

## Original Research Article

### **OCCURRENCE, PHYSICOCHEMICAL PROPERTIES AND ANTIBIOTIC RESISTANCE PATTERNS OF ENTERIC BACTERIA ISOLATED FROM WELL WATER IN ILARA-MOKIN, ONDO STATE, NIGERIA**

#### **ABSTRACT**

The occurrence of enteric bacteria isolated from well water sources, their resistance to antibiotics and their physicochemical profile were ascertained in this study. High bacterial counts ranging from 7 to 250 bacterial counts/100ml were recorded. Molecular analysis of bacterial isolates from the well water samples was conducted via polymerase chain reaction (PCR)-based identification. *Klebsiella pneumoniae*, *Escherichia coli*, *Salmonella typhi* and *Shigella dysenteriae* were the Gram-negative organisms enumerated and molecularly-identified as *Klebsiella pneumoniae* subsp. *Pneumoniae* HS11286, *Escherichia coli* 0157:H7, *Salmonella enterica* subsp. *Enterica* serovar *typhimurium* and *Shigella dysenteriae* HNCMB 20080 from the well water samples with percentage identity of 97.19 %, 87.44 %, 80.45 % and 96.19 % respectively. *Klebsiella pneumoniae* showed 67% resistance to augmentin during the dry season and 100% during the rainy season. *Shigella dysenteriae* and *E. coli* showed 8.3%, 67% resistance to augmentin during the dry season, and 75%, 58% resistance during the rainy season respectively. Water hardness had the highest mean of 98.5 and 99.5 mg/L in dry and rainy season respectively while turbidity, and alkalinity had the least mean value at 1.2 (NTU) and 0.62 mg/L, 1.4 (NTU) and 0.7mg/L in both dry and wet seasons respectively. Findings provided information on the poor quality of the well water, these information will be useful in groundwater treatment strategies and policy formulation by appropriate groundwater source protection bodies.

**Keywords:** Enteric bacteria, well-water, physicochemical profile, dry season, rainy season

#### **Introduction**

Water is one of the most indispensable requirements in life. It is a substance that is well valued and appreciated. For human consumption and good health, water must be free from pathogenic organisms, poisonous minerals and organic substances (Folorunso *et al.*, 2014). Most human population in semi-urban and rural areas in Nigeria rely mostly on well water as the main source of water supply for domestic use and drinking, due to inadequate provision of potable pipe borne water (Aboh *et al.*, 2015). Groundwater such as wells can easily be fecally contaminated and thus, increase the incidence and outbreaks of water borne diseases (Aboh *et*

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al., 2015). Up to 80% of all illnesses and diseases in the world are implication of inadequate sanitation, polluted water or non-availability of water (Olowe *et al.*, 2016). The infectious diseases caused by drinking unsafe water are the leading cause of mortality and morbidity for children under the age of 5 years and about 1.5 million deaths occur annually in developing countries (Bahiru *et al.*, 2013). Water is vital both as a solvent in which many of the body's solutes dissolve and as an essential part of many metabolic processes within the body (Gaseca and Zahnle, 2019).

There are greater chances of water-borne diseases with increase turbidity of water. This is because contaminants like viruses and bacteria can be attached to these suspended solids which protected them from disinfection by chlorination or ultraviolet (UV) sterilization (Jung *et al.*, 2021). The inhibited rays of sunlight by suspended particles can influence the rate of photosynthetic activity and thus reduce the dissolved oxygen level of the water (Yisa *et al.*, 2012). Dissolved oxygen level in water bodies can be influenced because suspended particles absorb sunlight and increase the temperature of the water which consequently reduces the oxygen level of such water. Total dissolved solids are a general indicator of overall water quality. It is a measure of inorganic and organic materials dissolved in water. Increased total dissolved solids (TDS) may impart a bad odour or taste to drinking water, as well as cause scaling of pipes and corrosion (Napacho and Manyele, 2010). Water hardness is the traditional measure of the capacity of water to react with soap (Soni *et al.*, 2013). The WHO permissible level for total hardness is 500 mg/l as CaCO<sub>3</sub>. Water hardness can be classified as soft, moderate soft, slightly soft, slightly hard, moderate hard and excessively hard (Benard and Ayeni, 2012).

