

30(2): 1-10, 2020; Article no.MRJI.55043 ISSN: 2456-7043 (Past name: British Microbiology Research Journal, Past ISSN: 2231-0886, NLM ID: 101608140)



R. R. Nrior¹, M. Okpokiri¹ and N. P. Akani^{1*}

¹Department of Microbiology, Faculty of Science, Rivers State University, Port Harcourt, Rivers State, Nigeria.

Authors' contributions

This work was carried out in collaboration among all authors. Author RRN supervised the study. Author MO managed the analyses of the study, wrote the protocol, wrote the first draft of the manuscript and managed the literature searches. Author NPA designed the study and performed the statistical analysis. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/MRJI/2020/v30i230192 <u>Editor(s):</u> (1) Dr. Juliano De Dea Lindner, Federal University of Santa Catarina (UFSC), Brazil. <u>Reviewers:</u> (1) Opeyemi U. Lawal, Portugal. (2) Pinar Sanlibaba, Ankara University, Turkey. (3) R. D. Mavunda, University of Johannesburg, South Africa. Complete Peer review History: <u>http://www.sdiarticle4.com/review-history/55043</u>

> Received 25 December 2019 Accepted 02 March 2020 Published 13 March 2020

Original Research Article

ABSTRACT

Antibiotic resistance has become a great global problem. Thus, it has emerged as a public health challenge. The antibiotic susceptibility pattern of bacteria in well water was characterized with a view of determining the level of resistance in the environment. Fifty well water samples were collected from ten different points in Ula-Ubie community, Ahoda, Rivers State for a period of five months. Standard microbiological methods were used to analyse the population and types of bacteria in the water while methods recommended by the American Public Health Association (APHA) was used to determine the physicochemical parameters of the samples. The antibiotic susceptibility profile of the bacterial isolates was carried out using the disc diffusion methods. The total heterotrophic bacteria of the water samples ranged from 0.93 ± 0.46 to $2.02\pm1.06 \log_{10} CFU/ml$. The coliform counts ranged from $0.45\pm0.42 - 2.55\pm2.33 \log_{10} CFU/ml$, respectively. Despite the variations in the counts of the different bacterial population, there was no significant differences (P > 0.05) in the different well water samples. The physicochemical parameters except the pH were all within the permissible



limits. *Klebsiella* spp, *Pseudomonas* spp, *Serratia* spp and *Enterobacter* spp were identified in the well water. The pH of the water stations ranged from 4.66 to 5.80. The temperature ranged from 24.0 to 24.7. The electrical conductivity, salinity, dissolved oxygen, total hardness, alkalinity, total suspended solids, biochemical oxygen demand, nitrate, chloride, calcium and magnesium ranged from 22.9 – 219, 0.03-0.13, 4.50-4.90, 5.00-22.0, <0.01-3.00, <0.01, 49.6-84.5, 1.00-17.4, 3.00-24.5, 4.25-12.9 and 0,722-1.55 respectively. The antibiotic susceptibility profile showed that all the isolates were resistant to ceftazidime and augmentin, whereas *Enterobacter* spp were the most resistant bacteria amongst other bacterial genera to the antibiotics. Meanwhile there is an existence of multi-drug resistance. Thus, the wells could be considered not potable due to the presence of these bacterial isolates and the level of antibiotic resistant. Proper sanitation and cleanliness of well should be encouraged.

Keywords: Antibiogram; gram-negative bacteria; well water; Klebsiella spp; Pseudomonas spp.

