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Original Research Article

Evaluation of the bacteriological quality of underground well water in Oyi local government area of Anambra State, Nigeria

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ABSTRACT

Background: Water is indispensable for man's existence on earth. In urban and predominantly rural communities in Nigeria, with over 85% of the population living below an average income, traditional drinking water sources such as open reservoirs, springs and open wells are still being used. The study assessed the bacteriological qualities of underground well water in Oyi L.G.A of Anambra State.
Methods: Water samples collected by random sampling from various wells in the selected thirteen (13) wards of the study area were subjected to bacteriological analysis using standard methods. The bacteriological analysis examined differential and presumptive coliform counts. Confirmatory coliform tests were carried out using a loopful of presumptive positive and negative tests already sub-cultured on MacConkey agar plate and incubated at 37 0c for 24 hours to obtain bacterial isolates.
Results: *Escherichia coli* was the most frequently occurring isolate of all the bacteria identified. Other isolates include *Streptococcus* spp., *Staphylococcus aureus, Shigella* spp., *Enterococcus* spp., *Salmonella* spp., *Pseudomonas* spp., *Proteus* spp. *and Bacillus* spp. The majority of these organisms are Gram-negative microorganisms which are most times implicated in gastrointestinal abnormalities.
Conclusions: There is a high incidence of contamination of well waters by pathogenic organisms in most well waters from the Study area. Underground well water sources to be utilized for domestic purposes such as cooking should be treated or disinfected before use, either by boiling and filtration or by chemical sterilization or a combination of both.

Keywords: Bacteria, Gastrointestinal abnormalities, Underground well, Water quality, Water treatment

INTRODUCTION

Water is a natural chemical substance which consists of the elements; hydrogen and oxygen in the ratio of two is to one (2:1). It is indispensable for man's existence on earth as about two-thirds of the human body consists of water and requires between one to seven (1-7) liters of water per day for its appropriate functioning to avoid dehydration.[1,2] In urban and predominantly rural communities in Nigeria, with over 85% of the population living below an average income, traditional drinking water sources such as open reservoirs, springs and open wells are still being used. Water from such sources seldom complies with World Health Organization (WHO)

limits for drinking water.[3] The quality of water depends on its physical, chemical, and biological characteristics, which determines its utility for different purposes.[4] Water quality is affected by fecal matter, domestic and industrial sewage and agricultural and pasture runoff, in addition to a lack of awareness and education among the users.[5]

Water fit for human consumption is referred to as potable or drinking water and should be of safe quality, which entails that it does not present any significant health risk over life time consumption; and the only way to tell whether the water is potable is to have it tested.[6,7] Potable water is one that is free from unsafe bacteria and chemical impurities. It must be clear, bright, colourless, and odourless and should contain no suspended matter. Availability of potable public water supply is of great concern to families and communities especially in developing countries where provision of safe drinking water is not available.[8] Lack of safe drinking water is a threat to public health and well-being of the people and exposes them to risk of waterborne diseases such as diarrheal and dysentery as well as chemical intoxication.[9,10] Therefore, drinking water contaminated from any source is of primary importance due to the danger and risk of waterborne diseases.[11]

Well water is one of the budding sources of water for human consumption especially in developing countries. It is regarded as a reliable source of water supply because it is often unpolluted, as a result of restricted movement of pollutants in the soil profile in contrast to shallow and permeable water aquifers.[11,12] However, water from wells that are poorly constructed and maintained remains an important source of infectious diseases caused by pathogenic bacteria, viruses and parasites.

There are three broad types of contaminants present in leachates that can pollute groundwater and subsequently affect public health. These are hazardous chemicals, conventional and non-conventional contaminants.[13] The leachate from some landfills is highly concentrated that small amount of leachate can pollute large amounts of groundwater rendering it unsuitable for use in domestic activities. Drinking contaminated well water can have serious health effects which include diseases such as hepatitis and dysentery which are caused by contamination from septic tank waste. To maintain good health, however, water should be safe to drink, meet the local standards, and ensure the sustainability of national and internal criteria and guidelines established for water quality standards.[14] Safe location of the borehole or well requires careful consideration of factors such as where the borehole or well is about surface drainage and groundwater flow. Pollution of groundwater stems from different sources and these include insanitary conditions during borehole construction, splashing of runoff into open wells, flooding at borehole site, leachate from buried waste pits or latrine, industrial wastes and sewage into the hole through cracks in the aquifer and annular of the hole.[15,16]