Groundwater pollution occurs when pollutants are released to the ground and make their way down into groundwater by erosion or leaching (Ackah *et al.*, 2011). The presence of enteric pathogens in drinking water sources is of great concern, therefore, legislation either in Europe, United States and other countries requires analysis of indicators to determine the microbiological quality of these water sources. The analysis of several microorganisms classed as either indicator or index organisms are the most useful tool to determine the potential presence of pathogens in waters (Odonkor and Ampofo, 2013). Hence, the occurrence and antibiotic resistance patterns of enteric bacteria isolated from well water in Ilara-Mokin metropolis was ascertained in this study. This study set out to isolate and characterize molecularly the enteric bacteria isolated from selected well water sources in Ilara-Mokin, Ondo State, carry out sensitivity tests on the isolates, determine the resistance of the isolates and estimate the physicochemical properties such as pH, conductivity, hardness, alkalinity, acidity, total dissolved solids, temperature and turbidity of the well water.

## MATERIALS AND METHODS

### Study area

The study took place in Ilara-Mokin, which is located in the central part of Ifedore local government in Ondo state, Nigeria. Ilara-Mokin is an urban settlement, well known for her rich

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and preserved culture, academics, agriculture and tourism. It is about 12km from Akure, the state capital of Ondo State (Adu, 2019).

### Sample sites

Well water samples were collected from selected compounds of political zones of ward one and ward two in Ilara- mokin town, Ifedore Local Government, Ondo State, Nigeria. Assessments of the selected compounds were done by using a well-planned questionnaire and their addresses were noted.

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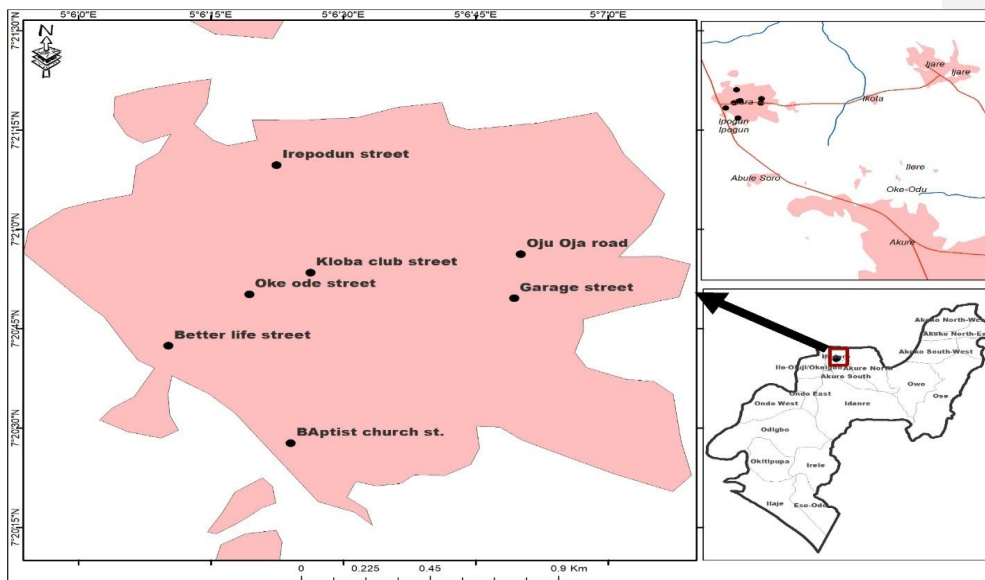


Figure 1. Locality map of Ilara-Mokin, Nigeria showing sample collection locations

### Sample collection

Total of 12 wells were used for this study. Samples were collected in triplicate from each well, and mean values were obtained. The first batch of samples were collected during the dry season in January and February, 2020. The second batch of samples were collected during the

rainy season in July 2020. The well water samples were aseptically collected from selected areas in Ilara-Mokin, Ifedore, Nigeria, using sterile well fetcher and seven hundred and fifty milliliters (750 ml) polypropylene sample bottles. The samples were collected according to internationally recommended methodology. Samples were kept at 4 °C until arrival in the laboratory.

**Comment [A7]:** Was the staff trained for sample collection packing and transportation?

**Comment [A8]:** Kindly mention the methodology in brief

**Comment [A9]:** How was the temperature maintained ?

### **Microbiological analysis of well water samples**

The test used for the detection of coliforms and other enteric bacteria in this study was the most probable number (MPN) method.

