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Physicochemical Properties, Bacteriological Quality and Antimicrobial Resistance Profile of Isolates from Groundwater Sources in Ile-Ife Suburbs, Southwest Nigeria.

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Abstract*: Groundwater resources generally considered safe source of drinking water are commonly vulnerable to pollution. Hence, this study investigated the physicochemical, bacteriological qualities as well as the patterns of antibiotic resistance in bacterial isolates from selected groundwater sources in Ile-Ife. Groundwater samples were obtained in triplicates from random locations near septic facilities (test) and sites with no septic facilities (control) in Ile-Ife.Physiochemical and bacteriological assays were conducted according to standard methods described by APHA and Kirby-Bauer disc diffusion method was used for the antibiotic sensitivity test.Result from this study showed that; 23 out of the 25 wells studied were heavily contaminated with microorganisms ranging from $4x10^3$cfu/ml to $1.21x10^5$cfu/ml above WHO limits of $1x10^2$cfu/ml. The pH of the well water samples ranged from 5.6 to 8.4, the temperature was between 24.5^{o}C to 29.5^{o}C, acidity and alkalinity were 0.7-4.9 mg/l and 0.7-8.6 mg/l respectively. The isolates showed high resistance to Cefuroxime, Augmentin, Ampicillin, mild resistance to Ofloxacin and Nitrofurantoin but highly susceptible to Ceftazidime, Gentamicin and Ciprofloxacin. Above all, about 86% of the isolates were found to be multi Drug Resistant (MDR). This study concludes that most groundwater sources in Ile-Ife especially those near septic facilities were contaminated with antibiotic resistant bacteria which can lead to severe health issues.*

Key words: *Antibiotic resistance, Bacteriological, Coliforms, Multi-drug resistant, Groundwater.*

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I. Introduction

Groundwater (also well water) serves as an important drinking water source to an estimated 1.5 billion population worldwide majority of which comprises Sub–Saharan Africa population and the 2006 Nigerian household population census showed the dependence of an estimated 49.4% households on groundwater as the main source of water for domestic use (MacDonald and Davies, 2002). Generally, groundwater quality varies due to seasonal changes; however, its quality is currently being threatened by hosts of human activities resulting in over-abstraction, microbiological and chemical contamination. Khan et al (2012), have reported anthropogenic activities such as poor sewage disposal and open defecation as the most common and widespread cause of water contamination.Physicochemical parameters such as temperature, pH, turbidity, nitrate concentration also affect microbial activities and population in the well which influences the overall quality of well water (Trivede et al., 2010).

In Sub-Saharan Africa, due to poor sanitation systems, it is often a common practice to dump environmental pollutant such as pharmaceutical wastes, agricultural discharges and other industrial wastes into aquatic systems.This results in thedevelopment of antimicrobial resistance by aquatic microflora.

Nelson et al., (2019) attributed antimicrobial resistance in bacteria to the misuse and overuse of antibiotics as well as the possession of drug resistant plasmids while Jose and Cesar, (2016) reported that such resistance could also arise from the acquisition of mobile genetic elements such as plasmids, transposons, through horizontal gene transfer, both of which play crucial roles in the development of antimicrobial resistance among clinically relevant organisms. Evolutionarily, it has become possible for bacterial species to transfer antibiotic resistant genes not only between members of a particular species but also between different bacteria species, thus creating pathotypes with new combinations of different virulence genes which either due to selective pressure or antibiotics overuse by humans have demonstrated significant increase in resistance to specific antibiotics over a short time period (Brown et al., 2019).

In Sub-Saharan Africa where many still rely on open defecation, there is the transmission of antibiotic resistant bacteria via fecal-oral route, possibly due to the fact that drugs and their metabolites eliminated in fecal matter find their way through sewage systems into water supplies

Contamination of water with faecal and antibiotic resistant bacteria remains a global health challengeas this has resulted in several episodes of water borne diseases outbreak which accounts for 3.4million death annually especially in under-developed and developing countries Although several authors (such as; Okafor et al., 2015; Abu and Wondikom, 2018; Osumanu et al., 2019) have conducted studies on the incidence of antimicrobial resistance in Sub-Saharan Africa, however, there is paucity of empirical information as regards multi-antibiotics resistance by microorganisms in local water supplies.Hence, the objectives of this study were to; determine the physicochemical parameters of groundwater and how they influence its bacteriological quality, characterize multi antimicrobial resistant bacterial coliforms from groundwater and determine the antibiotics of interest that would be most effective in the treatment and management of enteric diseases such as; cholera, typhoid fever, dysentery, diarrhea particularly of bacterial origin that may become non-self limiting.

II. Materials and Methods

Study Area: The study area, Ile-Ife, geographically lies on longitude 4^0 69'E and latitude 70^0 50'N. It covers a total land mass of 1,791km^2.

