

Bacteriological Assessment of Well and River Water in North Bank Area of Makurdi Benue State, Nigeria

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ABSTRACT

A study was carried out on Bacteriological assessment of Well and River Water in North Bank Area of Makurdi, Benue State, Nigeria. A total of 82 water samples were collected, fifty two (52) from well water and thirty (30) from river water and were analyzed for both bacterial counts and Most Probable Number (MPN) index. The results showed that the mean bacteria count from well water ranged from 1.11×10^6 – 9.25×10^6 cfu/ml, while the MPN index ranged from 4 – 34. The river water samples had a mean bacteria count ranging from 7.09×10^6 – 12.33×10^6 cfu/ml and an MPN index ranging from 26 – 2634. The cultural, morphological, and biochemical characteristics of coliform bacteria isolated from the water samples were also examined. The results revealed the presence of *Escherichia coli* (*E. coli*), *Klebsiella* species, *Enterobacter* species, and *Citrobacter* species. The highest occurrence of coliform bacteria in well water was *Klebsiella* species (66.6%), followed by *E. coli* (33.3%), while in river water, *Klebsiella* species (58.3%) and *Enterobacter* species (41.6%) were the most predominant. The pathogenicity of the isolated coliform bacteria was assessed using hemolysin production, Congo red dye binding, and survival in blood serum assays. The results showed that 50.0% of *E. coli* isolated from well water produced hemolysin, while 25.0% of *E. coli* from river water produced hemolysin. *Klebsiella* species from well water and river water showed 33.3% and 42.8% hemolysin production, respectively. Congo Red dye binding was observed in 33.3% of *E. coli* from well water and 75.0% of *E. coli* from river water. *Klebsiella* species from well water and river water showed 25.0% and 28.5% Congo Red dye binding, respectively. *Enterobacter* species from well water and river water showed 25.0% and 50.0% Congo red dye binding, respectively. *Citrobacter* species from well water and river water showed 60.0% and 33.3% Congo red dye binding, respectively. Survival in blood serum was observed in 40.0% of *E. coli* from well water and 50.0% of *E. coli* from river water. *Klebsiella* species from well water and river water showed 41.6% and 42.8% survival in blood serum, respectively. *Enterobacter* species from well water and river water showed 25.0% and 33.3% survival in blood serum, respectively. *Citrobacter* species from well water showed 50.0% survival in blood serum. The study revealed the poor bacteriological quality of well and river water in the North Bank area of Makurdi, Benue State, and the potential health risks associated with the consumption of contaminated water. This result therefore, emphasizes the need for constant monitoring and treatment of water sources to ensure the safety of drinking water for wellbeing of the communities.

Keywords: Bacteriological Assessment, Well water, River Water, North Bank, Benue State

INTRODUCTION

The quality of water is a vital concern for mankind since it is directly linked with human welfare. Since it is a dynamic system containing living as well as non-living organic, soluble as well as insoluble substances, its quality is likely to change day by day and from source to source. Only one percent of water is available on land for drinking, agriculture, domestic power generation, industrial consumption, transportation and waste

disposal (Iboet *al.*, 2020). The quality of water is more important compared to quantity in any water supply planning, especially for drinking purposes. Water quality standards are the foundation for the quality based control program and required for the treatment process. These standards support efforts to achieve and maintain protective water quality conditions (Omakaet *al.*, 2014; AlSuhaimiet *al.*, 2017). A primary concern of people living in developing countries is that of obtaining clean