1. INTRODUCTION

Water is one of the most important and most valuable natural resources. It is essential in the life of all living organisms including plants and animals [1]. Good drinking water or potable water is water that is free from microbial contaminants and other substances which could cause diseases. Due to the continued pollution of water bodies, potable water has become a public health concern in many countries, especially in developing countries [2]. The bacterial qualities of groundwater, pipe borne water and other natural water supplies in Nigeria, have been reported to be unsatisfactory, with coliform counts far exceeding the levels recommended by WHO [3]. The quality of water may vary from place to place due to the type of activities carried out in that environment. For instance, the quality of ground water sources (like wells, tube wells) sited close to dump sites could be more polluted than those sited far away from dumpsites due to the fact that some contaminants inherent in the dumpsites could enter into the aquifer via seepage of water. Palamuleni and Akoth [4] posited that the quality of groundwater is not always constant especially for different water sources since certain factors such as periodic changes, rock and soil types and areas via which the water flows from could influence the substances present in the water. Contaminants which could be present in the rocks and sediments due to previous seepage from a highly contaminated source (like dump sites) could contaminate the water body and as groundwater moves across the sediments, metals such as iron and manganese are dissolved and may later be found in large amounts in the water. Additionally, the pollution of most water bodies is orchestrated by certain human activities (the disposal or dumping of chemicals and microbial matter on the land surface and into soils, or via the direct contamination caused by human activities adversely affects the health of people who consumes them without treatment [5]. More so, ground water sources like well water could be contaminated by poor hygienic practices such as the indiscriminate use of dirty fetching buckets to scoop water from deep wells as well as talking or sneezing when fetching water. Infectious diseases caused by pathogenic bacteria, viruses and parasites (e.g. protozoa and helminths) are the most common and widespread health risk associated with drinking-water [6]. Consumption of untreated water has been reported to cause different types of water borne diseases including cholera, typhoid, hepatitis A and diphtheria [7] For instance, cholera outbreak has been reported in Zimbabwe, India and Nigeria which was caused by the presence of Vibrio cholerae (gram negative bacterium) in municipal taps and wells [8]. 80% of sicknesses and deaths among children worldwide have been associated with the consumption of unsafe water [9]. Most gramnegative bacteria are involved in food and water borne diseases. Prescott et al. [10] highlighted Salmonella sp, Vibrio cholera, Campylobacter sp, E. coli, Shigella, to be associated with food and water borne diseases. An antibiogram is a chart that displays the

injection of wastes into groundwater). This

susceptibility test or responses of microorganisms against the antibiotics to which they were tested for [11]. Parkyz [12] posited that the antibiogram could be used as a guide by the clinicians and pharmacists towards choosing the most appropriate empiric antimicrobial treatment in the event of pending microbiology culture and susceptibility result. With the rate at which microorganisms are becoming very resistant to antibiotics, there is a need to develop antibiogram for microbial isolates so as to ascertain the antibiotics which are more potent in treating infections caused by these microbes. Well water is the major source of drinking water in many communities in Ahoada, Rivers State, Nigeria. Thus, evaluating the bacteriological properties and determining the antibiotic susceptibility profile would help us understand the extent of contamination or potability of these water sources, the prevalence of bacterial isolates especially Gram-negatives as well as the right antibiotics suitable in the treatment of diseases caused by microorganisms associated with the wells.

2. MATERIALS AND METHODS

2.1 Description of Study Area

The study was carried out in Ula-Ubie community. Ula-Ubie is one of the communities located in Ahoada, Ahoada West Local Government Area of Rivers state, Nigeria. Ahoada is a city in Orashi Region of Rivers State, Nigeria, found northwest of Port Harcourt.

The map of the stations where samples were collected is presented in Fig. 1.

2.2 Collection of Samples

Fifty (50) well water (underground water) samples were collected in sterile containers from ten different stations in the community. The collected samples were placed in ice pack container and sent to the microbiology laboratory of the department of Microbiology, Rivers State University for analysis.

2.3 Microbiological Analysis

The microbiological analysis of the samples involved enumeration and isolation of the bacteria present in the different samples. The microbial population in the water samples was enumerated using the tenfold serial dilution as described by Wemedo et al. [13]. In this method, one milliliter of the water sample was transferred

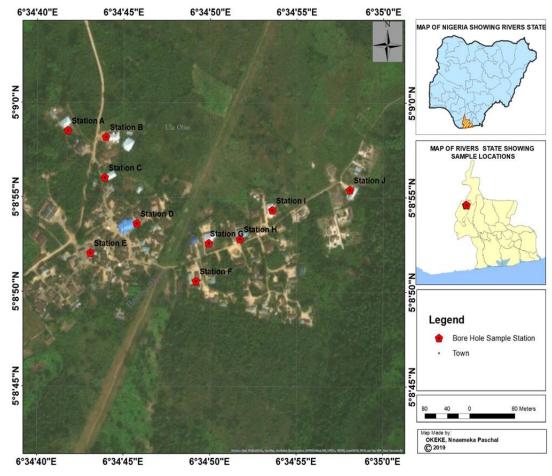


Fig. 1. Map showing the various stations under study

into test tube containing 9 mL of prepared sterile saline. After which a step wise dilution was made by transferring 1 mL from the previous dilution into another test tube containing 9 mL sterile saline. This was done until a dilution of 10⁻⁶ was reached. Aliquot (0.1 ml) from 10⁻¹, 10⁻² and 10⁻³ dilutions were seeded into prepared Nutrient agar. Brain Heart infusion agar (BHI), MacConkey agar, and Bile esculin agar plates. Swabs were inoculated directly on the respective agar plates. All the inoculated plates were incubated at 37°C for 24-48 hours. After incubation, plates which showed bacterial growth were used in enumerating the bacterial population and distinct colonies were subcultured for further identification.