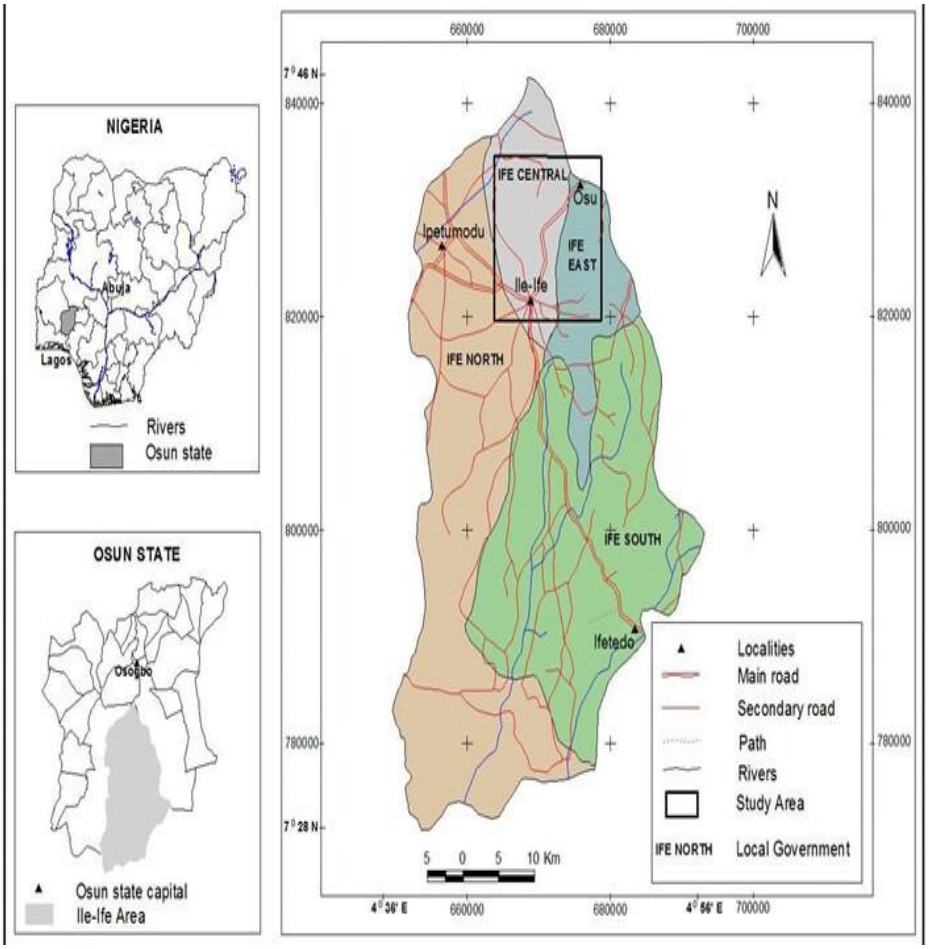

Fig. I: Map description showing the location of Ile-Ife, Osun State, Nigeria
(Source: Digital archives of the Department of Geography, Obafemi Awolowo University, Ife)

Sample Collection: The well water samples were collected from twenty-five (25) dug wells at different locations in Ile-Ife and its suburb town, Modakeke between October 2016 and February, 2017. The samples were transported in ice-packs to the Microbiology Laboratory, Obafemi Awolowo University, Ile-Ife for analysis immediately after collection.

Preparation of Media: All media used were prepared according to manufacturer's instruction and sterilized in an autoclave at 121^{o}C for 15 minutes.

Physicochemical Analysis: Temperature, pH, electrical conductivity (EC), dissolved oxygen (DO) and biological oxygen demand (BOD) were determinedaccording to Nollet, (2000). Temperature was determined at

the point of sampling via a thermometer. Groundwater samples (50ml) were measured into a beaker and the pH and EC were measured using properly calibrated pH meter and conductivity meter respectively while DO and BOD were determined by iodometric titration.

Bacteriological Analyses: Samples were processed according to methods described by Cheesbrough, (2005). 1ml of each test and control samples were aseptically transferred into test tubes containing 9ml of sterile distilled water. The mixture was serially diluted up to 10^{-5} dilution factor. 0.1ml inocula from 10^{-3} to 10^{-5} test tubes were aseptically transferred to the surface of a solidified nutrient agar contained in sterile petri dishes and incubated in an inverted position at 37^0C for 24-48h. The Total viable count of bacteria in each sample was counted after incubation.

For the total coliform count (TCC) determination; three (3) tube dilution series of inoculum quantities; 10ml, 1ml and 0.1ml were used in the Most Probable Number Analysis. Presumptive, confirmatory and completed tests were used to identify isolates capable of lactose fermentation at 37^0C after 48 hwith gas production.

Purification of Isolates: Sub culturing was done on solidified sterile nutrient agar to obtain pure cultures. The pure cultures were maintained at 4°C in nutrient agar as stock culture for further tests

Characterization and Identification of Isolates: Isolates were characterized and identified using biochemical procedures (Gram staining, catalase, coagulase,sugar fermentation, starch hydrolysis, Citrate utilization, motility, oxidase, Voges Proskauer and endospore tests) according to protocols described in Bergey's manual of Systemic Bacteriology (Krieg and Holt, 1994).