drinking water. Groundwater sources are getting contaminated due to human interference, such as waste dumping, effluent and sewage discharge without proper treatment. Municipal and industrial wastes, application of fertilizers, herbicides, pesticides, burning of coal, leaching from mining activity further add to contamination of groundwater. These different sources of contamination may influence physical, chemical, and biological variables of groundwater (Olajuba and Ogunika, 2014). Open dumping of municipal solid wastes, is mainly the existing method of waste disposal used even in capital cities except perhaps among few and affluent institutions in Nigeria (Onwughara *et al.*, 2010). Groundwater contamination by leachates can transmit bacteria and disease. Typhoid fever is a common problem for the people of developing nations, many of them cannot afford to dig wells deep enough to reach fresh aquifers (Onwughara *et al.*, 2010; Reidl and Klose, 2002). Faecal coliform bacteria are used as an indicator for the presence of any of these water-borne pathogens. Their presence in water however possibly detects the existence of disease causing organisms (Anhwange *et al.*, 2012). The detection of bacterial indicators in drinking water suggests the presence of pathogenic organisms that are sources of waterborne diseases (Yassin *et al.*, 2016). Indicator microorganisms survive better and longer than pathogens, with uniform and stable properties, and may be easily detected using standard laboratory techniques (Chatterjee *et al.*, 2017). The need to assess the microbiological quality of water has become imperative because it has a direct effect on the health of individuals (Anyanwu and Okoli, 2012). In response to the public health problems caused by contaminated well and river waters. 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. limits for drinking water (Peter-Ikechukwu *et al.*, 2015). The quality of water depends on its physical, chemical, and biological characteristics, which determines its utility for different purposes. 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 (Ngwa and Chrysanthus, 2013). The paucity and unreliable water supply within Makurdi has forced residents to increasingly depend on shallow wells and boreholes as the source of water for drinking and domestic use. These boreholes are dug shallow wells connected to constantly open overhead tank and pumped with sumo machine many of them are located close to household drainage systems and septic tanks and are therefore susceptible to contamination (Ibo *et al.*, 2020).

A proper knowledge of the bacteriological properties of water meant for drinking and domestic purposes is crucial to avert a possible health hazard, therefore in this study focus on pathogenicity and bacteriological assessment of well and river water in north bank area of Makurdi Benue State

MATERIALS AND METHODS

Study Area

The study was conducted in Makurdi, the capital city of Benue State. It is situated on the flood plains of the lower Benue valley in North Central Nigeria on latitude 7°53'44" N and longitude 8°22'54" E. It covers a 10 km² radius and the River Benue passed through Makurdi and split it in the north and south banks. Makurdi was stratified into four sections, South, North, East, and West, represented by Modern Market community (Location A), Federal Low-cost North Bank community (Location B), Fiidi community (Location C), and Kanshio community (Location D) (Agyo *et al.*, 2020)

Sample size

The sample size for this study was determined using the formula as reported by Naing *et al.* (2006).

$$n = z^2[pq]/d^2$$

Where n= minimum sample size

z=standard error [1.96] at 95% confidence limit

p=local prevalence of 0.31% % or 0.31 (Agyo *et al.*, 2020).

$$q = [1.0-p]$$

d = degree of accuracy of 5% or 0.05

$$n = (1.96)^2[0.31 \times (1.0-0.31)]/0.05^2$$

$$n = z^2 [pq]/d^2$$

$$n = [1.96]^2 \times 0.31 \times 0.758/[0.05]^2$$

$$n = 3.8416 \times 0.343/0.0025$$

$$n = 0.704688/0.0025$$

$$n = 72$$

Attrition rate of 10% = 10

Total minimum sample to be collected = 82

The total minimum number of samples to be collected was 82, however, 82 samples was collected to minimize error.

Collection of well water samples

Fifty two (52) well water and thirty (30) river water samples was collected in sterile bottles tied with a strong string to a piece of metal (about 500g) as the weight. The bottle cap was aseptically removed and the weighted bottle lowered into the well to a depth of about 1-2 meters in non-cased wells, burnt brick cased wells, concrete cased wells and shallow wells. The bottle was brought up to a surface and covered with a screw cap when no air bubbles was seen inside.

Presumptive coliform test

Presumptive test was carried out using a method described by Cheesbrough, (2006). Five tubes each containing 10 ml of MacConkey broth, fitted cap and inverted Durham's tube was prepared in Triplicates. The MacConkey broth contained in the first set of the tubes is double strength while single strength in the other sets. 10 ml of the water sample was added to each of the five tubes of the first set and labelled 1ml and 0.1 ml of the sample was added to each of the five tubes of the second and third sets respectively; and labelled accordingly. The tubes were loosely capped and incubated at 37°C for 24 hours after which was examined for gas and acid productions. Positive tubes were identified by both gas production, shown by collection of bobbles in the inverted Durham's tubes; and acid production shown by change in colour of MacConkey broth from purple to yellow. Positive tubes were subjected to confirmatory test. The negative tubes were re-incubated at the same condition for total of 48 hours and reexamined for gas and acid productions.

Confirmatory test

Positive tubes from the presumptive test were paired with new tubes each containing similar content to its positive pair. Using sterile wire loop, the new pairs were inoculated with their corresponding positive pairs and inoculated for 24 hours at 35-37°C. Positive tubes confirmed the presence of lactose fermenters in the water sample.