### **The most probable number analysis of well water samples**

The MacConkey broth (Hi-Media, India), was prepared in single and double strength in test tubes with Durham's tubes in inverted position and was autoclaved. Three sets of test tubes containing five tubes in each set; one set with 10ml double strength (DS) other two sets containing ten millilitre of single strength (SS). Using sterile pipettes, 10ml of the well water was transferred into each of Double Strength broth tubes. One milliliter of the well water sample was transferred into one set of single strength broth and 0.1ml well water sample was transferred into the last set of Single Strength broth tubes. The tubes were incubated at 37 °C for 24 hours, after which they were observed for gas production in Durham's tube and for colour change of the media. Number of positive result from each set was recorded and compared with the standard chart to give presumptive bacterial counts per 100 ml of well water sample as described by Sagar, (2018).

To ascertain the presence of coliforms, confirmatory test was done as some bacteria may produce acid and gas from lactose fermentation. A loop full of suspension from a positive tube was inoculated into 3 ml lactose broth and brilliant green lactose fermentation tube and the inoculated lactose broth fermentation tubes was incubated at 37°C and were inspected for gas formation after 24 hours and 48 hours.

A loop full of the suspension from a positive tube was inoculated on to selective media agar plates; Eosin Methylene Blue (EMB) agar (Hi-Media, India), Simion Citrate agar (Hi-Media, India), and Salmonella-Shigella agar (Hi-Media, India). The plates were incubated at 37°C for 24 h, after which colonies were examined macroscopically. Pure isolates were achieved by sub-culturing on nutrient agar plates as described by Sagar (2018).

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### **Enumeration and Identification of bacterial isolates**

Serial dilution and standard pour plate method using one (1) ml of 10<sup>-4</sup> diluent of the well water samples was employed as bacterial colonies were enumerated on nutrient agar (Hi-Media, India) and MacConkey agar (Hi-Media, India) plates as demonstrated by Fawole and Osho, (2001). The bacteria petri-plates were incubated for duration of 18-24 hours at 37 °C. The bacterial colonies were then sub-cultured for identification through molecular analysis. Biochemical confirmatory tests were conducted on the isolated bacteria including; Gram reaction, motility, urease, indole, citrate utilization and sugar fermentation tests for their identification and compared with Bergey's manual of systematic bacteriology (Don et al., 2006).

### Molecular analysis of bacterial isolates from well water samples

Polymerase chain reaction (PCR)-based identification and characterization of bacterial isolates were carried out with DNA extraction of bacterial isolates according to the technique described by Gurakan *et al.* (2008). The 16SrRNA gene of the bacteria was amplified using the primer pair 27F-5'-AGAGTTTGATCCTGGCTCAG-3', and 1492R 5'GGTTACCTTGTTACGACTT-3'. PCR extension was carried as described by Sambrook *et al.* (2001); the PCR profile used was at initial denaturation temperature of 94 °C for 3 mins, followed by 30 cycles of 94 °C for 60 sec, 56 °C for 60 sec, 72 °C for 120 seconds and the final extension temperature of 72 °C for 5 minutes followed by sequencing and genetic make-up blasting using the National centre for biotechnological information (NCBI) server. PCR-sequencing was conducted using DNA Sanger sequencing and data was analyzed by ABI Sequencing Analysis software (version 5.2).

Comment [A12]: manual or automated method?

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Comment [A14]: Kindly mention the laboratory where gene sequencing was conducted

### Antibiotics Sensitivity Test

Antibiotic susceptibility test was carried out on all the identified isolates from the twelve wells sampled, during the dry season and during the rainy season, using standard disc diffusion techniques as recommended by Clinical Laboratory Standard Institute (CLSI) (2018). Ten (10) antibiotics of different classes were tested. Ten (10) antibiotics of different classes were tested. The antibiotics and their concentration were as follow; **aminoglycosides**; gentamycin (30ug), streptomycin, (30ug); **betalactam**: augmentin (10ug), **fluroquinolones**; ciprofloxacin (30ug), sparfloxacin (10ug), pefloxacin (30ug) ofloxacin (10ug), **penicillin**; amoxicillin (30ug), **folate pathway inhibitors**; co-trimoxazole(septrin)(30ug), **phenicols**; chloramphenicol (30ug). The antibiotics were chosen based on their importance in treating human infections caused by Gram negative bacteria such as *Esherichia coli*, *Salmonella typhi*, *Shigella dysentariae* and *Klebsiella pneumoniae*. Standardized inoculum was prepared by making a direct broth suspension of discrete colony selected from 18 – 24 hours culture using sterile peptone water. The suspension was adjusted to match the 0.5 McFarland for study standard. The dried surface of Nutrient agar plate was inoculated by pouring the standardized inoculum on the plate and then rotated for even distribution on the plate. Excess inoculum was removed by decanting it into a bowl containing disinfectant liquid. The surface of the inoculated plates was allowed to dry before applying the drug-impregnated disk. The antibiotic discs were dispensed aseptically onto the surface of the