Determination of Antibiotics Sensitivity: Agar disc diffusion method was used for Antibiotics sensitivity testing as described by Bauer et al., (2000). A 24 hour old culture was inoculated into a10ml sterile distilled water in a test tube to give a concentration of one million cfu/ml and standardized to a turbidity of 0.5 MacFarland standard with subsequent inoculation on sterilized Mueller Hinton agar. Gram negative antibiotics impregnated discs containing; Ofloxacin (5µg), Augmentin (30µg), Nitrofurantoin (300µg), Ampicillin (10µg), Ceftazidime (30µg), Cefuroxime (30µg), Gentamicin (10µg) and Ciprofloxacin (5µg) were placed on inoculated agar by means of a pair of sterile forceps and incubated at 37^0C for 18-24 hours. The zone of inhibition was recorded in mm and interpreted according to Clinical Laboratory Standard (CLSI, 2014).

Statistical Analysis of Data: Data were subjected to one-way analysis of variance (ANOVA) and compared by Tukey multiple test range at $p \leq 0.05$.

III. Results

Bacteriological Quality of the Groundwater Samples

TableI shows the total viable cell counts per test (JK) and control (WW) sample.The microbial load is highest in JK 25 (1.21×10^5cfu/ml) and least in JK 24 (4×10^3cfu/ml). For the control samples, the highest and least bacterial counts were recorded at WW 5 (4.5×10^3) and WW8 (2×10^2) respectively.

Biochemical Characterization of Isolates

The biochemical characterization and identification of isolates is as shown in Table II. Thirty (30) coliform bacteria belonging to nine different genera; Salmonella, Citrobacter, Klebsiella, Aeromonas, Vibrio, Pseudomonas, Enterobacter, Escherichia and Serratia were identified.

Percentage Occurrence of the Bacterial Isolates

Figure II depict the percentage occurrence of the isolates. Salmonella spp had the highest prevalence (23.3%). Conversely, Enterobacter spp and Pseudomonas spp were the least occurring isolates with prevalence of only 3.3%

Antibiotics Susceptibility Pattern of Isolates

Table III illustrates the susceptibility pattern of the thirty isolates tested against eight (8) different antibiotics. Cefuroxime (CRX), Augmentine (AUG), Ampicillin (AMP), moderate susceptibility to Ofloxacin (OFL) and Nitrofurantoin (NIT) but high susceptibility to Ceftazidime (CAZ), Gentamicin (GEN) and Ciprofloxacin (CPR).

Table I: Total Viable Counts of isolates

Test Samples(JK)	Colony_count(cfu/ml)	Control (WW)	Colony_count(cfu/ml)
JK1	19800	WW1	450
JK2	28000	WW2	550
JK3	10600	WW3	660
JK4	16900	WW4	500
JK5	83000	WW5	4500
JK6	31000	WW6	700
JK7	32000	WW7	1000
JK8	5900	WW8	200
JK9	9000	WW9	780
JK10	10000	WW10	467
JK11	7000	WW11	556
JK12	16000	WW12	770
JK13	12500	WW13	3000
JK14	16200	WW14	980
JK15	24400	WW15	950
JK16	8000	WW16	990
JK17	25000	WW17	1560
JK18	9000	WW18	554
JK19	14300	WW19	681
JK20	9500	WW20	500
JK21	8600	WW21	910
JK22	9900	WW22	440
JK23	14100	WW23	730
JK24	4000	WW24	300
JK25	121000	WW25	855

Table II: Biochemical Characterization of Isolates and Probable Organisms Identified