Isolation of bacteria

Isolation of bacterial was carried out using the method described by Iroha *et al.* (2018), the positive tubes from confirmatory test were inoculated on Eosin methylene blue (EMB) agar, MacConkey broth, Salmonella Shigella (SSA) agar using streaking method and incubated for 24 hours at 35-37°C.

Identification of bacterial isolates

Identification of bacteria was carried out as described by Cheesbrough (2006) which was done using cultural, morphology characteristics and biochemical test such as Catalase test, Indole, Methyl red Voges-Proskauer tests, nitrate reduction tests, Urease production tests, citrate utilisation and Glucose fermentation tests.

Gram Staining Examination

The gram staining technique was carried out as described by Cheesbrough (2006) with some modifications; A small portion of cultural organism was transferred onto clean grease-free glass slide, and emulsified in a drop of distilled water until a thin homogeneous film is obtained, then the wire loop was re-sterilized and the thin homogeneous film was allowed

to air dry and heat fixed by passing it through the flame. The slide was flooded with crystal violet for 1 minute and then rinsed with distilled water. The stain was again flooded with Lugol's iodine for 1 minute, and rinsed with distilled water and the decolorized, rapidly with acetone alcohol until no colour appear to flow from preparation and rinsed appropriately with distilled water and allowed to air dry and viewed under microscope using x 100 oil immersion objective. Gram positive retain the dark blue colour inferred by the iodine/crystal violet complex, while Gram negative organisms appear red; maintaining the colour of the secondary dye.

Biochemical tests

The following biochemical tests were carried out on the suspected bacteria isolates: Catalase test, Indole, Methyl red Voges-Proskauer tests, nitrate reduction tests, Urease production tests, citrate utilisation and Glucose fermentation tests.

Indole Test

The Indole test for the suspected organism was carried out as described by Cheesbrough (2006). A colony of the organism from culture plates was inoculated onto 5ml tryptone broth and incubated at 37°C for 24hrs. After which a few drops of Kovac's reagent was added to the overnight tryptone broth culture, and shaken. A positive is indicated by the development of red ring colour in the reagent layer above the broth within 10 minutes observed.

Methyl Red/Voges-Proskauer Test

The methyl red/Voges-Proskauer for the suspected organism was carried out as described by Cheesbrough (2006). A pure culture of the test organism was inoculated in to MR-VP MEDIUM and incubated at 37°C for 72hrs after which the culture was divided into two portions. To the first portion, three drops of methyl red was added and formation of red colour was an indication of methyl red positive. To the second portion, 10 drops of 40% KOH (Potassium hydroxide) was added and observed for 30 minutes. Formation of pink/red colour indicates Voges-Proskauer positive and formation of yellow colour indicates Voges-Proskauer negative.

Utilisation Test

The citrate utilization test for the suspected organism was carried out as described by Cheesbrough (2006). A pure culture of the organism was inoculated as a single streak on the slant surface of citrate agar and was incubated at 37°C for 24hrs, blue colour on the medium indicated the presence of alkaline product and it is therefore positive, while green colour is negative.

Catalase Test

Catalase test was performed as described by Cheesbough (2006). A pure colony of the organism was streaked aseptically on the nutrient agar slant and incubated at 37°C for 24hrs. Three drops of hydrogen peroxide (H₂O₂) was added to the slant and observed for bubbling gas.

Urease Test

This was performed by inoculating the organism into Urea broth and incubated at 37°C for 24hrs. Intense pink colour indicated positive, otherwise, was negative (Cheesbough, 2006).

Data analysis

Data was analysed using descriptive statistics and percentages. The association between water source and bacteriological contamination was evaluated using the chi-square test at a significance level of $p < 0.05$.