The detection of bacterial indicators in drinking water suggests the presence of pathogenic organisms that are sources of waterborne diseases.[17] Indicator microorganisms survive better and longer than pathogens, with uniform and stable properties, and may be easily detected using standard laboratory techniques.[18] The occurrence of waterborne illnesses has both economic and social impacts. Consequently, monitoring the levels of contamination and the prevention of disease outbreaks is important from both economic and public health perspectives. Moreover, the need to assess the microbiological quality of water has become imperative because it has a direct effect on the health of individuals.[19]

In response to the public health problems caused by contaminated well waters, this study proposes to investigate the bacteriological qualities of underground well water for domestic uses, in the Oyi local Government Area of Anambra state based on World Health Organization (WHO) guidelines for drinking water standards.

METHODS

Study area

The study was conducted using underground wells utilized by households in selected 13 wards in Oyi Local Government Area of Anambra state. Oyi is a local Government area in Anambra state, Nigeria with geographic coordinates Latitude: 6° 13' 60.00" N Longitude: 6° 56' 59.99" E. The towns that make up the local government are Nkwelle-Ezunaka, Awkuzu, Ogbunike, Umunya and Nteje. It has an estimated population of 239,700 as of the 2022 projected census and 139.7 km^2 of land area.[20]

The study was limited to households in the Oyi local government area of Enugu State faces a number of problems regarding both its drinking and domestic water quality and availability. Wells belonging to households who mainly use well water as their main source of drinking and household water, within the study area were recruited for the study. The selected 13 wards used for this study are designated A-M. Informed consent was obtained from the heads of the households whose wells were recruited as samples for the study, in the course of carrying out the research and presentation of the final work.

Study procedure and sample collection

Clustre sampling method was used for the quantitative study. Here, the households in each ward were divided into 3 multiple groups (clusters), based on the presence and usage of wells as the main source of drinking and domestic usage water source. Next using systematic random sampling, 3 households were picked from each sub-group. This shows that a two-stage sampling method

was used to draw 9 samples randomly from each of the selected 13 wards in the local government area, which gave a total of 117 well samples used in the study. Samples were collected in the morning, with sterile bottles. The bottles were also covered with lids, ensuring no air bubbles once the samples were drawn from the different wells.

The sampling was done between the hours of 7.30 am and 9.30 am. The water samples were aseptically collected with 200ml screw-capped, clean, heat-sterilized amber-coloured plastic bottles, from wells whose openings were covered with lids; which were removed and replaced during and after drawing (fetching) from it. The sample bottles were also rinsed with the sample water before filling them; a stone of suitable size was attached to the sampling bottle using a piece of string. The bottle was opened and lowered into the well and was completely immersed in the water without touching the sides of the well and without hitting the body or disturbing any sediment. The bottles were filled and then removed by rewinding the string. The bottles, once filled were covered with their respective screw caps with no air bubbles. All the sampled bottles were immediately labelled with complete details, transported in a light-proof insulated box containing ice packs to the laboratory and analyzed within 6 hours of collection. Sampling was as used.[21]

Microbiological analysis

Bacteriological analysis of water samples was done according to the method of American public health standard methods, for examination of water and wastewater.[22,23]

Presumptive coliform identification

A 50 ml of the test sample was transferred into a 50 ml bottle containing 50 ml double strength MacConkey broth. 5 ml of the test sample was transferred into the 5 tubes containing 5 ml of double-strength MacConkey broth. 1 ml of the test sample was transferred into the 5 tubes containing 1 ml of single-strength MacConkey broth. The whole tubes containing the test preparations and Durharm's tubes were incubated for 18-24 hours at 37 ^{0}c. At the end of the process, the tubes were observed for both acid and gas production. Those with acid and gas production give the presumptive coliform count.

Eijkman's test for E-coli (differential coliform test)

A pair of test tubes containing brilliant green lactose bile broth (BGLBB) and a tube containing tryptone water were used. These preparations were made in two sets. Each tube in each set was inoculated with a drop from the tube which produced acid and gas, while the other set was inoculated with a drop from a tube which did not produce acid and gas from the presumptive test above. The first group was incubated at 37^{0}c, while the second group was incubated at 44^{0}c for 48 hours. The tubes to be incubated at 44^{0}c must be pre-warmed at 44^{0}c by placing them in a water bath before sub-culturing. Coliforms produce gas from lactose only at 37^{0}c, while *E. coli* produce gas from lactose at 37^{0}c and 44^{0}c and also produce indole from tryptophan at 44^{0}c.