SAMPLES CODE	ISOATE CODE	GRAM REACTION	SPORE TEST	CAT	OXD	pH	H_2S	GAS	MOT	CIT	IND	NIT	STA	GLU	MR	VP	PROBABLE ORGANISMS
JK1	JK1A	GN Rod	-ve	+ve	-ve	A	+ve	+ve	-ve	-ve	-ve	+ve	+ve	A/G	+ve	-ve	*Salmonella spp*
JK2	JK2A	GN Rod	-ve	+ve	-ve	A	+ve	+ve	-ve	-ve	-ve	+ve	-ve	A/G	+ve	+ve	*Salmonella spp*
JK3	JK3A	GN Rod	-ve	+ve	+ve	ALK	+ve	+ve	-ve	-ve	-ve	+ve	-ve	A/G	+ve	-ve	*Citrobacter spp*
	JK3B	GN Rod	-ve	+ve	-ve	A	-ve	-ve	-ve	-ve	-ve	-ve	+ve	A	-ve	+ve	*Klebsiella spp*
JK4	JK4A	GN Rod	-ve	+ve	+ve	A	+ve	-ve	+ve	-ve	+ve	+ve	-ve	A/G	-ve	-ve	*Aeromonas spp*
JK5	JK5A	GN Rod	-ve	+ve	+ve	A	+ve	-ve	+ve	-ve	+ve	+ve	+ve	A/G	-ve	+ve	*Aeromonas spp*
	JK5B	GN Rod	-ve	+ve	+ve	A	+ve	-ve	-ve	-ve	-ve	+ve	+ve	A/G	+ve	-ve	*Salmonella spp*
JK6	JK6A	GN Rod	-ve	+ve	+ve	A/ALK	+ve	-ve	+ve	-ve	+ve	-ve	-ve	A	-ve	-ve	*Vibrio spp*
JK7	JK7A	GN Rod	-ve	+ve	-ve	ALK	+ve	-ve	+ve	+ve	-ve	-ve	+ve	A	+ve	-ve	*Salmonella spp*
	JK7B	GN Rod	-ve	+ve	+ve	A	+ve	-ve	+ve	-ve	+ve	-ve	-ve	A	-ve	+ve	*Vibrio spp*
JK8	JK8A	GN Rod	-ve	+ve	-ve	A	+ve	-ve	+ve	+ve	-ve	+ve	-ve	A	-ve	-ve	*Aeromonas spp*
	JK8B	GN Rod	-ve	+ve	-ve	A	+ve	+ve	-ve	-ve	-ve	+ve	+ve	A/G	+ve	-ve	*Salmonella spp*
JK9	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	*NCB*
JK10	JK10A	GN Rod	-ve	+ve	-ve	ALK	-ve	-ve	+ve	+ve	-ve	+ve	+ve	A	+ve	-ve	*Seratia spp*
	JK10B	GN Rod	-ve	+ve	-ve	A	-ve	+ve	+ve	+ve	-ve	+ve	-ve	A/G	-ve	+ve	*Klebsiella spp*
JK11	JK11A	GN Rod	-ve	+ve	+ve	A/ALK	-ve	+ve	+ve	+ve	+ve	+ve	+ve	A/G	-ve	-ve	*Citrobacter spp*
JK12	JK12A	GN Rod	-ve	+ve	+ve	A	-ve	+ve	+ve	+ve	+ve	+ve	-ve	A/G	-ve	-ve	*Aeromonas spp*
JK13	JK13A	GN Rod	-ve	+ve	-ve	A/A	-ve	-ve	-ve	-ve	+ve	+ve	+ve	A/G	+ve	-ve	*Escherichia spp*
JK14	JK14A	GN Rod	-ve	+ve	+ve	A/ALK	-ve	-ve	-ve	-ve	+ve	-ve	+ve	A	-ve	+ve	*Vibrio spp*
JK15	JK15A	GN Rod	-ve	+ve	+ve	ALK	-ve	+ve	+ve	-ve	-ve	+ve	+ve	A/G	-ve	+ve	*Pseudomonas spp*
JK16	JK16A	GN Rod	-ve	+ve	-ve	A/A	-ve	-ve	-ve	-ve	+ve	+ve	+ve	A/G	+ve	-ve	*Escherichia spp*
JK17	JK17A	GN Rod	-ve	+ve	-ve	A/ALK	-ve	+ve	+ve	+ve	-ve	-ve	-ve	A	-ve	+ve	*Serratia spp*
	JK17B	GN Rod	-ve	+ve	-ve	A/ALK	+ve	+ve	+ve	-ve	-ve	+ve	+ve	A/G	-ve	-ve	*Enterobacter spp*
JK18	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	NCB	*NCB*
JK19	JK19A	GN Rod	-ve	-ve	+ve	A/ALK	+ve	-ve	-ve	-ve	+ve	-ve	+ve	A/G	-ve	-ve	*Aeromonas spp*
JK20	JK20A	GN Rod	-ve	-ve	+ve	A/ALK	+ve	-ve	-ve	-ve	+ve	-ve	+ve	A/G	-ve	+ve	*Aeromonas spp*
JK21	JK21A	GN Rod	-ve	+ve	+ve	A/ALK	-ve	-ve	+ve	+ve	-ve	-ve	+ve	A/G	-ve	-ve	*Vibriospp*
JK22	JK22A	GN Rod	-ve	+ve	-ve	ALK	+ve	-ve	-ve	-ve	+ve	+ve	-ve	A/G	+ve	-ve	*Salmonella spp*
JK23	JK23A	GN Rod	-ve	+ve	-ve	A/A	-ve	-ve	+ve	-ve	+ve	+ve	+ve	A/G	+ve	-ve	*Escherichia spp*
JK24	JK24A	GN Rod	-ve	+ve	-ve	A	-ve	+ve	+ve	-ve	-ve	+ve	+ve	A	+ve	-ve	*Escherichia spp*
JK25	JK25A	GN Rod	-ve	+ve	-ve	A/ALK	+ve	-ve	-ve	-ve	+ve	+ve	-ve	A/G	+ve	-ve	*Salmonellaspp*
	JK25B	GN Rod	-ve	+ve	-ve	A/A	-ve	-ve	-ve	-ve	+ve	-ve	+ve	A/G	+ve	-ve	*Escherichia spp*

Legend: CAT= Catalase test, OXD= Oxidase test, MOT= Motility test, CIT= Citrate Utilization, IND= Indole test, NIT= Nitrate test, STA= Starch Hydrolysis, GLU= Glucose Utilization, MR= Methyl red, VP= Vogue-Proskauer, A= Acid, ALK= Alkaline, G= Gas, +ve= Positive, -ve= Negative, ND= Not Determined, NCB= No Coliform Bacteria.