RESULTS

The bacteria count from selected water sources in different location is as given in Table 1. The mean bacteria count from Yagba well water ranges from 4.08×10^6 - 9.25×10^6 cfu/ml and the most probable number (MPN) index ranges from 9 – 26 while river water ranges from 11.41 – 12.33×10^6 cfu/ml . From Agan well water the mean bacteria count ranges from 3.29×10^6 - 6.29×10^6 cfu/ml and the MPN index ranges from 11 – 34 while the river water ranges from 10.21 - 11.09×10^6 cfu/ml and the MPN index ranges from 26–34. From Asase the mean bacteria count ranges from 3.19×10^6 - 5.19×10^6 cfu/ml and the MPN index ranges from 8–12 while the river water bacteria count ranges from 9.31×10^6 - 10.19×10^6 cfu/ml and the the MPN index ranges from 26– 26 . From Agwan Ochounu the mean bacteria count ranges from 1.11×10^6 – 5.45×10^6 cfu/ml while the MPN index ranges from 4– 12. From Kpege the mean bacteria count ranges from 1.45×10^6 – 2.11×10^6 cfu/ml while the MPN index ranges were 4 and the river water bacteria count ranges from 7.09×10^6 – 9.21×10^6 cfu/ml. From Day spring the mean bacteria count ranges from 3.09×10^6 – 5.98×10^6 cfu/ml while the MPN index ranges from 6 –11 while the bacteria count from the river ranges from 9.15×10^6 – 9.15×10^6 cfu/ml. The cultural, morphological and biochemical characteristics of coliform bacteria isolated from selected water sources in water sources in different location in North bank, Makurdi is as given in Table 2. *E. coli* grow Pinkish colony on MaConkey agar and greenish metallic sheen colony EMB agar, Indole positive, methyl-red positive. Pink and mucor colony on MaConkey agar, gram negative, rod shape, Indolenegative, methyl-red positive, Voges-Proskauer positive, Citrate utilization negative, Oxidative

negative, Triple sugar iron negative was recorded as *Klebsiella* species. Mucoid, pale, opaque cream to pink on MaConkey agar , gram negative, rod shape, Indolenegative, methyl-red negative, Voges-Proskauer positive, Citrate utilization negative, Oxidative negative, Triple sugar iron positive was recorded as *Enterobacter* species The percentage of bacteria occurrence from selected water sources in North bank, Makurdi is as given in Table 3. The highest coliform bacteria isolated from well water were *Klebsiella* species (66.6 %) followed by *E. coli* (33.3 %), *Citrobacter* species (27.7 %) and the lowest was *Enterobacter* species (22.2 %). The highest occurring coliform bacteria isolated from river water in north bank were *Klebsiella* species (58.3 %) followed by *Enterobacter* species and *Citrobacter* species and the lowest was *E. coli* (33.3%). The haemolysin production by coliform bacteria isolated from water sources is as shown in Table 4. Out of 6 *E. coli* isolated from well water 3 (50.0 %) produced halo zones, from from river 4 *E. coli* isolated 1 (25.0 %) produced halo zones. Out of 12 of *Klebsiella* species isolated from well water 4 (33.3 %) produced halo zones, out of 7 from river water 3 (42.8 %) were able to produced halo zones. Four (4) *Enterobacter* species isolated from well water 1 (25.0 %) produced halo zones, 6 *Enterobacter* species isolated from river 2 (33.3 %) produced halo zone. Out of 5 *Citrobacter* species isolated from well water 2 (40.0 %) produced halo zones, 6 *Citrobacter* species isolated from river water 4 (66.6 %) produced halo zones respectively. Table 5 shows the congo red dye binding of coliform bacteria isolated from water sources in North bank, Makurdi. Out of 6 *E. coli* isolated from well water 2 (33.3 %) bind with congo red dye,. Four (4) *E. coli* from river water 3 (75.0) bind with congo red dye. Out of 12 *Klebsiella* species isolated from well water 3 (25.0 %) bind congo red dye. Out of 7 *Klebsiella* species isolated from river water 2 (28.5 %) were able to bind congo red dye. Out of 4 *Enterobacter* species isolated from well water 2 (25.0 %) bind congo red dye. Of 6 *Enterobacter* species isolated from river water 3 (50.0 %) bind congo red dye. Out of 5 *Citrobacter* species isolated from stream water 3 (60.0 %) was able to bind with congo red dye. Out of 6 *Citrobacter* species isolated from well water 2 (33.3 %) to bind with congo red dye respectively. The Survival in blood serum by coliform bacteria isolated from water sources in North bank, Makurdi as shown in Table 6. Out of 6 *E. coli* isolated from well water 2 (40.0 %) survived in blood serum. Out of 4 *E. coli* isolated from river water 2 (50.0%) were able to survived in blood serum. Out of 12 *Klebsiella* species isolated from well water 5 (41.6 %) were able survive in blood serum, 7 *Klebsiella* species from river water 3 (42.8%) survive in blood serum. Out of 4 *Enterobacter* species isolated from well water 1 (25.0%)

survived in blood serum. Total of 6 *Citrobacter* species isolated from well water 3 (50.0 %) were found to survive in blood serum.