Confirmatory coliform test

A loopful of presumptive positive and negative tests was sub-cultured on a MacConkey agar plate and incubated at 37 0c for 24 hours. The significant bacterial isolates obtained were inoculated on nutrient agar slopes for biochemical identification.

Biochemical identification of isolates

Conventional microbiology tests; Gram stain, indole test, catalase test, oxidase test, citrate utilization test, and triple iron sugar test were carried out on the isolates.

Urease test: The slants of urea agar base medium were prepared and inoculated with the isolates obtained during early investigation, kept at 37ºC and then examined after 24 hours. The ability of the organisms to produce urease, which breaks down the urea incorporated in the medium; thus liberating ammonia gas, which then increases the pH of the medium to alkalinity was observed. The change in pH was detected by the change of the colour of the indicator (phenol red) used from yellow to reddish pink.

Catalase test: The test detects the ability of the organisms to produce the enzyme catalase, which catalyzes the release of Oxygen (O_2) from hydrogen peroxide giving bubbles from the bacterial suspension. The organisms were picked up aseptically with the help of a sterile wire-loop on a slide and then colonies were diluted with distilled water. Further to that, 2-3 drops of 3% hydrogen peroxide were dropped on diluted colonies containing organisms, immediately bubbling took place and the tests were considered to be positive.

Oxidase test: The purpose of this test was to examine the ability of the bacterium to produce the enzyme oxidase, which indicates the bacterium's ability to exchange electrons with a dye, tetra methyl-p-phenylenediamin di-hydrochloride leading to the reduction of the dye to a deep blue colouration. About 0.1g of tetra methyl-p-phenylenediamine di-hydrochloride (dye) was added to 10 ml distilled water and dissolved. Ascorbic acid (vitamin C) 0.01g was then added to the strips of this reagent, it can also be made by soaking the strips of filter papers in the reagent. For confirmation of this test, a glass rod streak was used to pick a generous amount of the bacterial culture and place it on a moist portion of the filter paper. A positive reaction indicates an intense blue colouration of the paper within 10 seconds.

Indole test: The test organism was inoculated into a broth that contained tryptophan and incubated at 370C for 48

hours. Then 2ml of the broth suspension was transferred to another test tube under aseptic conditions. About 0.5ml of Kovac's reagent was added to the broth. The mixture was shaken properly to ensure a thorough mixing and then observed for colour reaction. A positive result was indicated by a pink-coloured ring around the interface between the broth suspension and alcohol reagent which rose to the surface.

Sugar fermentation activities of bacterial species

Two grams of different sugars (glucose lactose) were dissolved in 200 distilled water and bottled in a 20 ml bottle. The medium was then sterilized by an autoclave slightly opened. The contents of the 20ml bottle were added in 180ml of the basal medium, mixed well and dispensed in 3ml volumes in bijoux bottles. The medium was sterilized under 15lb pressure for 15 minutes and then stored at room temperature for up to 5-6 consecutive days. A bottle of each medium was inoculated with a streak of solid culture (by a single colony). The inoculated bottles were incubated aerobically at 37ºC for the required period. The change in colour of the indicator from red to yellow indicates acid production organisms. The changes were noted after every 24 hours, for five to six consecutive days.

Data analysis

Water and microbial data analysis were done using statistical software, a statistical package for social sciences (SPSS version 22) developed by IBM Corporation. Means and Standard deviation in the same column with the same superscript were not significantly different at p>0.05. The means were separated using the least significant difference (LSD).

RESULTS

Microbial quality of underground well water

Table 1 shows that *Escherichia coli* is the highest occurring microbial isolate in the water sample of the wards studied, and most occurrences were noticed in wards A, B, C, E, F and G. Most probable number per 100ml for *Proteus spp.* ranges from 122.22 MPN/100ml to 233.33 MPN/100ml.

Table 1: Microbial parameters of underground well water in Oyi local government area.

