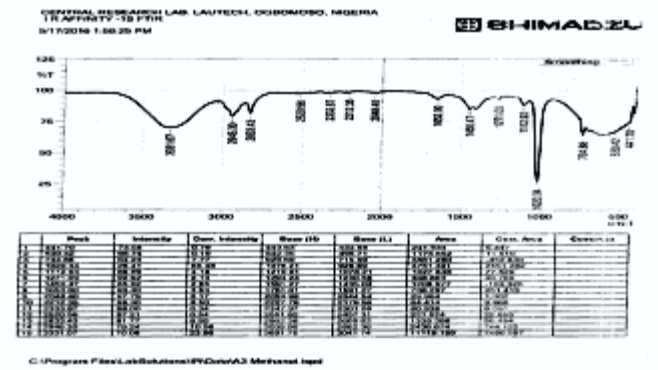
Supplement 1: Chromatogram for sample A1.



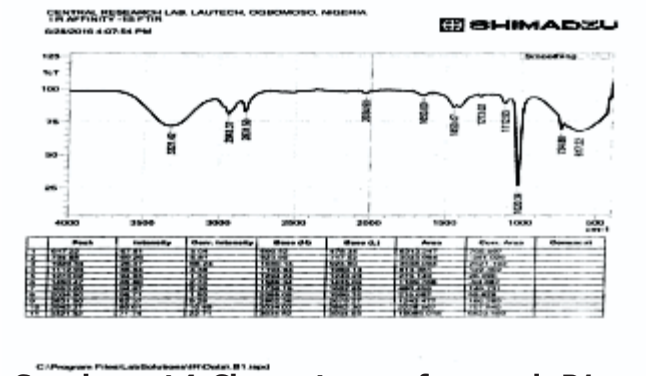
Supplement 2: Chromatogram for sample A2

For sample A3 the strong peak is observed at 3331.07, 2945.30, 1450.47, 1112.93, 1020.34cm^{-1}as shown in Supplement 3 which shows that the biogenically synthesized methanol was capped and stabilized by proteins. The band at 3331.07cm^{-1} is indicative of N-H stretch of 1^{0},2^{0}amines, 2945.30cm^{-1}band is indicative of C-H stretch of alkanes, 1450.47cm^{-1}band is indicative of C-H bend of alkanes.

For sample B1 the strong peak was noted at 3321.42, 2943.37, 1450.47, 1020.34, 734.88cm^{-1} as shown in Supplement 4 which shows that the biogenically synthesized methanol was capped and stabilized by proteins.



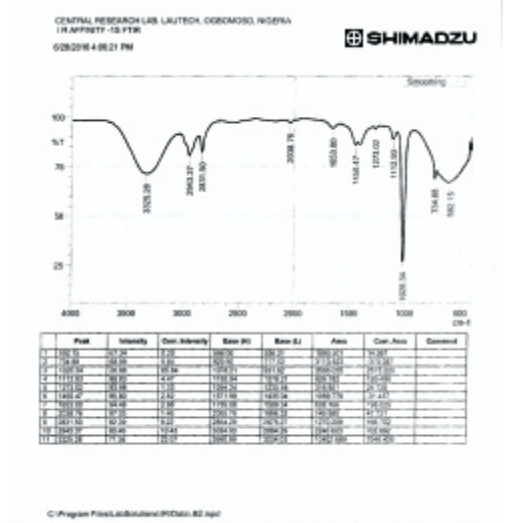
Supplement 3: Chromatogram for sample A3



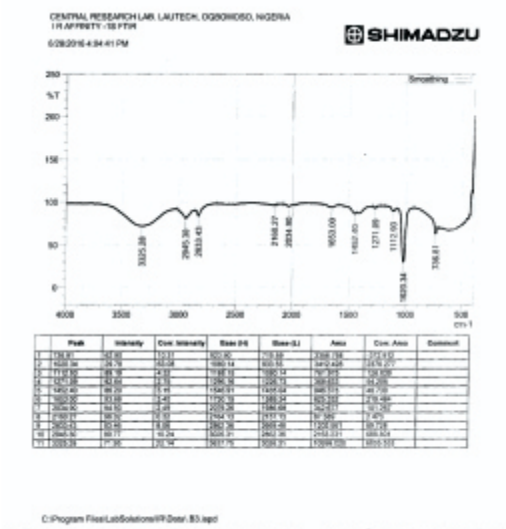
Supplement 4: Chromatogram for sample B1

For sample B2 the strong peak was recorded at 3325.28, 2943.37, 1450.47, 1020.34, 738.88cm^{-1} as shown in Supplement 5 which shows that the biogenically synthesized methanol was capped and stabilized by proteins. The band at 3325.28cm^{-1} is indicative of N-H stretch of 1^0,2^0amines.