Table 1 Bacteriological counts and most probable number (MPN) of some selected well water and river water in different location in North bank, Makurdi

Sample	Mean bacteria count (CFU/mL)	MPN index 100ml ^{-L}
Yagba		
w1	6.48×10^6	12
w2	9.25×10^6	26
w3	4.08×10^6	9
Rp 1	12.33×10^6	140
Rp 2	11.41×10^6	34
Agan		
w1	6.29×10^6	12
w2	4.19×10^6	9
w3	3.29×10^6	14
Rp 4	10.21×10^6	26
Rp 2	11.09×10^6	34
Asase		
w1	5.19×10^6	12
w2	3.59×10^6	8
w3	3.19×10^6	8
Rp 1	10.19×10^6	26
Rp 2	9.31×10^6	24
AgwanOchounu		
w1	1.11×10^6	4
w2	5.45×10^6	12
w3	3.59×10^6	9
Rp 1	8.12×10^6	17
Rp 2	12.09×10^6	140
Kpege		
w1	1.45×10^6	4
w2	2.11×10^6	4
w3	1.32×10^6	4
Rp 1	7.09×10^6	11
Rp 2	9.21×10^6	17
Day spring		
w1	3.09×10^6	6
w2	3.45×10^6	7
w3	5.98×10^6	11
Rp 1	11.22×10^6	34
Rp 2	9.15×10^6	17

Table 2 Cultural, morphological and biochemical characteristic of coliform bacteria isolated from selected water sources in different location in North bank in Makurdi

Cultural	Morphology	Gram test	Biochemical characteristics					TSI	OF	Inference
			In	MR	VP	CuT	Ox			
Pinkish colony on MCA and greenish metallic sheen colony	Rod shape	Gram negative	+	+	-	-	+	+	+	<i>E. coli</i>

EMB agar										
Pink and mucor colony on MaC agar	Rod shape	Gram negative	-	+	+	-	-	-	+	<i>Klebsiella</i> species
Mucoid, pale, opaque cream to pink on MCA	Bacilli	Gram negative	-	-	+	+	-	+	+	<i>Enterobacter</i> species
Entire, creamy, raised	Cocci	Gram negative	-	-	+	-	-	+	-	<i>Citrobacter</i> species

Note: - = Negative; + = positive; OF= Oxidative/Fermentation, CT = Citrate; VP = Voges-Proskauer; MR= methyl-red, In = Indole; TSI=Triple sugar iron, CuT= Citrate utilization test

Table 3 occurrence of coliform bacteria from water sources in different location in North bank in Makurdi Benue State

		No (%) isolated		
Bacteria isolated	No. sample	Well water	No. sample	River water
<i>E. coli</i>	18	6(33.3)	12	4 (33.3)
<i>Klebsiella</i> species	18	12(66.6)	12	7(58.3)
<i>Enterobacter</i> species	18	4(22.2)	12	6(50.0)
<i>Citrobacter</i> species	18	5(27.7)	12	6(50.0)

Table 4. Haemolysin production activity of coliform bacteria from water sources in North bank in Makurdi

Isolates	Well water	Halo zone (%)	River water	Halo zone (%)
<i>E. coli</i>	6	3 (50.0)	4	1 (25.0)
<i>Klebsiella</i> species	12	4(33.3)	7	3(42.8)
<i>Enterobacter</i> species	4	1 (25.0)	6	2(33.3)
<i>Citrobacter</i> species	5	2(40.0)	6	4(66.6)

Table 5 Congo Red Dye binding of coliform bacteria from water sources in different location in North bank in Makurdi Benue State

Isolates	Well water	No. (%) Bind	River water	No. (%) Bind
<i>E. coli</i>	6	2 (33.3)	4	3 (75.0)
<i>Klebsiella</i> species	12	3 (25.0)	7	2(28.5)
<i>Enterobacter</i> species	4	2 (50.0)	6	3(50.0)
<i>Citrobacter</i> species	5	3 (60.0)	6	2 (33.3)

Table 6 Survival in blood serum by coliform bacteria from water sources in different location in North bank, Makurdi

Isolates	Well water	No. (%) Survival	River water	No. (%) Survival
<i>E. coli</i>	6	2 (33.3)	4	2 (50.0)
<i>Klebsiella</i> species	12	5(41.6)	7	3(42.8)
<i>Enterobacter</i> species	4	1 (25.0)	6	0(0.0)
<i>Citrobacter</i> species	5	1 (20.0)	6	3(50.0)

DISCUSSION

The microbiological quality of drinking water remains an important public-health concern because contaminated water can serve as a vehicle for transmission of enteric pathogens and other disease-causing microorganisms. Poor water quality, inadequate sanitation and inappropriate hygiene practices are major environmental determinants of waterborne disease, particularly in low- and middle-income settings. Diakite et al. (2019), for example, reported widespread microbiological contamination of commonly used water sources in Mali and emphasized the importance of safe water, sanitation and hygiene in preventing waterborne diseases.