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inoculated agar plate. Each disc was pressed down to ensure complete contact with the agar surface. The plates were inverted and incubated at 35°C for 18 – 24hours and diameter of the zone of inhibition was read and recorded. The results of the susceptibility testing were interpreted as Resistance (R), Intermediate (I), or susceptible (S) using standard interpretative charts of CLSI (2018).

#### **Determination of the physicochemical properties of the well water samples**

The physicochemical properties of the water samples comprising pH, electrical conductivity (mS/cm), and total dissolved solids (mg/l) of the water samples were determined using a multi-parameter analyzer (HI98194, PH/ORP/EC/DO), temperature (°C) was determined using mercury-in-glass thermometer (ACCU-SAFE Thomas Scientific, New Jersey, US). Alkalinity (mg/l), and acidity (mg/l) was determined using titration method, turbidity (NTU) was determined via spectrophotometer (Benchtop Spectrophotometer S6003, China). These physical and chemical properties were selected in order to evaluate their influence on the microbial

Sample	Bacterial counts /100ml	Bacterial counts/100ml
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indicators and enteric bacteria in the water sample.

## **RESULTS**

### **Total viable bacterial counts during dry season and rainy season**

Table 1 shows the total viable bacterial counts during dry season and rainy season. Large bacterial counts ranging from 7 to 250 bacterial counts/100ml were recorded. In the dry season, sample one had 17 bacterial counts/100ml which increased to 39 bacterial counts/100ml in the rainy season. Sample two had a high count of 140 bacterial counts/100ml which increased to 250 bacterial counts/100ml. However, sample three had a decrease from 47 bacterial counts/100ml to 26 bacterial counts/100ml in the rainy season. Sample six bacterial counts remained the same at 21 bacterial counts/100ml. Sample 7 in the dry season had 250 bacterial counts/100ml but in the rainy season was reduced to 200 bacterial counts /100ml. Sample 8 to 12 had values ranging from 7 to 20 bacterial counts/100ml.

	Dry season	Rainy season
1	17	39
2	140	250
3	47	26
4	14	20
5	35	39
6	21	21
7	250	200
8	20	17
9	35	17
10	14	12
11	14	7
12	15	12

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**Table 1. Total viable bacterial counts during dry season and rainy season**

**Occurrence of bacteria in well water samples**

Isolates	Samples												% occurrence
	1	2	3	4	5	6	7	8	9	10	11	12	

Table 2 reveals the bacteria isolated from the well water samples. Four organisms were isolated, which were identified as *Escherichia coli*, *Klebsiella pneumoniae*, *Shigella dysenteriae* and *Salmonella typhi*. *Escherichia coli* were 100 % present in all the samples in the dry season and in the rainy season. *Klebsiella pneumoniae* and *Shigella dysenteriae* were 100 % present in the rainy season but 83 % and 75 % present respectively in the dry season. *Salmonella typhi* were the least isolated with 58 % presence rate in the dry season and 50 % in the rainy season.

**Table 2. Occurrence of bacteria in well water samples**

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**Dry season**

<i>Escherichia coli</i>	+	+	+	+	+	+	+	+	+	+	+	+	100
<i>Klebsiella pneumoniae</i>	+	+	-	+	+	+	+	+	+	+	+	-	83
<i>Shigella dysenteriae</i>	+	-	+	+	+	+	+	-	+	+	+	-	75
<i>Salmonella typhi</i>	+	-	-	+	+	+	-	+	-	+	-	+	58

**Rainy season**

<i>Escherichia coli</i>	+	+	+	+	+	+	+	+	+	+	+	+	100
<i>Klebsiella pneumoniae</i>	+	+	+	+	+	+	+	+	+	+	+	+	100
<i>Shigella dysenteriae</i>	+	+	+	+	+	+	+	+	+	+	+	+	100
<i>Salmonella typhi</i>	+	-	-	-	-	+	+	-	-	+	+	+	50

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Key: - = not isolated, + = isolated

**Biochemical characteristics of bacterial isolates from well water**

*Klebsiella pneumoniae*, *Escherichia coli*, *Salmonella typhi* and *Shigella dysenteriae* were the Gram-negative bacteria enumerated from the well water samples in this study as illustrated in Table 3.