Fig II: Percentage Occurrence of Isolates

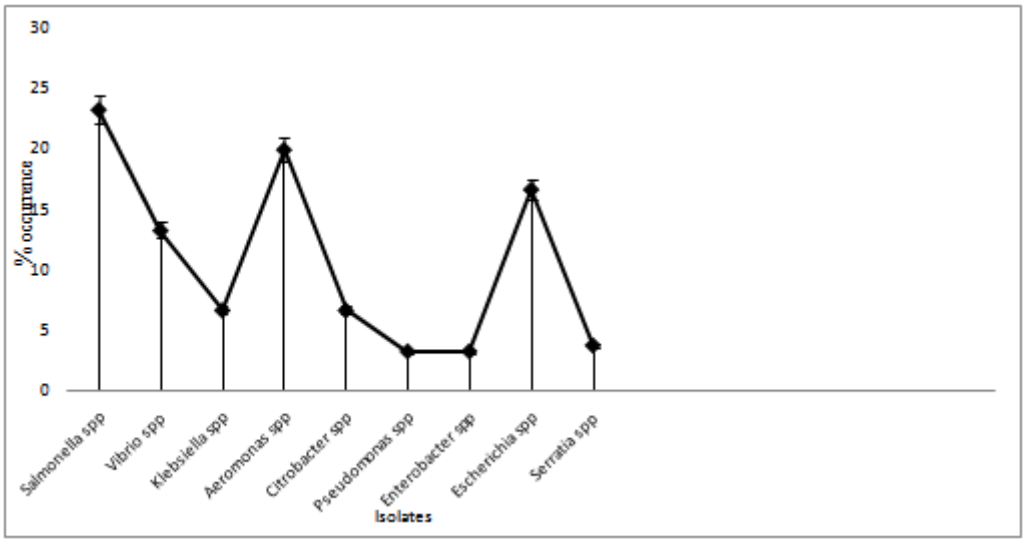

Table III: Antibiotic Resistance profiles and Multi Antibiotic Resistance (MAR) Index of Isolates

Code	Isolates	AUG	CAZ	GEN	OFL	CRX	NIT	AMP	CPR	MAR index
JK1A	Salmonella spp	R	R	R	I	R	S	R	S	0.6
JK2A	Salmonella spp	R	S	R	R	S	S	R	S	0.5
JK3A	Citrobacterspp	R	S	R	R	R	S	R	S	0.6
JK3B	Klebsiellaspp	R	S	R	R	R	S	R	S	0.6
JK4A	Aeromonas spp	R	R	R	R	R	S	R	S	0.8
JK5A	Aeromonas spp	R	R	R	R	R	I	R	S	0.8
JK5B	Salmonella spp	R	R	R	I	R	I	I	S	0.5
JK6A	Vibrio spp	R	R	S	S	R	R	R	S	0.6
JK7A	Salmonella spp	R	S	S	S	R	I	R	S	0.4
JK7B	Vibrio spp	S	R	S	S	S	S	S	S	0.1
JK8A	Aeromonas spp	R	R	R	R	R	I	R	S	0.8
JK8B	Salmonella spp	R	S	S	S	R	R	R	S	0.5
JK10A	Serratiaspp	I	S	S	S	S	S	S	S	0.0
JK10B	Klebsiellaspp	R	S	R	R	S	S	R	S	0.5
JK11A	Citrobacterspp	I	S	S	S	R	S	R	S	0.3
JK12A	Aeromonas spp	R	S	S	S	R	S	R	S	0.4
JK13A	Escherichia spp	R	R	I	I	S	S	I	I	0.3
JK14A	Vibrio spp	R	S	S	S	R	I	R	S	0.4
JK15A	Pseudomonas spp	R	S	S	I	R	I	R	S	0.4
JK16A	Escherichia spp	I	S	S	S	S	S	S	S	0.0
JK17A	Serratiaspp	R	S	S	I	R	I	I	S	0.3
JK17B	Enterobacterspp	R	S	S	S	R	R	R	S	0.5
JK19A	Aeromonas spp	R	S	S	S	R	I	R	S	0.4
JK20A	Aeromonas spp	R	R	R	I	R	I	R	S	0.6
JK21A	Vibrio spp	R	S	S	S	R	I	R	S	0.4
JK22A	Salmonella spp	R	S	S	I	R	S	R	I	0.4
JK23A	Escherichia spp	R	S	S	I	R	I	R	S	0.4
JK24A	Escherichia spp	R	S	S	I	R	I	R	S	0.4
JK25A	Salmonella spp	R	I	S	S	R	R	R	S	0.5
JK25B	Escherichia spp	I	S	S	S	S	S	S	S	0.0

Legend: OFL= Ofloxacin;CAZ= Ceftazidime; CRX= Cefuroxime; NIT= Nitrofurantoin .
GEN= Gentamicin; AUG= Augmentin; CAZ= Ceftazidime; AMP= Ampicillin
CPR= Ciprofloxacin; S= Susceptible; I= Intermediate; R= Resistant