2.4 Characterization of Bacterial Isolates

The morphological and biochemical characteristics of the bacterial isolates were determined using the method of Cheesbrough [14]. The morphological and biochemical test used include; Gram staining, motility, catalase, indole production, methyl red, citrate utilization, Vogue's Proskauer test, blood haemolysis test and sugar fermentation (raffinose, arabinose, mannitol, glucose, lactose and sucrose). The probable identities were gotten from the advanced bacteriological identification system (ABIS) after imputing the biochemical responses of various isolates. Prior to the use of the ABIS software, identities were first compared with similar isolates in the Bergy's manual of determinative bacteriology [15].

2.5 Antibiotic Sensitivity

This was prepared as described by Chesbrough [14]. Twenty-four (24) hours old culture were aseptically introduced into 4 ml sterile normal saline, turbidity of the organism in the tube and was compared to the turbidity of the 0.5 McFarland Standard. Unto a sterile solid Muller Hinton agar plates the already standardized isolates were aseptically inoculated using sterile swab sticks and allowed to dry [11] after which antibiotic disc was aseptically placed on the solid media using sterile forceps. The inoculated plates were incubated at 37°C for 24 hours. After 24 hours, the diameter of the zone of inhibition around each antibiotic was measured to the nearest millimeter and the readings recorded and presented as described by CLSI [16]. The abtek antibiotics disc was used and it contained the following antibiotics; Gentamycin (10 µg), Ciprofloxacin (5 µg), Nitrofurantoin, Augmentin (30 µg), Ofloxacin (5 µg), Cefixime (5 µg), Ceftazidime (30 μ g), Cefuroxime (10 μ g), Ceftriaxone (30 μ g), Cloxacillin (5 μ g) and Erythromycin (5 μ g).

3. RESULTS AND DISCUSSION

3.1 Microbial Load of Well Water

The total heterotrophic bacterial load and coliform counts of the ten (10) well water samples is illustrated in Table 1.

The total heterotrophic bacteria of the water samples ranged from 0.93 ± 0.46 to 2.02 ± 1.06 Log₁₀ CFU/ml. The coliform counts ranged from $0.45\pm0.42-2.55\pm2.33$ Log₁₀ CFU/ml.

The result for the coliform count showed that coliform was detected in all the well water samples. The station with the highest coliform load was well station H ($2.55\pm2.33 \log_{10} CFU/mI$) followed by station I ($1.90\pm2.75 \log_{10} CFU/mI$), G ($1.18\pm0.55 \log_{10} CFU/mI$), E ($1.10\pm1.14 \log_{10} CFU/mI$) and C ($1.10\pm1.13 \log_{10} CFU/mI$). The least coliform load of $0.45\pm0.42 \log_{10} CFU/mI$ was observed in station A.

The aerobic bacteria) of all the well water samples in this study exceeds the limit of 1.0×10^2 CFU/mL, which is the limit of aerobic bacteria accepted in water [17]. Some of the wells are covered with metal lids to prevent run off from the ground. This could be the reason for the varied bacterial load. Also, the fluctuation and high microbial load could be attributed to the fluctuation in rainfall. More so, the water might have been contaminated from the scoop (felting bucket) which is usually used in fetching water. It could also be that these microorganisms got into the well water via activities like talking or coughing especially when fetching water from the well. The heterotrophic bacteria load in this study are higher than the values $(1.8 \times 10^4 - 6.8 \times 10^4)$ reported by Azuonwu et al. [18] of well water in Khana Local Government Area of Rivers State. The total coliform in this study are above the acceptable/ permissible limits recommended by the world health organization (WHO). The WHO has recommended that the acceptable limit of coliform in drinking water (underground water) should be between 0-10 CFU100/mL, while total faecal coliform should be zero (0) CFU/100 mL [19].