The present study demonstrated substantial bacterial contamination of well and river water sources in North Bank, Makurdi. The mean bacterial counts obtained from Yagba well water ranged from 4.08×10^6 to 9.25×10^6 CFU/mL, while the MPN index ranged from 9–26. River-water samples from the same area recorded bacterial counts ranging from 11.41×10^6 to 12.33×10^6 CFU/mL. Similarly, Agan well water had mean bacterial counts ranging from 3.29×10^6 to 6.29×10^6 CFU/mL, with MPN values of 11–34, whereas river water recorded counts of 10.21 – 11.09×10^6 CFU/mL and MPN values of 26–34. At Asase, mean bacterial counts ranged from 3.19×10^6 to 5.19×10^6 CFU/mL in well water, with MPN values of 8–12, while river-water counts ranged from 9.31×10^6 to 10.19×10^6 CFU/mL.

The high bacterial loads observed in the present investigation are consistent with previous Nigerian studies. Agyo et al. (2020), working in Makurdi, reported that total coliform counts and MPN indices in private wells and boreholes exceeded WHO permissible limits. Their study further demonstrated significantly higher coliform counts during the wet season, suggesting that environmental conditions and surface runoff may contribute to contamination of groundwater sources (Agyo et al 2020). The similarity between their findings and those of the present study is particularly important because both investigations were conducted in Makurdi, suggesting that faecal contamination of local water sources may represent a persistent environmental-health problem.

Similarly, Yusufu and Egwujeh (2019) reported that water sources in Anyigba, Kogi State, did not comply with bacteriological standards. Their investigation detected *Escherichia coli*, *Salmonella*, *Staphylococcus aureus*, *Shigella* and *Bacillus* species, with river water being among the most polluted sources (Yusufu and Egwujeh, 2019). The high bacterial counts recorded in the river samples in the present study may likewise be associated with direct or indirect contamination from

human activities, domestic wastewater, animal waste, agricultural runoff and poor protection of water sources.

The detection of total and faecal coliforms in the water samples is of considerable public-health significance. According to WHO drinking-water guidelines, *E. coli* or thermotolerant coliform bacteria should not be detectable in any 100 mL sample of water intended for drinking (WHO, 2017). Therefore, the detection of faecal indicator organisms in the investigated well and river waters indicates recent or continuing faecal pollution and makes the water unsuitable for direct human consumption without appropriate treatment.

The predominance of *Klebsiella* spp. and *E. coli* among the organisms isolated in the present study further strengthens the evidence of microbial contamination. *E. coli* is widely used as an indicator of recent faecal contamination because it occurs abundantly in human and animal faeces. WHO identifies *E. coli* as the most appropriate indicator organism for assessing faecal contamination of drinking water (WHO, 2017). The occurrence of *Klebsiella* and other members of the Enterobacteriaceae in the investigated sources may reflect faecal contamination as well as environmental contamination associated with soil, sewage and organic matter.

The findings are also comparable with more recent evidence from Makurdi. Agbendeh and Ogbonna (2022) detected several potentially pathogenic organisms, including *E. coli*, *Klebsiella*, *Salmonella*, *Shigella*, *Staphylococcus aureus* and *Pseudomonas aeruginosa*, in packaged drinking water sold within Makurdi metropolis (Agbendeh and Ogbonna, 2022). The occurrence of similar organisms in both packaged water and environmental water sources suggests that microbial contamination remains an important water-safety issue in the Makurdi area.

The high bacterial burden observed in river water compared with most well-water samples may be explained by the greater exposure of surface water to environmental contamination. Rivers are directly exposed to domestic sewage, animal faeces, refuse disposal, agricultural runoff and other anthropogenic activities. Diakite et al. (2019) similarly observed substantial microbiological contamination of surface-water sources and attributed contamination partly to poor protection of surface-water structures and contamination from domestic and animal sources (Diakite et al., 2019).

The detection of potentially pathogenic bacteria also has important implications for community health. Consumption of untreated contaminated water can expose residents to enteric infections, particularly diarrhoeal diseases. The WHO emphasizes that microbial contamination remains one of the greatest

risks associated with drinking-water and that control of faecal contamination is fundamental to protecting public health (WHO, 2017).