**Table 3. Biochemical characteristics of bacterial isolates from well water**

Biochemical test	<i>Klebsiella pneumoniae</i>	<i>Escherichia coli</i>	<i>Salmonella typhi</i>	<i>Shigella dysenteriae</i>
Gram stain	-	-	-	-
Indole test	-	+	-	-
Citrate utilization test	+	-	-	-
Motility	-	+	+	-
Urease test	+	-	-	-

Sugar fermentation;				
Glucose	+	+	+	+
Sucrose	+	+	-	-
Lactose	+	+	-	-

Key; - = negative, += positive

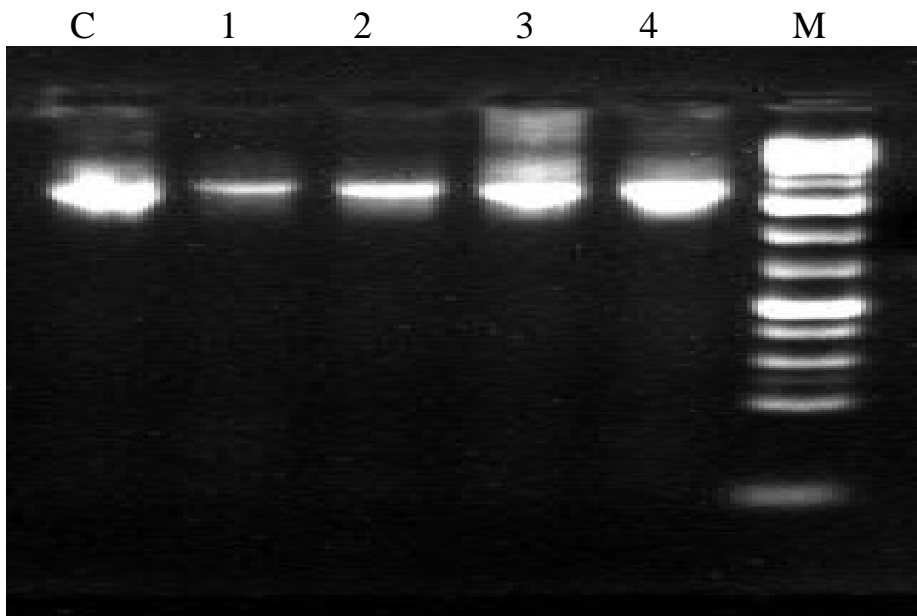
#### Molecular identity of bacterial isolates from well water samples

*Klebsiella pneumoniae* subsp. *Pneumoniae* HS11286, *Escherichia coli* 0157:H7 strain sakai DNA, *Salmonella enterica* subsp. *Enterica* serovar *Typhimurium* strain LT2 and *Shigella dysenteriae* strain HNCMB 20080 were molecularly-identified from the well water samples with percentage identity of 97.19 %, 87.44 %, 80.45 % and 96.19 % respectively (Table 4). Plate 1 shows the Polymerase chain reaction (PCR) of the bacterial isolates on ethidium bromide electrophoresic gel.

**Table 4. Molecular identification of bacterial isolates from the well water samples**

Isolate Codes	Similarity %	Molecular identity	NCBI Gene bank accession number	Isolates identified
C1	97.19	<i>Klebsiella pneumoniae</i> subsp. <i>Pneumoniae</i> HS11286	NC-016845.1	<i>Klebsiella pneumoniae</i>

C2	87.44	<i>Escherichia coli</i> 0157:H7 strain sakai DNA	<i>Escherichia coli</i>
			NC-002695.2
C3	80.45	<i>Salmonella enterica</i> subsp. <i>Enterica</i> serovar <i>Typhimurium</i> strain LT2.	<i>Salmonella typhi</i>
			NC-003197.2
C4	96.19	<i>Shigella dysenteriae</i> strain HNCMB 20080	<i>Shigella dysenteriae</i>
			NZ-CP061527.1