3.2 Bacteria Diversity

The bacterial isolates identified from the various well water samples include; *Klebsiella* sp

Enterobacter sp, Pseudomonas sp, and Serratia sp. Amongst the identified isolates, *Klebsiella* sp Enterobacter sp, and Serratia sp were the most prevalent organisms in the well water recording frequency of 26.32%. *Pseudomonas* sp was the least predominant isolates with frequency of 21.05%. Contamination of the wells with these bacterial types could be attributed to when leachates sips down into the underground aquifer or when water in dumpsites sips into the underground. Species of, Enterobacter, Serratia and *Pseudomonas* which are present in this study have been reported by previous studies [18,20,13]. *E. coli, Salmonella* species, and *Klebsiella* sp have been identified in spring water which is a source of drinking water in lhitte/Uboma of Imo State, Nigeria [21]. Thus, the prevalence of gram-negative bacteria in drinking water especially underground water is well documented. Most of the bacteria identified in this study are of public health importance since they are associated with different types of diseases ranging from food poisoning, boils, skin infections, and urinary tract infections [10].

Stations	THB(X10 ⁴ Cfu/ml)	TCC(X10 ³ Cfu/ml)
А	1.33±0.80 ^a	0.45±0.42 ^a
В	1.25±0.93 ^a	0.60±0.71 ^a
С	1.31±1.10 ^a	1.10±1.13 ^a
D	0.93±0.46 ^a	0.50±0.80 ^a
E	1.17±0.73 ^a	1.10±1.14 ^a
F	1.68±0.64 ^a	0.73±0.51 ^a
G	1.99±1.13 ^a	1.18±0.55 ^ª
Н	1.90±0.94 ^a	2.55±2.33 ^a
	2.02±1.06 ^a	1.90±2.75 ^a
J	1.33±1.01 ^a	0.95±0.21 ^a

*Means with same superscript across the column shows no significant difference at (p>0.05) Key: TFC(Total fungi count), THB (Total heterotrophic bacteria) and TCC(Total coliform count) The above result is presented in Mean ± SD

Antibiotics	Resistant (%)	Intermediate (%)	Susceptible (%)	
Ceftazidime	4(100.0)	0(0.00)	0(0.00)	
Cefuroxime	3(75.0)	1(25.0)	0(0.00)	
Gentamycin	0(0.00)	1(25.0)	3(75.0)	
Ofloxacin	2(50.0)	2(50.0)	0(0.00)	
Augmentin	3(75.0)	1(25.0)	0(0.00)	
Cefixime	3(75.0)	1(25.0)	0(0.00)	
Nitrofurantoin	4(100.0)	0(0.00)	0(0.00)	
Ceftriaxone	4(100.0)	0(0.00)	0(0.00)	

Table 2. Susceptibility pattern of Pseudomonas Sp isolated from water samples

Table 3. Susceptibility pattern of Enterobacter Sp isolated from water samples

Antibiotics	Resistant (%)	Intermediate (%)	Susceptible (%)
Ceftazidime	5(100)	0(0.00)	0(0.00)
Cefuroxime	3(60.0)	2(40.0)	0(0.00)
Gentamycin	4(80.0)	1(20.0)	0(0.00)
Ofloxacin	4(80.0)	1(20.0)	0(0.00)
Augmentin	5(100)	0(0.00)	0(0.00)
Cefixime	3(60.0)	2(40.0)	0(0.00)
Nitrofurantoin	3(60.0)	2(40.0)	0(0.00)
Ceftriaxone	5(100)	0(0.00)	0(0.00)

Antibiotics	Resistant (%)	Intermediate (%)	Susceptible (%)	
Ceftazidime	5(100.0)	0(0.00)	0(0.00)	
Cefuroxime	3(60.0)	2(40.0)	0(0.00)	
Gentamycin	0(0.00)	2(40.0)	3(60.0)	
Ofloxacin	0(0.00)	1(20.0)	4(80.0)	
Augmentin	4(80.0)	1(20.0)	0(0.00)	
Cefixime	4(80.0)	1(20.0)	0(0.00)	
Nitrofurantoin	0(0.00)	1(20.0)	4(80.0)	
Ceftriaxone	0(0.00)	1(20.0)	4(80.0)	

Table 4. Susceptibility pattern of *Klebsiella* Sp isolated from water samples

Table 5. Susceptibility patter	n of Se <i>rratia</i> sp isolate	d from water samples
rubic c. cuccoptibility pattor		