	Microbial isolates								
Ward	***Enterobacter* sp (MPN/100 ml)**	***Salmonella* sp (MPN/100 ml)**	***Bacillus* sp (MPN/100 ml)**	***Escherichia* coli (MPN/100 ml)**	***Proteus* sp (MPN/100 ml)**	***Staphylococus* sp (MPN/100 ml)**	***Shigella* sp (MPN/100 ml)**	***Pseudomonas* sp (MPN/100 ml)**	***Streptococcus* sp (MPN/100 ml)**
A	188.89±77.8	276.67±38.4	128.89±24.2	325.56±64.2	140±37.7	256.67±36.7	134.44±28.7	126.67±17.3	238.89±39.1
B	216.67±35	266.67±53.8	151.11±36.2	340±32.01	222.22±38.3	274.44±42.4	184.44±34.6	163.33±26.4	216.67±33.5
C	214.44±30.4	170±36.0	132.22±25.8	334.44±60.2	233.33±32.0	224.44±53.6	138.88±17.6	160±48.4	241.11±40.1
D	204.44±45.3	153.33±34.6	136.66±25	273.33±25.9	196.66±40.6	158.88±36.2	120±17.3	204.44±39.0	251.11±33.3
E	226.67±27.3	243.33±31.22	178.89±16.9	352.22±67.7	193.33±38.4	231.11±33.3	193.33±2	217.78±19.8	245.56±27.8
F	225.56±35.7	275.56±24.5	223.33±2	363.33±48.4	185.56±24.0	274.44±29.2	212.22±21.0	188.89±26.1	252.22±35.9
G	200±48.7	153.33±34.6	180±31.2	315.56±41.8	125.56±21.2	286.67±43.8	190±33.5	190±31.2	214.44±28.8
H	190±25.9	231.11±28.0	207.78±28.1	303.33±37.4	173.33±31.2	255.56±30.4	187.78±17.8	197.78±22.7	214.44±25.5
I	201.11±30.1	225.55±42.7	126.66±21.7	284.44±23.5	205.56±507	185.56±18.7	136.67±18.7	198.89±38.2	228.89±26.1
J	196.67±24.4	212.22±26.3	210±27.3	305.56±26.6	160±18.7	252.22±3	163.33±17	196.67±31.2	251.11±31.4
K	154.44±20.6	156.67±24.4	151.11±22.6	281.11±26.6	122.22±18.5	275.56±24.5	167.78±26.8	172.22±15.6	188.89±29.7
L	124.44±17.4	188.89±16.9	137.78±19.2	250±20	130±18.71	217.78±24.8	176.67±20.6	142.22±24.0	198.89±20.8
M	124.44±17.4	135.56±15.0	124.44±17.4	286.67±30	147.7824.3	236.67±22.3	203.33±31.6	150±18.7	188.89±27.1

*mean and standard deviation values for *Enterobacter* spp., *Salmonella* spp., *Bacillus* spp., *Escherichia coli*, *Proteus* spp., *Staphylococcus* spp, *Shigella* spp, *Pseudomonas* spp., and *Streptococcus* spp. ^{a} = p ≤ 0.05, ^{ab} = p ≥ 0.05

The facultative bacteria identified include Enterobacter *spp*., *Salmonella spp*., *Bacillus spp*., *Escherichia coli*, *Proteus spp.*, *staphylococcus spp*, *Shigella spp*., *Pseudomonas sp*., and *Streptococcus spp.* All the bacteria identified were present in high numbers in all the samples and their values were reported as most probable number (MPN). Highest occurrence is *E. coli*, with most probable number (MPN) of 363.33 per 100 ml of sample was reported in ward F samples. Also lowest occurrence is *Shigella spp*, with most probable number (MPN) of 120.00 per 100 ml of sample reported in ward D samples.

In A, B, and C-wards, all the well water samples had a significant count of microbial content, which does not agree with the value of 0MPN/100ml specified by WHO. In ward A household 5 had the highest count of *E. coli* at 440 (MPN/100ml) while household 3 had the lowest count at 250 (MPN/100ml); in ward B household 2 had the highest count of *Salmonella spp* at 340 (MPN/100ml) while household 1 had the lowest count at 200 (MPN/100ml) and also, in ward C household 4 had the highest count of *Enterobacter spp.* at 270 (MPN/100ml) while household 3 had the lowest count at 170 (MPN/100ml) (Table 2).

Table 2: Bacteriological properties of well water samples in ward-A, B and C.