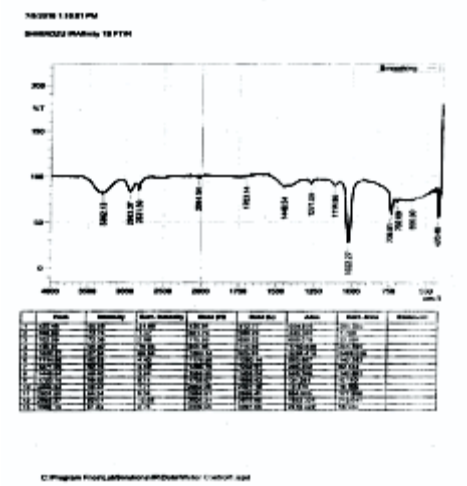
For sample B3 the strong peak was observed at 3325.28, 2945.30, 1452.47, 1020.34, 736.81cm^{-1} as shown in Supplement 6 which shows that the biogenically synthesized methanol was capped and stabilized by proteins. The band at 3325.28cm^{-1} is indicative of N-H stretch of 1^0,2^0amines, 2945.30cm^{-1} band is indicative of –C-H stretch of alkanes, 1452.47cm^{-1} of C-H bend of alkanes,1020.34cm^{-1}band is indicative of C-O stretch of alcohol, carboxylic acid, 736.81cm^{-1} band is indicative of C-CL stretch of alkyl halides. The strong peak observed has revealed that the samples are capped and stabilized by proteins. While Supplement 7 shows the result of the control, water sample from a river free from feacal contamination.



Supplement 5: Chromatogram for sample B2



Supplement 6: Chromatogram for sample B3



Supplement 7: Chromatogram for Control

Discussion

The results from this study indicated the presence of total coliform (TC) and total heterotrophic (TH) bacteria in the water samples, some of them being coliforms/enteropathogenic species. The presence of these bacteria might be attributed to indiscriminate deposition of animal waste, human, and agricultural wastes (Adetunde et. al. 2011); Adekoyeni and Salako (2012); Adegbola et. al. (2014) and Ayandele et. al. (2015).) The presence of Coliforms and *E. coli* in the water samples studied indicated faecal contamination, this shows that the water is not fit for human consumption.

Comparing the sampling areas, there was a high presence of TH and TC bacteria in Papa-Osiagoro water source than Oke-Baaki. This difference may be attributed to the difference in the human population characterized by the increased generation of animal or human waste, and low-socioeconomic status of the community dwellers. In addition, the TC and TH detected in all samples were above WHO standards. According to WHO (2011) recommendations for drinking water, there should not be a single coliform growth per ml of drinking water. The poor environmental planning, management, indiscriminate wastes disposal and organic matter infiltration and leaching might have contributed to microbial activities in the samples.

According to Harakeh et. al. (2006), the emergence of antimicrobial resistant bacteria increases in an environment where antimicrobials are indiscriminately used by the public, particularly in Nigeria and other developing countries. The resistant of the isolated bacteria to most of the antibiotics used might be as a result of the discharge of active antibiotics in considerable amounts in the form of human waste (Dahunsi et. al., 2014). Also, native bacteria in natural environments can be exposed to these antibiotics, especially those with higher persistence in the environment, facilitating bacterial antibiotic resistance selection (Ma Carmen et. al., 2016). It might also be due to the ineffective control of using antibiotics to treat gastrointestinal infections, resulting in lower alternatives for therapeutic treatments. Ayandiran et. al. (2014) also reported the presence of multiple antibiotic resistant bacteria in Oluwa river, Nigeria. All the bacteria isolated in this study showed multiple resistant to all the antibiotics used in this study, resistant of microorganisms to different antibiotics had also been reported in many studies (Rakic-Martinez et. al., 2011; Kosak et. al., 2012; Mohammed et. al.,. 2013)

There was no disparity between the mineral contents observed in the water samples and the WHO standard as well as Nigeria standard for Drinking Water Quality as all fell below the standard (SON, 2007). This shows that the water sources are free from chemical hazards. This conformed to the findings of (Egwuonwu et. al., 2012) and (Ayandele et. al., 2015) where the mineral content of the water samples studied in their works fell within the WHO standard (WHO, 2011). However, the higher quantity of zinc recorded with a comparison to NSZWQ might be ascribable to the natural introduction of the metal by erosion of minerals from rocks and lands or through artificial pathways such as combustion of waste materials, use of coal, or leaching of some plant materials.

Fecal sterols are important biomarkers for determining the intensity of marine pollution. Coprostanol has been the principal human fecal sterol derivative used as a sensitive indicator for sewage pollution (Black et. al., 2007; Tyagi et. al., 2008). The result of the water samples showed the presence of high concentrations of fecal sterols in all the water samples analyzed. (Isobe et. al. (2002) reported coprostanol of < 0.0001 to 13.47µg/L in the Tropical River and estuarine water in Malaysia and Vietnam, while Hussain (2010) also reported a high concentration of faecal sterol in an Australian water supply.

Conclusion

The high percentage of *E. coli* recorded revealed feacal contamination of the water samples, indicating unsuitability of these water samples for human consumption since water is being fetched directly from these surface directly for both domestic and agricultural purposes. The incidence of multiple antibiotic resistant (MAR) bacteria is another area of concern in the studied dams. Proactive measures are therefore recommended in order to avert severe contamination before exposure to public use.

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