The haemolysin production observed among some of the bacterial isolates in this study is also noteworthy. Haemolysins are bacterial virulence-associated factors capable of damaging host-cell membranes and contributing to tissue injury. Their detection among isolates recovered from water intended for domestic use suggests that the organisms present may possess pathogenic potential. However, the haemolysis result should be interpreted as evidence of a virulence-associated phenotype rather than direct proof of human pathogenicity, since pathogenicity depends on multiple bacterial and host factors.

The Congo-red-binding results are similarly relevant because surface-associated properties and biofilm formation can facilitate bacterial persistence on environmental surfaces and resistance to environmental stresses. Consequently, the detection of isolates exhibiting Congo-red-binding or other adhesion-associated characteristics suggests that contaminated water sources may provide opportunities for persistence of potentially pathogenic bacteria. These findings reinforce the need for routine microbiological surveillance and appropriate treatment of well and river water before domestic consumption.

STRENGTHS

This study has several strengths. First, it assessed the bacteriological quality of both well and river water from multiple locations in the North Bank area of Makurdi, providing a broader local assessment of water contamination. Second, a total of 82 water samples were investigated, and both bacterial counts and the Most Probable Number (MPN) method were used to evaluate microbial contamination. Third, the study included cultural, morphological, Gram-staining, and biochemical characterization of the isolated coliform bacteria. In addition, selected virulence-associated characteristics, including haemolysin production, Congo-red dye binding, and survival in blood serum, were evaluated. These findings provide useful information regarding the microbiological quality and potential public-health significance of contaminated water sources in the study area.

LIMITATIONS

This study has some limitations. The investigation was conducted within the North Bank area of Makurdi, and therefore the findings may not be directly generalizable to other geographical regions. The study did not provide a detailed assessment of seasonal variations in bacterial contamination. Bacterial identification was primarily based on culture and biochemical methods, without

molecular confirmation of the isolates. Physicochemical parameters of the water, such as pH, turbidity, temperature, and chemical contaminants, were not assessed. Antimicrobial susceptibility and antibiotic-resistance profiles of the bacterial isolates were also not investigated. Furthermore, the haemolysin production, Congo-red binding, and serum-survival assays represent selected virulence-associated characteristics and should not be interpreted as direct evidence of human pathogenicity. Future studies should therefore incorporate broader microbiological, molecular, physicochemical, and antimicrobial-resistance assessments.

FUTURE DIRECTIONS

Future research should include larger and multicentre investigations covering additional communities and water sources in Makurdi and other regions of Benue State. Seasonal sampling during both wet and dry periods would help determine temporal variations in bacteriological contamination. Molecular identification and characterization of bacterial isolates could provide more definitive identification and improve understanding of the organisms present. Further studies should also investigate antimicrobial susceptibility and resistance patterns among waterborne bacterial isolates. Assessment of physicochemical parameters, sanitation conditions, sources of contamination, and household water-treatment practices would provide a more comprehensive understanding of factors contributing to water contamination. Intervention-based studies evaluating the effectiveness of water treatment, improved sanitation, and regular monitoring could also help develop practical strategies for reducing the health risks associated with contaminated water.

CONCLUSION

Overall, the results demonstrate that well and river water sources in North Bank, Makurdi are bacteriologically compromised and should not be considered safe for direct consumption without appropriate treatment. The findings agree with previous investigations in Makurdi and other Nigerian communities and are consistent with WHO requirements for drinking-water safety (Diakite et al., 2019; Yusufu and Egwujeh, 2019). Improved protection of wells, prevention of indiscriminate waste disposal, adequate sanitation, regular water-quality monitoring and appropriate household water-treatment practices are therefore recommended.

DECLARATIONS

Ethics Approval and Consent to Participate

Ethical approval and informed consent were not applicable to this study because it involved the microbiological assessment of environmental water

samples and did not involve human participants or identifiable human data.

Consent for Publication

Not applicable.

Availability of Data

The data generated and analyzed during the present study are available from the corresponding author upon reasonable request.

Competing Interests

The authors declare that they have no competing interests.

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Authors' Contributions

All authors contributed to the study conception, methodology, data collection, analysis, interpretation of results, and preparation and revision of the manuscript. All authors read and approved the final manuscript.