**Plate 1. Polymerase chain reaction (PCR) of bacterial isolates on ethidium bromide electrophoresis gel**

1=-*Escherichia coli*, 2- *Klebsiella pneumoniae*, 3- *Salmonella typhi*, 4- *Shigella dysenteriae*  
M=Marker, C=control

**Comment [A18]:** Kindly label the base pair

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Each bacteria amplicon had to be at different levels

### Resistance of bacterial isolates from well water samples to antibiotics

Figure 2 revealed the resistance of the bacterial isolates to ten different antibiotics during the dry season. *E. coli* and *Klebsiella pneumoniae* showed resistance of 67% to augmentin, *Salmonella typhi* showed resistance rate of 41% while *Shigella dysenteriae* showed 8.3% resistance rate to augmentin. *Salmonella typhi* showed 50% resistance to amoxicillin, *Klebsiella pneumoniae* showed 41% resistance rate, while *Escherichia coli* showed 18% resistance to amoxicillin. *Shigella dysenteriae* showed 41% resistance to Streptomycin, while *Salmonella typhi* and *Klebsiella pneumoniae* gave 25% resistance rate.

*Klebsiella pneumoniae* gave higher resistance rate to augmentin, amoxicillin, and streptomycin at 87%, 100% and 87% respectively during the rainy season as shown in figure 3

**Comment [A20]:** How was this performed kindly explain method adopted

**Comment [A21]:** Disk diffusion is interpreted as zone of inhibition in mm.

Kindly explain the method used to get percentage resistance in disk diffusion method

**Figure 2. Resistance of bacterial isolates from well water samples during dry season.**

**Figure 3. Resistance of bacterial isolates from well water samples during the rainy season.**

**Physicochemical profile of well water samples**

Hardness mean value obtained was 98.5 and 99.5 mg/L in dry and rainy season respectively while turbidity, mean values were 1.2 and 1.4 Nephelometric turbidity unit (NTU), acidity mean values were 1.9 and 2.0mg/L. Alkalinity mean value were 0.6 and 0.7mg/L respectively. Also, Total Dissolved Solids in both dry and rainy season were 14.0 and 15.3mg/L (Figure 4).

**Figure 4. Physicochemical properties of the well water samples during the dry and rainy season.**

### **Discussion**

The high value of bacterial counts recorded ranged from 7 to 250/bacterial counts per 100ml from the wells indicated that the well water were faecally contaminated probably as a result of agricultural surface runoff, seepage or exposure to birds and other pest faeces. This is in agreement with Tambe *et al.* (2008) who also recorded that ground water samples were frequently contaminated with human faecal organisms. There was an increase in the total bacterial count in the rainy season, increase from 140 bacterial counts per 100ml during the dry

season, to 250 bacterial counts per 100ml during the rainy season. This may be due to rain fall. Erosion may wash these organisms from areas where they had been deposited to the well resulting in increased contamination. *Escherichia coli* was isolated from all the well samples, while *Salmonella typhi* was isolated from 58% of the well water samples.

The detection of *E. coli* is an indication of faecal organisms present in the water samples in low and high concentration. The high concentrations of *E. coli* in the groundwater samples in this study is similar to the findings of related studies such as Ghimire *et al.* (2013); Sharma *et al.* (2017) as they observed high concentrations of *E. coli* in surface drinking water samples. Kirstein *et al.* (2017) also reported *E. coli* values that ranged between 1 and >200 per 100 mL sample in drinking water of Sagarmatha national park, Nepal. The results of relatively high concentrations of *Salmonella* species in this study is consistent with the findings of Kovacic *et al.* (2017) who enumerated *Salmonella* species from groundwater sources. Possible sources and reason of *Salmonella* in ground water may be attributed to inappropriately composted manure that may be transferred to fresh water via the flow paths of the soil or within the surface run-off water in line with the observation of Jacobsen and Bech (2012) as the groundwater source is surrounded by arable farm lands. The detection of *Shigella dysenteriae* in the well water samples indicated the presence of faecal materials present in different concentrations. The relative concentrations of *Shigella dysenteriae* in this current study is in agreement with the findings reported by Rasel *et al.* (2002), who isolated *Shigella* species from surface water. Similarly, a study conducted in Yaounde by Yongsu (2008) observed that *Shigella dysenteriae* had 0.24% occurrence from variety of drinking water. The presence of *Shigella dysenteriae* in household well water could be due to poor sanitation and contamination with faecal materials.