Table IV: Statistical Analysis of the Relationship between Physicochemical Parameters and Bacterial Population of the Groundwater Samples

Table IV: Statistical Analysis of the Relationship between Physicochemical Parameters and Bacterial Population of the Groundwater Samples

Groundwater	pH	Temperature(^{0}C)	DO(mgl$^-$)	BOD(mgl$^-$)	EC	Colony counts(cfu/ml)
JK1	6.80 ± 0.12	28.00 ± 0.23	3.20 ± 0.24	50.00 ± 3.24	466.00 ± 48.02	19800.00 ± 5190.35
JK2	6.13 ± 0.12	26.00 ± 0.23	1.40 ± 0.24	20.00 ± 3.24	271.00 ± 48.02	28000.00 ± 5190.35
JK3	5.81 ± 0.12	26.50 ± 0.23	2.80 ± 0.24	40.00 ± 3.24	236.00 ± 48.02	10600.00 ± 5190.35
JK4	6.23 ± 0.12	24.50 ± 0.23	1.10 ± 0.24	30.00 ± 3.24	360.00 ± 48.02	16900.00 ± 5190.35
JK5	6.11 ± 0.12	27.00 ± 0.23	2.20 ± 0.24	60.00 ± 3.24	182.00 ± 48.02	83000.00 ± 5190.35
JK6	6.66 ± 0.12	28.00 ± 0.23	2.50 ± 0.24	50.00 ± 3.24	388.00 ± 48.02	31000.00 ± 5190.35
JK7	6.37 ± 0.12	27.00 ± 0.23	1.30 ± 0.24	40.00 ± 3.24	130.00 ± 48.02	32000.00 ± 5190.35
JK8	6.17 ± 0.12	27.00 ± 0.23	1.20 ± 0.24	60.00 ± 3.24	194.00 ± 48.02	5900.00 ± 5190.35
JK9	6.01 ± 0.12	29.00 ± 0.23	5.70 ± 0.24	38.00 ± 3.24	500.00 ± 48.02	9000.00 ± 5190.35
JK10	6.33 ± 0.12	28.00 ± 0.23	3.80 ± 0.24	19.00 ± 3.24	530.00 ± 48.02	10000.00 ± 5190.35
JK11	5.87 ± 0.12	29.50 ± 0.23	5.00 ± 0.24	28.00 ± 3.24	340.00 ± 48.02	7000.00 ± 5190.35
JK12	6.80 ± 0.12	29.00 ± 0.23	4.50 ± 0.24	29.00 ± 3.24	440.00 ± 48.02	16000.00 ± 5190.35
JK13	7.25 ± 0.12	28.70 ± 0.23	3.00 ± 0.24	16.00 ± 3.24	870.00 ± 48.02	12500.00 ± 5190.35
JK14	5.63 ± 0.12	28.50 ± 0.23	2.90 ± 0.24	13.00 ± 3.24	250.00 ± 48.02	16200.00 ± 5190.35
JK15	6.25 ± 0.12	28.00 ± 0.23	2.70 ± 0.24	13.00 ± 3.24	950.00 ± 48.02	24400.00 ± 5190.35
JK16	6.53 ± 0.12	29.00 ± 0.23	4.90 ± 0.24	20.00 ± 3.24	800.00 ± 48.02	8000.00 ± 5190.35
JK17	7.36 ± 0.12	29.00 ± 0.23	3.70 ± 0.24	16.00 ± 3.24	980.00 ± 48.02	25000.00 ± 5190.35
JK16	6.73 ± 0.12	27.00 ± 0.23	1.80 ± 0.24	9.0.00 ± 3.24	287.00 ± 48.02	9000.00 ± 5190.35
JK19	5.95 ± 0.12	28.00 ± 0.23	3.20 ± 0.24	14.00 ± 3.24	407.00 ± 48.02	14300.00 ± 5190.35
JK20	6.54 ± 0.12	28.50 ± 0.23	3.50 ± 0.24	14.00 ± 3.24	430.00 ± 48.02	9500.00 ± 5190.35
JK21	6.15 ± 0.12	28.00 ± 0.23	2.70 ± 0.24	9.00 ± 3.24	386.00 ± 48.02	8600.00 ± 5190.35
JK22	6.61 ± 0.12	28.50 ± 0.23	3.70 ± 0.24	16.00 ± 3.24	251.00 ± 48.02	9900.00 ± 5190.35
JK23	5.93 ± 0.12	28.50 ± 0.23	2.90 ± 0.24	11.00 ± 3.24	276.00 ± 48.02	14100.00 ± 5190.35
JSK24	5.60 ± 0.12	28.00 ± 0.23	3.60 ± 0.24	16.00 ± 3.24	286.00 ± 48.02	4000.00 ± 5190.35
JK25	8.42 ± 0.12	27.00 ± 0.23	2.00 ± 0.24	8.0.00 ± 3.24	203.00 ± 48.02	121000.00 ± 5190.35

Standard error of each parameter was calculated. When subjected to Tukey. Test (α=0.05, 95% confidence interval), p value=0.039(i.e. < 0.05).