Antibiotics	Resistant (%)	Intermediate (%)	Susceptible (%)
Ceftazidime	5(100.0)	0(0.00)	0(0.00)
Cefuroxime	3(60.0)	2(40.0)	0(0.00)
Gentamycin	4(80.0)	1(20.0)	0(0.00)
Ofloxacin	0(0.00)	1(20.0)	4(80.0)
Augmentin	5(100.0)	0(0.00)	0(0.00)
Cefixime	3(60.0)	2(40.0)	0(0.00)
Nitrofurantoin	0(0.00)	1(20.0)	4(80.0)
Ceftriaxone	5(100.0)	0(0.00)	0(0.00)

3.3 Antimicrobial Susceptibility Profile

The response to the antibiotics by *Pseudomonas* sp showed that they were highly resistant to Ceftazidime, Nitrofurantoin and Ceftriaxone. They were only susceptible to Gentamycin (Table 2). Also, resistance to Ofloxacin, Augmentin and Cefixime was recorded and were in the order of 50%, 75% and 75%, respectively. Out of the five Enterobacter sp subjected to determine their antimicrobial susceptibility, five were completely (100%) resistant to Ceftazidime, Augmentin and Ceftriaxone, while four (80%) were resistant to Gentamycin and Ofloxacin (Table 3). The result also showed that while some of the Enterobacter isolates had intermediate response to the antibiotics, none was susceptible to any of the antibiotics (Table 3). The antibiotics susceptibility pattern of Klebsiella sp showed that out of the five isolates of Klebsiella, five were completely (100%) resistant to Ceftazidime, while four (80%) were resistant to Augmentin and Cefixime. respectively (Table 4). The result also showed that 80% of the isolates were susceptible to ofloxacin, nitrofurantoin and ceftriaxone, while 60% were susceptible to Gentamycin. It is worthy to note that though there was no resistance recorded against ofloxacin, nitrofurantoin and ceftriaxone. 20% had intermediate response. Intermediate response could mean that the Klebsiella isolates are developing some sort of resistance towards these antibiotic agents. The

all the isolates were 100% resistant to Ceftazidime, Augmentin and Ceftriaxone. While only 80% resistance was recorded for Gentamycin. Sixty percent (60%) resistance was recorded for Cefuroxime and Cefixime (Table 5). Also, despite 20% of the isolates being exhibiting intermediate response to Ofloxacin and Nitrofurantoin, 80% of the Serratia isolates were completely sensitive (Table 5). The susceptibility pattern of Klebsiella, Serratia, and Enterobacter sp showed that they were all resistant to Ceftazidime and Cefuroxime. As a result of indiscriminate disposal of antimicrobial agents, bacterial isolates could develop or synthesize substances or routes which would confer immunity to antimicrobial agents and they could transmit the resistance to other bacteria in the environment via conduction, transformation or conjunction. This statement agreed [10]. All the bacterial isolates were resistant to more than two antibiotics. The MAR index of all the isolates were greater than 0.2 (Table 7). Thus, we could posit that greater proportion of these isolates could have resulted from high risk source of environments with high use of antibiotics. The level of resistance in this study could also be drawn from the indiscriminate use of antibiotics, alteration of antibiotic target sites by the bacterial isolates, use of antibiotics in livestock feeds and self-medication. Also, the activities surrounding an environment could be responsible for the level of resistance. For instance, environments were