The molecular identity of the enteric bacteria enumerated from the well water samples in this study is similar to the observations of Abada *et al.* (2019). Recently, universal primers have been used to amplify the conserved region of 16S rRNA through the PCR technique (Amir *et al.*, 2013). The outcome of the molecularly-characterized enteric bacteria in this study could be attributed to the fact that most common health hazards associated with drinking water resulted from contamination by pathogenic Gram-negative bacteria as supported by Abada *et al.* (2019).

The findings in the present study indicated that the enteric bacteria recovered showed high levels of resistance to antibiotics that are commonly used in treating infectious water borne related diseases in the study areas. This could contribute to the spread and persistence of antibiotic-resistant bacteria and resistance determinants in humans and the environment. *Klebsiella pneumoniae* gave the highest resistance rate, the ability of the organism to produce the enzymes extended spectrum beta lactamases may be a contributing factor for this resistance. One of the most important factors contributing to the spread of antibiotic-resistance in bacteria has been attributed to the fact that in most developing countries including Nigeria, diarrheal diseases are treated with inadequate regimen of antimicrobials and often empirically without first identifying the pathogens. Nontongana *et al.* (2014) had reported high resistance rate of coliforms to antibiotics.

Comment [A22]: Spelling correction

Antibiotics used in animal husbandry as growth promoters could be another factor contributing to antibiotic-resistant bacteria in ground water sources as the gut microbial flora of these animals end up developing resistance to these antibiotics when they get to the environment, and passing the same to autochthonous bacteria in ground water. The dissemination of antibiotic resistance in the environment may have potential negative clinical implications for therapeutic advancement (Samie *et al.*, 2012; Akhter *et al.*, 2014). Resistance of *E. coli* from drinking water sources to commonly used antibiotics has been documented (Mishra *et al.*, 2013; Oluyeye *et al.*, 2014).

The mean values of the physicochemical parameters of the well water samples were evaluated. The mean value for pH in dry and rainy season was 6.5 which is within the range of standard maximum permissible limit set by WHO (2009) which range from 6.0 to 8.5. A similar result was also reported by Chinedu *et al.* (2011). They recorded pH values between the range of 5.96 and 7.17 for surface water samples collected from Ota, Ogun State, Nigeria. The findings from this study in respect of the pH are similar to the findings of Oyem *et al.* (2014). Acidic water has been identified to cause damage to cells of mucous membrane, eyes and skin irritation (Meinhardt, 2006; Popoola *et al.*, 2019). The alkalinity of water samples may be due to the presence of bicarbonates lost into the soil and percolated into the underground soil via rain water essentially in the rainy season. The temperature values of the well water samples reported in this study could be attributed to an increase in environmental temperature and imbalances the environment, may also be a factor increase in temperature and biological productivity (Togue *et al.*, 2017). A high water temperature can cause damage to some organisms which require cold water and high oxygen. The hotter the water, the less dissolved oxygen it contains. The temperature of the water does not change at the same speed as that of the air: it cools less quickly. Indeed, water has a higher thermal capacity than that of air. The high conductivity value reported could be attributed to the dissolution of ionic heavy metals from industrial activities of heavy machines which later found their ways into groundwater via leaching of sub-soil layers (Popoola *et al.*, 2019). The increased variation of the total dissolved solids in the well water samples may be as an indication of the presence of inorganic salts and small amount of organic matter in excess concentration which could make water objectionable and shorten the duration of hot water heaters. The concentration of hardness in the groundwater samples is as a result of metallic ions dissolved in the water as concentration of calcium carbonate, which is known to decrease the lather formation of soap and increase scale formation in hot-water heaters and low-pressure boilers at high levels.

## Conclusion

This study provided information on the poor quality of well water in Ilara-Mokin, Ondo State, Nigeria. It also revealed the extent of contamination of well water sources. The observations from this study suggest the need for focused intervention on water source protection and sanitation practices, especially during the rainy season by appropriate authorities to conduct

quality assessment of well water sources from time to time in order to ensure good quality drinking water availability. Also, the results obtained may be useful in the management strategies and decision making as well as planning and policy formulation by the appropriate water source protection bodies or agencies.

Comment [A23]: Well written

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