Legend:EC= Electrical Conductivity, DO = Dissolved Oxygen, BOD = Biological Oxygen Demand.

IV. Discussion

This study investigated the physicochemical properties and the extent of bacterial contamination of various groundwater sources in Ile-Ife as well as the antimicrobial resistance pattern of the isolates. Results from the study showed that thirty isolates (30) belonging to nine genera were isolated (Table II) with Salmonella having the most occurrence (23.3%) while Enterobacter and Pseudomonas, each with 3.3% occurrence were the least isolated genera.

Virtually all the groundwaterin test sites were heavily contaminated with microorganisms, having a viable count within the range; $4x10^3$to $1.21x10^5$cfu/ml.This high total viable count is way beyond that obtained for the controls and significantly exceeds WHO recommended limits for potable water (WHO, 2018).Similar results have been reported in recent studies within Nigeria (Giwa et al., 2015; Elemile et al., 2019; Ibe et al., 2019) and other developing countries (Chourasia, 2018; Kawo and Karuppannan, 2018; Odiyo and Makungo, 2018).

Lutterodt et al., (2018) and Olasoji et al., (2019)have attributed high microbiological contamination of groundwater to poor sanitary conditions and practices as well as proximity to septic tanks and pit latrines uphill or downhill

Furthermore, enteric organisms such as Escherichia spp, Klebsiella spp, Enterobacter spp, Citrobacter spp, Salmonella sppwere isolated from the samples.This corroborates with the findings of Okafor et al., (2015) where enteropathogens were isolated from sachet water brands and borehole water sold in Abakaliki metropolis, Southern Nigeria. The presence of enteric organisms in water is indicative of pollution with faecal matter and can predispose consumers of such water to gastroenteritis.

The results of the physicochemical analysis in Table IV, showed mild to moderate acidity, temperature andelectrical conductivity. However, the Dissolved oxygen (DO) and Biochemical oxygen demand (BOD) values were beyond WHO limits (WHO, 2018).

Several studies have established a relationship between physicochemical parameters and bacteriological quality. For instance, Waziri, (2010), directly linked the decomposition of dead organic matter present in the wastewater (BOD)to increased microbial populations and anoxic conditions (less DO). According to Oyem et al., (2014), high temperature negatively impact water quality by enhancing microbial growth and activities. In addition, pH shapes the composition and activity of microbial communities as extremes of acidity and alkalinity can inhibit microbial growth and activities (Jin and Kirk, 2018). This is typical of the findings of this study as seen in Table IV. The statistical analysis of this relationship between physicochemical parameters and bacteriological population yielded a p value of 0.039 (@ α=0.05, 95% confidence interval) and this

connotes that mild or harsh physicochemical conditions can inhibit or stimulate bacterial growth and activity in the groundwater.

The antibiotics profile showed about 86% of the isolates to be multi antibiotic resistant with Aeromonas spp (JK4A and JK5A) having the most MAR index and Cirobacter spp (JK11A), Escherichia spp (JK13A) and Serratia spp (JK17A) having the least.

Multi antimicrobial resistance as observed in this study can be ascribed to; irrational use of antibiotics in the study area which must have reached the groundwater through seepages from ruptures or cracks in septic devices, possession of drug resistant plasmids or acquisition of antibiotic resistance genes by bacterial organisms.The alarming occurrence of antibiotic resistant coliforms to commonly used antibiotics in medicine and agriculture has been labeled a public health challenge due to their decreased therapeutic activities against bacterial infections.

V. Conclusion

This study concludes that groundwater from the study areas were contaminated with faecal and antibiotic resistant bacteria which remains a global health challenge as this may result in severe episodes of water borne diseases outbreak such as cholera, typhoid fever, dysentery and diarrhea. In cases of outbreaks of enteric diseases, fluoroquinolones should be considered as the preferred class of antibiotics in the first line of treatment since it showed the best antimicrobial activity against enteric pathogens in this study.

References

[1]. Abu, G.O., and Wondikom, A.C. (2018). Isolation, Characterization and Antibiotic Resistance Profile Studies of Bacteria from an Excavated Pond in Port Harcourt Metropolis, Nigeria.J. Appl. Sci. Environ. Manage. Vol. 22 (8) 1177–1184 .

[2]. Bauer A.W., Kirby W.M., Sherris J.C. and Jurck M. (2000). Antibiotic sensitivity testing by a standard single disk method. American Journal of Clinical Pathology 451: 493-496.

[3]. Brown, E.E., Cooper, A., Carrillo, C., and Blais, B. (2019). Selection of multi-drug resistant bacteria in medicated animal feeds. Front Microbiol. 10:456.

[4]. Cheesbrough M. (2005). District Laboratory Practice in Tropical Countries, Part1, Second Edition, Cambridge University Press.

[5]. Chourasia, L.P. (2018). Assessment of groundwater quality using water quality index in and around Korba city, Chhattisgarh, India. Am J Softw Eng Appl. 7:15-21.