susceptibility pattern of Serratia sp showed that

Parameters	Well water stations									
	SASA	SBSA	SCSA	SDSA	SESA	SFSA	SGSH	SHSA	SISA	SJSA
pН	5.50±0.00	5.34±0.00	5.14±0.00	4.66±0.00	5.48±0.00	5.91±0.00	5.32±0.00	5.40±0.00	6.17±0.00	5.80±0.00
Temperature (°C)	24.5±0.00	24.0±0.00	24.1±0.00	24.1±0.00	24.4±0.00	24.2±0.00	24.7±0.00	23.9±0.00	24.4±0.00	24.3±0.00
Electrical Conductivity	219±0.00	59.6±0.00	98.0±0.00	289±0.00	115±0.00	22.9±0.00	73.7±0.00	55.4±0.00	58.2±0.00	91.4±0.00
(µS/cm)										
Salinity (ppt)	0.10±0.00	0.03±0.00	0.05±0.00	0.13±0.00	0.05±0.00	0.01±0.00	0.03±0.00	0.02±0.00	0.03±0.00	0.04±0.00
Dissolved Oxygen (mg/ml)	4.80±0.00	4.50±0.00	4.90±0.00	4.60±0.00	4.80±0.00	4.70±0.00	4.80±0.00	4.70±0.00	4.80±0.00	4.70±0.00
Total Hardness (mgCaCO3/l)	22.0±0.00	7.00±0.00	5.00±0.00	8.00±0.00	14.0±0.00	7.00±0.00	6.00±0.00	6.00±0.00	6.00±0.00	7.00±0.00
Alkalinity (mg/ml)	3.00±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00
Total Suspended Solids (mg/ml)	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00	<0.01±0.00
Biochemical Oxygen Demand (mg/ml)	62.0±0.00	84.5±0.00	55.8±0.00	68.5±0.00	49.6±0.00	66.5±0.00	57.4±0.00	65.0±0.00	50.5±0.00	52.0±0.00
Nitrate (mg/ml)	5.05±0.00	4.26±0.00	3.39±0.00	17.4±0.00	6.76±0.00	1.00±0.00	3.58±0.00	1.93±0.00	2.73±0.00	2.85±0.00
Chloride (mg/ml)	24.5±0.00	5.00±0.00	14.5±0.00	25.0±0.00	12.5±0.00	3.00±0.00	8.50±0.00	9.00±0.00	9.00±0.00	12.5±0.00
Calcium (mg/ml)	12.4±0.00	6.94±0.00	6.61±0.00	12.9±0.00	7.33±0.00	5.57±0.00	6.20±0.00	5.64±0.00	4.25±0.00	7.96±0.00
Magnesium (mg/ml)	1.49	0.753	0.754	1.55	1.03	0.819	0.997	0.830	0.722	0.834

Table 6. Chemical parameters of the well water stations

Key: SASA: Station A Water Sample, SASB: Station B Water Sample, SASC: Station C Water Sample, SASD: Station D Water Sample, SASE: Station E Water Sample, SASF: Station F Water Sample, SASG: Station G Water Sample, SASH: Station H Water Sample, SASI: Station I Water Sample, SASJ: Station J Water Sample

MAR Index	Number (%)						
	Pseudomonas	Enterobacter	Klebsiella	Serratia			
0.3	0(0.00)	2(40)	2(40)	0(0.00)			
0.4	0(0.00)	0(0.00)	0(0.00)	2(100)			
0.5	2(50)	3(60)	3(60)	0(0.00)			
0.6	1(25)	0(0.00)	0(0.00)	0(0.00)			
0.7	1(25)	0(0.00)	0(0.00)	0(0.00)			

Table 7. MAR indices of bacterial isolates from the water samples

wastes especially wastes of pharmaceutical products or livestock feeds are dumped could habour more resistant microorganisms than those environments were such activities are minimized or not practiced. More so, excretory products of live stocks which are fed with feeds containing antibiotics in the environment could be decomposed by a particular organism which in turn could use such substances in building itself against similar agents. According to Adeleke and Omafuvbe [22] the continuous inclusion of antimicrobial agents in feeds for animals could result to the proliferation of zoonotic pathogens which could be selectively resistant to some antibiotics and could be transferred to humans. It is well documented that in other to adapt in an environment, microorganisms try to synthesize substance or modify antibiotics target sites that could aid them, others known as competent cells are able to pick up resistant DNA in the environment and incorporate it in their DNA, while other bacteria could receive resistance gene from a donor [10,23]. Furthermore, the bacterial isolates showed varying level of resistance to Ofloxacin. Ofloxacin is considered to be a fluoroquinolone antibiotic which possess broad spectrum activities and is used in treatment of bacterial infections of skin, urinary tract, bronchitis, pneumonia, chlamydia and gonorrhea [10]. Resistance of bacterial isolates to fluoroquinolone have been reported. Ramya et al. [24] in a study of the Detection of Vancomycin Resistance among Enterococcus faecalis and Staphylococcus aureus reported that 79.03% of Enterococcus faecalis were resistant to Ciprofloxacin (a fluoroquinolone) while 57.7% Staphylococcus aureus were resistant to Ciprofloxacin. High resistance to Gentamycin by isolates in this study were also recorded. Gentamycin is an aminoglycoside and carries out its antimicrobial effects by attaching to the 30S ribosomal subunit of the bacteria; thus, altering the proof-reading function which leads to the synthesis of toxic proteins caused by wrong interpretation of the mRNA [25]. Resistance of

the bacterial isolates in this study agreed with previous studies [24,26].