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REFERENCES

1. Agbendeh L and Ogbonna I (2022). Bacteriological and physicochemical assessment of sachet and bottled drinking water sold in Makurdi Metropolis, Benue State, Nigeria. *African Journal of Clinical and Experimental Microbiology*. 4(5) <https://doi.org/10.1099/acmi.ac2021.po0346>
2. Agyo RA, Ofukwu RA, Okoh A EJ, Agada CA (2020). Bacteriological quality of water in private wells and boreholes in Makurdi Metropolis, Benue State, Nigeria. *International Journal of One Health*, 6(1), 76–82.
3. AlSuhaimi AO, AlMohaimidi KM and Momani KA (2017). Preliminary assessment for physicochemical quality parameters of groundwater in Oqdus Area, Saudi Arabia. *Journal Saudi Society of Agricultural Science*, 12:2
4. Anhwange BA, Agbaji EB and Gimba EC. (2012). Impact assessment of human activities and seasonal variation on River Benue within Makurdi Metropolis. *International Journal of Science and Technology*, 2(5): 248-254
5. Anyanwu CU and Okoli EN (2012). Evaluation of the bacteriological and physicochemical quality of water supplies in Nsukka, Southeast, Nigeria. *Afr J Biotechnol*. 11(48):10868-73.
6. Chatterjee SN, Das D, Roy M, Banerjee S, Dey P and Bhattacharya T (2017). Bacteriological examination of drinking water in Burdwan India Concerning Coliforms. *Afr J Biotechnol*. 6(22):2601-2.
7. Cheesbrough M (2006). District laboratory practice in tropical countries. New York, NY: Cambridge University Press, 2006:149-54.
8. Diakite H, Gao Y and Toure A (2019). Assessment of the microbiological quality of drinking water in light of water quality in the Pelengana Commune of Segou Region. *Computational Water, Energy, and Environmental Engineering*, 8, 79–89. <https://doi.org/10.4236/cweee.2019.83005>
9. Ibo EM, Umeh OR, Uba BO and Egwuatu PI (2020). Bacteriological assessment of some borehole water samples in Mile 50, Abakaliki, Ebonyi State, Nigeria. *Archives of Agriculture and Environmental Science*, 5(2): 179-189
10. Iroha IR, Afiukwa NF, Afiukwa CA, Ayogu TE, Onwa, NC, Nwuzo AC (2018). Presence of antibiotic resistant coliforms in sachet water sold in some parts of South Eastern Nigeria. *Advanced Journal of Microbiology Research*, 17(1), 1–6.
11. Naing L Winn T and Rusli BN (2006). Practical issues in calculating the sample size for prevalence studies. *Archives of Orofacial Sciences*, 1, 9–14.
12. Ngwa NR and Chrysanthus N (2013). Bacteriological analysis of well water sources in the Bambui student residential area. *J Water Res Protect*. 5(11):1013-7
13. Olajuba FA and Ogunika F (2014). Assessment of the Physicochemical and Microbiological properties of borehole water samples from Akungba-Akoko, Ondo State, Nigeria. *International Journal of Pharmaceutical Science and Research*, 5 (7): 367–374.
14. Omaka ON, Offor IF and Onwe IM (2014). Hydrogeochemical attributes and ground water quality of Ngbo Community in Ohaukwu Area Council, Ebonyi State, Nigeria. *Revista Ambient Água* 10(1): 35-47

15. Onwughara IN, Nnorom IC and Kanno OC (2010): Issues of roadside disposal habit of municipal solid waste, environmental impacts and implementation of sound management practices in developing country: Nigeria. *International Journal of Environmental Science and Development*, 1(5): 409-417
16. Peter-Ikechukwu A, Omeire GC, Okafor DC, Eluchie C, Odimegwu NE and Nze SN (2015). Assessment of the quality of borehole water sample in federal housing estate and sites and services areas of Owerri, Imo State, Nigeria. *Food Sci Qual Manag*. 42(1):5-12.
17. Reidl J and Klose KE (2002). *Vibrio cholerae* and cholera: Out of the water and into the host. *FEMS Microbiology Reviews*, 26 (2): 125–139
18. World Health Organization (2017). *Guidelines for Drinking-water Quality*, 4th ed., incorporating the first addendum. Geneva: WHO.
19. Yassin MM, Abu-Amr SS and Al-Najar HM (2016). Assessment of microbiological water quality and its relation to human health in Gaza Governorate, Gaza Strip. *Public Health*. 120(12):1177-87.
20. Yusufu PA and Egwujeh SID (2019). Safety assessment of drinking water in Anyigba Town, Kogi State, Nigeria. *ASUU Journal of Science*, 6(1–2), 105–117.