Household	*Enterobacter* sp (MPN/100ml)	*Salmonella* sp (MPN/100ml)	*Bacillus* sp (MPN/100ml)	*E. coli* (MPN/100ml)	*Proteus* sp (MPN/100ml)	*Staphylococus* sp (MPN/100ml)	*Shigella* sp (MPN/100ml)	*Pseudomonas* sp (MPN/100ml)	*Streptococcus* sp (MPN/100ml)
From well water samples in ward-A									
1	160	240	140	280	150	290	100	130	220
2	120	290	90	310	120	250	160	150	240
3	290	340	150	250	140	180	100	110	310
4	100	280	110	410	170	260	150	130	260
5	240	310	170	440	110	300	120	100	190
6	150	220	130	290	90	260	120	150	250
7	320	240	120	340	100	250	180	110	180
8	190	300	140	270	190	230	160	130	240
9	130	270	110	340	190	290	120	130	260
From well water samples in ward-B									
1	210	200	120	350	230	290	160	170	160
2	150	340	130	390	210	250	220	150	250
3	250	310	190	360	250	340	150	180	220
4	190	240	100	290	160	220	140	170	220
5	230	300	160	320	200	250	210	140	190
6	250	250	150	350	290	220	240	210	270
7	210	220	220	310	250	280	180	150	200
8	260	210	150	320	220	300	200	120	240
9	200	330	140	370	190	320	160	180	200
From well water samples in ward - C									
1	240	210	140	270	250	200	140	190	250
2	200	190	110	240	270	170	140	220	180
3	170	140	160	350	210	290	110	150	320
4	270	190	110	310	180	150	170	100	250
5	210	110	100	370	250	180	150	150	210
6	240	140	130	310	270	260	120	240	270
7	190	220	180	440	200	300	140	100	220
8	200	160	120	380	250	220	130	140	220
9	210	170	140	340	220	250	160	150	250

In D, E, and F-wards, all the well water samples had a significant count of microbial content, which does not agree with the value of 0MPN/100ml specified by WHO. In ward D households 8 and 9 had the lowest counts of *Bacillus. spp* at 100 (MPN/100ml) while household 4 had the highest count at 170 (MPN/100ml). In ward E household 2 had the highest count of *Streptococcus spp* at 280 (MPN/100ml) while households 3 and 7 had the lowest count at 200 (MPN/100ml). Also, in ward F household 5 had the highest count of *Proteus spp* at 250 (MPN/100ml) while household 4 had the lowest count at 140 (MPN/100ml) (Table 3).

In G, H, and I-wards, all the well water samples had a significant count of microbial content, which does not agree with the value of 0MPN/100ml specified by WHO. In ward G, household 3 had the highest count of *Shigella spp* at 250 (MPN/100ml) while household 2 had the lowest count at 180 (MPN/100ml). In ward H, household 6 had the highest count of *Staphylococcus spp* at 300 (MPN/100ml) while households 3 and 8 had the lowest count at 220 (MPN/100ml). And also, in ward I, household 3 had the highest count of *Pseudomonas spp* at 240 (MPN/100ml) while household 2 had the lowest count at 150 (MPN/100ml) (Table 4).

In G, H, and I-wards, all the well water samples had a significant count of microbial content, which does not agree with the value of 0MPN/100ml specified by WHO. In ward J, household 2 had the highest count of *Shigella spp* at 230 (MPN/100ml) while households 5 and 6 had the lowest count at 140 (MPN/100ml). In ward k, household 3 had the highest count of *Staphylococcus spp* at 310 (MPN/100ml) while household 4 had the lowest count at 240 (MPN/100ml). And also, in ward L, household 4 had the highest count of *Proteus spp* at 160(MPN/100ml) while household 7 had the lowest count at 100(MPN/100ml) (Table 5).

The well water samples examined in M-ward had a significant count of microbial content, which is not within WHO's acceptable limit of 0MPN/100ml. Household 2 had the highest count of *Staphylococcus spp* at 280

(MPN/100ml) while households 3 and 6 had the lowest count at 210 (MPN/100ml) (Table 6).

Table 3: Bacteriological properties of well water samples in ward-D, E and F.