3.4 Physicochemical Parameters

The pH of all the well water across the stations varied from acidic to slight acidity and they ranged between 4.66-6.17. With the exception of the SISA well water station which is within the acceptable limit, all the pH values of the other well water are below the 6.5 - 8.5 and 6.50-7.50permissible limits of the WHO and NIS. respectively [27]. The pH of the different well stations which were acidic could corrode pipes and iron buckets, produce bad odour in food and drinks and also stain fabrics. This statement agreed with Mwekaven et al. [28]. The range of pH in this current study, though slightly acidic are lower than those reported by Obire and Osigwe [21] of spring water, and Mwekaven et al. [28] in different well water. The temperature of the well water varied respectively. A study by Charkhabi and Sakizadeh [29] reported a correlation between the pH and temperature of water body. Thus, an increase in temperature causes an increase in the pH and the effect on the pH also affects the dissolved oxygen which affects the amount of BOD available in the water. In this current study, no correlation of temperature and pH was made but the result showed that the temperature varied across the various well water with variations also observed in the pH. The temperature ranges in this current study (Table 6) are less than those reported by previous studies [27,28,30]. More so, the increase of the physico-chemical parameters of water above the required limits or out of the range required have been reported to have detrimental effects on health [19]. Thus, all the physico chemical parameters are within the WHO recommended limits. According to Mwekaven et al. [28] there are no recommended standards for DO and BOD for water. However, the DO in this study are higher than the 2.00-4.00 Mg/L reported by Mwekaven et al. [28] and

lower than the 9.24 mg/L to 9.34 mg/L reported by Ajit and Padmakar [31].

4. CONCLUSION

The well water from the different stations are not safe for drinking as microbial loads as well as coliform values exceeded the acceptable limits. More so, the bacterial isolates as presented in this study could be pathogenic especially when the water in this area are consumed without proper treatment. Diseases ranging from gastroenteritis to urinary tract infections and other cases of infections could be prevalent especially to consumers of untreated water from these locations. Furthermore, the level of antimicrobial resistance exhibited by bacterial isolates in this study is a cause for alarm.

5. RECOMMENDATION

We therefore recommend that well water should be properly treated, water could be boiled and stored in clean containers. Strict hygiene which would include covering of wells, not washing close to wells and spitting inside wells should be practiced. It would also be of immense help if treated pipe borne water sources are made available in this communities. After all, safe drinking water is the right of all.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

- Adogo LY, Anyanwu NCJ, Ajiji MA, Bukola Ajide. Bacteriological and physio-chemical analysis of borehole water in Auta Balifi Community, Nigeria. British Microbiology Journal. 2016;11(4):1-7.
- Rajini Kuruf, Roland Persaud, John Ceaser, Vincent Raja. Microbiological and physiochemical analysis of drinking water George Town, Guyana. Nature and Science. 2010;8(8):261-265.
- Obafemi O. Olubanjo, Alade E. Adebolu, Olubanjo M. Abosede. Bacteriological. assessment of borehole and wells water in Akungba-Akoko, Nigeria. International Journal of Agriculture, Environment and Bioresearch. 2018;3(6):2456-8643.
- 4. Palamuleni L, Akoth M. Physico-chemical and microbial analysis of selected borehole water in Mahikeng, South Africa.

International Journal of Environmental Research and Public Health. 2015;12: 8619-8630.