[6]. Clinical Laboratory Standard Institute. (2014). Analysis and Presentation of Cumulative Antimicrobial Susceptibility Test Data: Approved Guideline-Fourth Edition. CLSI document m39-A4. Wayne, PA.pp.216-218.

[7]. Elemile, O.O., Raphael, D.O., Omole, D.O., Oloruntoba, E.O., Ajayi, E.O., and Ohwavborua, N.A. (2019). Assessment of the impact of abbatoir effluent in a residential area of Omu-Aran, Nigeria. Environmental Sciences. 31:16.

[8]. Giwa, F.J., Aboh, E.A., and Giwa, A. (2015). Microbiological assessment of well waters in Samaru, Zaria, Kaduna State, Nigeria. Ann AfrMed. 14(1): 32-38.

[9]. Ibe, P.I., Aigbedon, I.P., Marcellinus, M., Okoli, F.U., and Sola, A.B. (2019). Assessment of water quality index for groundwater in Ado Ekiti, Nigeria. WNOFNS. 22(2019): 93-101.

[10]. Jin, Q., and Kirk, M.F. (2018). pH as a primary control in Environmental Microbiology: 1. Thermodynamic Perspective. https://doi.org/10.3389/fenvs.2018.00021

[11]. Jose, M.M., and Cesar, A.A. (2016). Mechanisms of antibiotic resistance. Microbiol Spectr. 4(2): 10.

[12]. Kawo, N.S., and Karuppannan, S. (2018). Groundwater quality assessment using water quality index and GIS technique in Modjo river basin, Central Ethiopia. J Afri Earth Sci. 147:300-311.

[13]. Khan M. S. and Ahmad S. R. (2012). Microbiological contamination in groundwater of Wah area. Pakistan Journal of Science 64(1), 20-23.

[14]. Krieg, N.R. and J.G. Holt, 1994. Bergey's manual of systematic Bacteriology. William and Wikins, Baltimore Ltd.

[15]. Lutterodt, G., Vossenberg, J., Hoiting, Y., Kamara, A.K., Oduro-Kwarteng, S., and Foppen, J. (2018). Microbial groundwater quality status of hand-dug wells and boreholes in the Dodowa area of Ghana. Int J Environ Res Public Health. 15(4): 730.

[16]. MacDonald, A.M., Davies, J.A. (2002). A brief review of groundwater for rural water supply in Sub- Saharan Africa. British Geological Society: Nottingham, UK.

[17]. Nelson, D.W., Moore, J.E., and Rao, J.R. (2019). Antimicroial resistance (AMR): significance to food quality and safety. Food quality and safety. 3(1): 15-22.

[18]. Nollet, L.M. (2000). Handbook of Water Analysis, Marcel Dekker, New York, NY, USA, 2000.

[19]. Odiyo, J.O., and Makungo, R. (2018). Chemical and microbial quality of groundwater in Siloam village, implications to human health and sources of contamination. Int J Environ Res Public Health. 15: 317.

[20]. Okafor, C.O., Iroha, I.R., Nwadiogbu , I.A., Agumah , N., Eni, O., and Odinkemere, S.C (2015). Antimicrobial Resistance Pattern of coliform bacteria isolated from sachet and borehole waters sold in Abakaliki Metropolis of Ebonyi state, Nigeria. Int J Innov Sci Res. ISSN 2351-8014 Vol.16, pp. 526-532.

[21]. Olasoji, S.O., Oyewole, N.O., Abiola, B., and Edokpayi, J.N. (2019). Water quality assessment of surface and groundwater sources using a water quality index method: A case study of a peri-urban town in Southwest, Nigeria. Environments. Article ID: 6020023.

[22]. Osumanu, I.K., Kosoe, E.A., and Ategeeng, F. (2019). Determinants of open defecation in the Wa municipality of Ghana: Empirical findings highlighted sociocultural and economic dynamics among households. J Environ Public health. https://doi.org/10.1155/2019/3075840.

[23]. Oyem, H.H., Oyem, I.M., and Ezeweali, D. (2014). Temperature, pH, Electrical conductivity, Total dissolved solids, and Chemical oxygen Demand of groundwater in Boji-Boji, Agbor/Owa area and immediate suburbs. ResJ EnvironSci. 8: 444-450.
[24]. Trivede, P., Bajpai, A., and Thareja, S. (2010). Comparative study of seasonal variations in physico-chemical characteristics in drinking water quality of Kanpur, India with reference to 200 MLD filtration plant and groundwater. Nat. Sci. 8:11-17.
[25]. Waziri M. and Ogugbuaja V.O. (2010). Interrelationships between physicochemical water pollution indicators: A case study of River Yobe-Nigeria. Am. J. Sci. Ind. Res., 2010, Vol. 1(1): 76-80.
[26]. WHO. (2018). Guidelines for Drinking water Quality.World Health Organization, Recommendation,Geneva,p:16.Retrievefromhttp:/www.who.int/water_sanitation_health/WHS_WWD2010_guidelines_2018_6_en.

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