Household	*Enterobacter* sp (MPN/100ml)	*Salmonella* sp (MPN/100ml)	*Bacillus* sp (MPN/100ml)	*E. coli* (MPN/100ml)	*Proteus* sp (MPN/100ml)	*Staphylococus* sp (MPN/100ml)	*Shigella* sp (MPN/100ml)	*Pseudomonas sp* (MPN/100ml)	*Streptococcus* sp (MPN/100ml)
From well water samples in ward-D									
1	190	210	160	260	200	150	150	220	260
2	170	120	150	240	250	220	110	180	290
3	210	180	140	310	170	190	130	150	240
4	220	180	170	280	240	140	100	250	190
5	150	140	150	290	150	120	110	220	300
6	300	100	140	250	170	110	140	200	250
7	190	150	120	310	220	140	120	260	220
8	240	130	100	270	240	170	100	210	260
9	170	170	100	250	230	190	120	150	250
From well water samples in ward - E									
1	260	180	150	300	220	170	120	240	220
2	180	280	130	270	270	240	160	150	280
3	210	250	150	290	140	170	130	220	200
4	160	200	110	250	270	150	150	200	220
5	190	160	100	320	250	210	110	170	240
6	220	280	110	290	190	210	130	190	250
7	170	240	140	260	170	190	150	210	200
8	210	200	150	270	200	170	160	150	240
9	210	240	100	310	140	160	120	260	210
From well water samples in ward - F									
1	220	280	180	340	200	190	200	240	200
2	190	270	160	300	240	220	210	200	260
3	250	290	200	380	160	280	170	240	280
4	260	240	180	260	140	210	200	190	250
5	210	220	150	280	250	210	220	250	220
6	190	250	190	440	200	250	180	200	240
7	240	200	180	350	220	200	160	180	280
8	260	220	200	460	170	280	190	220	220
9	220	220	170	360	160	240	210	240	260

Table 4: Bacteriological properties of well water samples in ward- G, H and I.

Household	*Enterobacter* sp (MPN/100ml)	*Salmo-nella* sp (MPN/100ml)	*Bacillus* sp (MPN/100ml)	*E. coli* (MPN/100ml)	*Proteus* sp (MPN/100ml)	*Staphylococus* sp (MPN/100ml)	*Shigella* sp (MPN/100ml)	*Pseudomonas* sp (MPN/100ml)	*Streptococcus* sp (MPN/100ml)
From well water samples in ward-G									
1	200	250	220	430	160	240	220	210	200
2	290	240	220	400	190	310	180	230	290
3	250	310	240	350	220	290	250	160	270
4	210	290	260	370	190	320	200	190	270
5	190	300	230	410	210	260	210	170	240
6	190	270	190	320	170	240	210	170	220
7	200	250	230	390	160	280	230	190	310
8	260	280	240	300	160	250	190	220	250
9	240	290	180	300	210	280	220	160	220

Continued.

House hold	*Entero-bacter* sp (MPN/ 100ml)	*Salmo-nella* sp (MPN/ 100ml)	*Bacillus* sp (MPN/ 100ml)	*E. coli* (MPN/ 100ml)	*Proteus* sp (MPN/ 100ml)	*Staphy-lococus* sp (MPN/ 100ml)	*Shigella* sp (MPN/100 ml)	*Pseud-omonas* sp (MPN/100ml)	*Strepto-coccus* sp (MPN/ 100ml)
From well water samples in ward - H									
1	170	220	250	240	180	290	180	230	210
2	230	240	220	280	120	240	220	170	240
3	210	270	210	340	140	220	170	190	210
4	160	250	250	330	180	290	190	210	180
5	220	210	180	310	210	250	190	160	200
6	180	270	200	270	180	300	180	190	250
7	200	210	170	290	160	240	200	210	180
8	160	190	200	360	170	220	160	200	220
9	180	220	190	310	220	250	200	220	240
From well water samples in ward - I									
1	190	240	200	280	160	250	120	180	240
2	230	210	160	340	140	290	190	150	290
3	230	250	240	260	180	190	150	240	250
4	200	200	230	300	160	260	190	210	210
5	170	210	180	360	160	310	210	230	240
6	210	170	200	290	190	270	140	160	270
7	160	220	220	270	150	250	120	180	300
8	200	180	220	310	130	210	160	200	250
9	180	230	170	340	170	240	190	220	210

Table 5: Bacteriological properties of well water samples in ward-J, K and L.

House hold	*Entero-bacter* sp (MPN/100ml)	*Salmo-nella* sp (MPN/100ml)	*Bacill-us* sp (MPN/100ml)	*E. coli* (MPN/100ml)	*Proteus* sp (MPN/100ml)	*Staph-ylococus* sp (MPN/100ml)	*Shigella* sp (MPN/100ml)	*Pseu-domonas* sp (MPN/100ml)	*Strepto-coccus* sp (MPN/100ml)
From well water samples in ward - J									
1	150	210	190	310	120	330	200	160	210
2	170	150	140	290	140	230	230	210	180
3	200	120	190	360	100	280	200	250	260
4	160	160	220	290	120	280	170	190	220
5	130	100	170	360	160	320	140	200	230
6	190	190	190	240	100	350	140	170	220
7	200	150	220	350	110	250	190	210	200
8	150	180	170	290	150	310	220	150	170
9	130	140	130	350	130	230	220	170	240
From well water samples in ward - k									
1	170	130	160	280	140	270	210	190	240
2	130	160	120	300	110	290	160	190	200
3	130	110	170	260	160	310	200	160	160
4	160	170	140	330	120	240	170	150	150
5	190	150	190	270	110	250	150	160	190
6	170	160	120	250	110	300	130	170	160
7	160	190	150	290	130	280	150	190	200
8	140	160	150	300	100	250	190	160	180
9	140	180	160	250	120	290	150	180	220
From well water samples in ward - L									
1	130	100	150	240	130	200	160	130	190
2	150	130	130	270	150	180	200	110	220
3	100	110	140	270	120	250	180	160	160