- Obire O, Aguda M, Ramesh RP. Impact of human activities on drinking water quality. Journal of Basic and Applied Biology. 2008;2(3&4):52-58.
- World Health Organization. Guidelines for drinking-water quality: Fourth edition incorporating the first addendum. Geneva; 2017.
- Obioma A, Chikanka AT, Loveth NW. Evaluation of bacteriological quality of surface, well, borehole and river water in Khana Local Government Area of Rivers State, Niger Delta. Ann Clin Lab Res. 2017;5(3):183.
- Sur D, Sarka BL, Dean J, Delta S, Niyogi SK, et al. Epidemiological, microbiological and electron microscopic study of a cholera outbreak in a Kolkata slum community. Indian J Med Res. 2006;123: 31-36.
- WHO. Guidelines for drinking water quality (3rd Edn). WHO, Geneva, Switzerland; 2003.
- 10. Prescott LM, Harley J, klein DA. Microbiology 8th Ed, McGraw-Hill New York. 2011;809-811.
- Wemedo SA, Robinson VK. Evaluation of indoor air for bacteria organisms and their antimicrobial susceptibility profiles in a Government Health Institution. Journal of Advances in Microbiology. 2018;11(3):1-7.
- Parkyz AL. The utility of hospital antibiograms as tools for guiding empiric therapy and tracking resistance insights from the society of infectious diseases pharmacists. Pharmacotherapy. 2007; 27(9):1306-1312.
- 13. Wemedo SA, Obire O, Akani NP. Bacterial population of an oilfield wastewater in Nigeria. Asian Journal of Biological Sciences. 2012;5:46-51.
- 14. Chesbrough M. District laboratory practice in tropical countries, Part. Cambridge University Press U.K. 2005;55-80.
- Holt JG, Krieg NR, Sneath PHA, Staley JT, Williams ST. Bergey's manual of determinative bacteriology. Williams and Wilkins, Baltimore, Maryland, USA. 1994;151–157.
- Clinical and Laboratory Standard Institutes. Performance standards for antimicrobial disk susceptibility tests. CLSI Document M100. Clinical and Laboratory Standard Institutes, 28th Edition; 2013.

17. EPA. US Environment Protection Agency. Safe drinking water act ammendment; 2002.

Available:http:// www. epa. gov/safe water /mcl. Html

- Azuonwu O, Azuonwu TC, Nwizug WL. Evaluation of bacteriological quality of surface, well, borehole and river water in Khana Local Government Area of Rivers State, Niger Delta. Annals of Clinical and Laboratory Research. 2017;3:183.
- 19. World Health Organization (WHO). Guideline for drinking water quality 4 Edition, WHO, Switzerland. 2011;156.
- Augustín L, Adriana LS, Pedro MR, María MS. Assessment of the microbiological quality of groundwater in three regions of the Valencian Community (Spain). International Journal of Environmental Research and Public Health. 2014;11: 5527-5540.
- Obire O, Osigwe IS. Bacterial quality of spring water in Ihitte/Uboma LGA of Imo State, Nigeria. Current studies in comparative education. Science and Technology. 2016;3(2):149-155.
- Adeleke EO, Omafuvbe BO. Antibiotic resistance of aerobic mesophilic bacteria isolated from poultry faeces. Research Journal of Microbiology. 2011;6(4):356-365.
- 23. Suely APF, Erica MDS, Patricia FS, Paola CL, Lúcia MT. Antimicrobial resistance profiles of enterococci isolated from poultry meat and pasteurized milk in Rio de

Janeiro, Brazil. Mem Inst Oswaldo Cruz, Rio de Janeiro. 2007;102(7):853-859.

- Ramya R, Shanthi M, Uma S, Arunagiri K. Detection of vancomycin resistance among *Enterococcus faecalis* and *Staphylococcus aureus*. Journal of Clinical and Diagnostic Research. 2016;10(2):4-6.
- 25. Tom E, Anna C, Peter L, Jonathan S. Medical microbiology and infection (5th Edn). 2011;147.
- Shittu AO, Lin J. Antimicrobial susceptibility patterns and characterization of clinical isolates of *Staphylococcus aureus* in KwaZulu-Natal province, South Africa. BioMed Central Infectious Diseases. 2006;125–126.
- Aderibigbe SA, Awoyemi AO, Osagbami GK. Availability, adequacy and quality of water supply in llorin Metropolis, Nigeria. European. J. Sci. Res. 2008;23(4):528-636.
- Mwekaven SS, Aorkwagh MT, Gundu EG, Yange T. Physico-chemical and microbiological analysis of well water stations In settlements around Akperan Orshi College of Agriculture, Yandev. International Journal of Science and Technology. 2017; 6:1.
- 29. Charkhabi AH, Sakizadeh M. Assessment of spatial variation of water quality; 2006.
- 30. Baird C, Cann M. Environmental chemistry (3rd Edition). W. H. Freeman, USA; 2004.
- Ajit MK, Padmakar AS. Determination of physico-chemical parameters of deoli bhorus dam water. Advances in Applied Science Research. 2012;3(1):273-279.

© 2020 Nrior et al.; This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history: The peer review history for this paper can be accessed here: http://www.sdiarticle4.com/review-history/55043