Continued.

Household	*Entero-bacter* sp (MPN/100ml)	*Salmo-nella* sp (MPN/100ml)	*Bacill-us* sp (MPN/100ml)	*E. coli* (MPN/100ml)	*Proteus* sp (MPN/100ml)	*Staph-ylococus* sp (MPN/100ml)	*Shigella* sp (MPN/100ml)	*Pseu-domonas* sp (MPN/100ml)	*Strepto-coccus* sp (MPN/100ml)
4	120	100	120	220	160	220	180	170	200
5	140	130	170	240	110	250	210	120	230
6	120	140	150	280	130	210	150	150	200
7	100	120	120	250	100	230	160	170	180
8	120	140	110	230	130	230	190	160	210
9	140	100	150	250	140	190	160	110	200

Table 6: Bacteriological properties of well water samples in ward-M.

House hold	*Enterob-acter* sp (MPN/100ml)	*Salmo-nella* sp (MPN/100ml)	*Bacil-lus* sp (MPN/100ml)	*E. coli* (MPN/100ml)	*Proteus* sp (MPN/100ml)	*Staphyl-ococus* sp (MPN/100ml)	*Shig-ella* sp (MPN/100ml)	*Pseudo-monas* sp (MPN/100ml)	*Streptococcus* sp (MPN/100ml)
1	120	130	120	270	170	230	220	130	220
2	140	150	100	310	140	280	230	160	200
3	120	120	140	250	180	210	180	130	170
4	160	160	140	290	130	240	260	180	190
5	110	130	100	340	170	250	200	130	200
6	130	120	130	310	150	210	150	160	160
7	120	150	140	290	120	220	190	140	220
8	120	140	140	270	110	240	210	170	140
9	100	120	110	250	160	250	190	150	200

DISCUSSION

Generally, water users in the study area have traditionally relied on hand–dug wells for decades. Local indigenes and dwellers as well, depend mostly on this water source for daily water needs which include cleaning, cooking, bathing, agriculture and occasionally drinking. During the field survey, observations showed that there are many hand dug wells in the study area and almost all were properly caped. Wells with such properly caped conditions are not vulnerable to pollution from pollutants such as insects, small animals, refuse, sediments, and other forms of contaminants that can be prevented from gaining entry into the well water from the surface. Also, the method of abstraction of water from these hand-hand-dugdug wells could introduce pollutants into the wells. Field survey revealed that water for domestic purposes from all sampled hand-dug wells in the area, were drawn using bucket and rope of different types and different sources. These buckets and ropes are most often dirty, and kept in open spaces where contaminants access them; thus, users of these wells are exposed to high levels of contaminants and pollutants which pose threats to their health and livelihoods.

Faecal coliform bacteria are a collection of relatively harmless microorganisms that live in large numbers in the intestines of warm and cold-blooded animals. They aid in the digestion of food. A specific subgroup of this collection is the faecal coliform bacteria, the most common member being *Escherichia coli*. These organisms may be repeated from the total coliform group by their ability to grow at elevated temperatures and are associated only with the fecal material of warm-blooded animals. The presence of fecal coliform bacteria in aquatic environments indicate that the water has been contaminated with the fecal material of man or other animals. At the time this occurred, the source water may have been contaminated by pathogens or disease-producing bacteria or viruses which can also exist in fecal material. Some water-borne pathogenic diseases include typhoid fever, viral, and bacterial gastroenteritis and hepatitis A. The presence of faecal contamination is an indicator that a potential health risk exists for individuals exposed to this water source. Quite several bacteria species were isolated from well water samples located within the study area. The presence of a group of bacteria known as coliforms in water samples serves as an indicator of pollution.[24] Chief among them is *Escherichia coli*, which was isolated from the samples used in this study and whose presence indicates the possible presence of other intestinal pathogens. *Streptococcus* spp, *Staphylococcus aureus*, *Shigella* spp, *Enterococcus* spp, *Salmonella* spp, *Pseudomonas* spp, *Proteus* spp and *Bacillus* spp which were also isolated and identified from the samples are other pathogens of importance that have

been linked to gastrointestinal disorders, according to Nwidu et al study.[25]

One of the occurring microorganism in the samples was *Bacillus* spp. These are gram-positive aerobic or facultative anaerobes and catalase positive microorganisms.[26] They are heat-resistant spore-forming microorganisms that are most often found in soil. Due to their ability to form heat-resistant spores, they can survive and compete with other organisms while secreting metabolites that are antagonistic to other microorganisms in the form of antibodies.[27] Although they have been useful in the production of antibodies, their presence in drinking water and even food pose critical health risks that may lead to diseases such as anthrax. *Staphylococcus aureus* is another gram-positive microorganism that is often associated with nosocomial infections. It is a facultative anaerobe, coagulase and catalase-positive microorganism. Although they are commensals in the mucosa of mammals, reptiles and birds, they can also be opportunistic pathogens. One risk of infection by *S. aureus* is the issue of its resistance to beta-lactamase antibiotics, including penicillin and methicillin a derivative of penicillin. The presence of these species in water, thus calls for public health concern. *Streptococcus* spp is a gram-positive catalase-positive microorganism and has been associated with illnesses such as pneumonia and usually upper respiratory tract infections.

Escherichia coli, *Proteus* spp, *Pseudomonas* spp, *Salmonella* spp, *Enterobacter* spp. and *Shigella* spp are all gram-negative microorganisms and belong to the group referred to as Enterobacteriaceae. It is worthy of note that *Escherichia coli* is the highest-occurring microorganism among the wards studied. The gram-negative organisms listed above can cause illnesses such as watery and bloody diarrhoea, dysentery, and urinary tract infection and when introduced into the bloodstream, they can lead to bacteremia. In addition, some strains of *Escherichia coli* can produce enterotoxins in the small intestine which can also cause diarrhoea if not managed in good time.

The most probable number (MPN) per 100 ml obtained for the well water samples exceeded the standard limit set by WHO. This suggests that the well water samples have been contaminated by potentially dangerous microorganisms and are therefore not fit for drinking purposes. This was confirmed by the characterization of the isolates from the well water samples from the locations under study, which were highly contaminated with more than one bacteria species including *Salmonella typhi*, *Escherichia coli*, *Enterobacter* species and *Proteus mirabilis* are pathogenic organisms mainly of fecal origin. Any water source used for drinking or cleaning purposes should not contain any organism of faecal origin.[28] Presence of enteric coliforms especially *Escherichia coli* makes the water samples unsuitable for human consumption according to the guidelines set by WHO for the evaluation of the bacteriological quality of drinking water.[29] Apart from environmental hygiene and population density, the presence of *Salmonella* species among the samples in wells in the study area may also be attributed to drainage and flooding from contaminated surface water, which seeps into underground water sources. Findings from this study highlight the non-conformity of well water samples studied with the WHO standard recommendation for safe potable water.[30] A situation where enteric pathogens are grossly isolated from sources of water consumed by humans or other animals, is a serious problem which calls for vigilance on the part of the authorities; as it signals possible future outbreaks of waterborne diseases.[31] The reason for the gross contamination of well water in the study area could be due to poor sanitary conditions around the areas where such wells are located, or drawing water from the wells with contaminated containers, a practice that has been common among the users since individuals bring along their water containers (fetchers) in some cases.

However, as a limitation, this study did not investigate potential sources of contamination such as the sanitary features of the well samples in relation to well water quality in the study area.

CONCLUSION

The bacteriological properties of all the samples from the 13 wards of the study area indicate a significant count of microorganisms, especially *E. coli*. This indicates recent faecal contamination in well water in the study area which signifies the presence of pathogenic microorganisms in the well water. It is therefore evident that there is a high incidence of contamination of well waters by pathogenic organisms in most well waters from the Study area. Underground well water sources to be utilized for domestic purposes such as cooking should therefore be treated or disinfected before use, either by boiling and filtration or by chemical sterilization or a combination of both. In addition, responsible bodies should pay attention to the scarcity of potable drinking water in most Local Government Areas and should work towards the provision of alternative safe water sources.

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