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Research Article

Water Quality and Antibiogram of Bacteria Isolated from Drinking Water Supplies in Bonny Island, Rivers State, Nigeria

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ABSTRACT

Access to safe drinking water is essential for public health, and the bacteriological quality of water sources is a crucial factor in ensuring its safety. This study assessed the bacteriological quality and antibiotic susceptibility patterns of isolated bacteria of drinking water supplies in Bonny Island, Rivers State, Nigeria. Water samples were collected from public taps located at Finima, Hospital Road, Oguede, Akiama, and By-Pass over a five-month period (September, 2022-January, 2023) and analyzed using standard bacteriological techniques. The total heterotrophic bacteria (THB) counts exhibited variations, with Finima and Hospital Road samples showing significant differences ($P < 0.05$). Total Coliform Count (TCC), the counts ranged from 3.9±2.5 to 4.5±4.1 x 10^2 CFU/ml, Finima was significantly different ($p<0.05$). Faecal coliform count and total *Vibrio* count consistently remained at zero, preventing further analysis. The total *Shigella* count ranged from 1.6±3.2 to 2.5±3.6 x 10^2 CFU/ml, with Oguede, By-Pass, and Akiama samples exhibiting significant differences ($P < 0.05$). The most prevalent bacterial isolates included *Erythrobacter*, *Pseudomonas*, *Shigella*, and *Staphylococcus* spp with an occurrence of 18.2% each while *Bacillus*, *Enterococcus*, and *Serratia* spp were less frequent (9.1%). Antibiotic resistance patterns varied among isolates, including resistance to commonly used antibiotics. Isolates were most susceptible to Gentamicin and Vancomycin, while the highest resistance was recorded for Augmentin, Ceftazidime, Cefuroxime, and Cefotaxime. All tested isolates exhibited MAR indices 0.2 and above. This study underscores the need for improved water quality management and sanitation practices to ensure safe drinking water in Bonny Island, Nigeria.

Keywords: Bonny Island Nigeria, drinking water, bacteriology, *Vibrio*, *Shigella*, antibiogram

Introduction

Safe, clean and adequate water supply is vital to public health, it is essential for the efficient operation of ecosystems, communities, and economies. One of the greatest accomplishments in public health throughout the 20th century was the disinfection of water that resulted in improvements of water quality. The growth in human population, industrial and agricultural activity increases, and climate change threatens to expressively distort the hydrological cycle, declining water quality (Li *et al.*, 2020). Despite appearances to the contrary, clean water is one of the world's rarest substances (Singh, 2005). Water is safeguarded by a body of laws, policies, and regulations worldwide to prevent abuse, just like all rare resources that have rules regulating its exploitation, ownership, preservation, and sustenance (Khair *et al.*, 2019).

Although it doesn't contain any calories or organic nutrients, safe drinking water is necessary for both people and animals since it is the solvent in which all biochemistry occurs and the conveyor by which energy, nutrients, and wastes are delivered throughout the body. Although the availability of safe drinking water has increased globally in recent years, almost a billion people still lack access to it, and many of them suffer from water-borne illnesses that can be fatal (Fiore *et al.*, 2010). The contamination of water by human activities, such as industrialization and agricultural practices, is quite significant (Yang *et al.*, 2020). Human actions during any step of the hydrologic cycle, which includes precipitation, surface runoff, infiltration, percolation, evaporation, and transpiration, can change the quality of underground water (Allan *et al.*, 2020).

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In Nigeria, waterborne diseases are a significant public health concern, with millions of people affected each year. According to the Federal Ministry of Water Resources of Nigeria, 110,000 people die from water-related ailments each year (Akinde, 2019). A sizable share health outcomes or sickness and death in Nigeria is caused by waterborne illnesses like cholera, typhoid fever, and diarrhoea, particularly in young children under the age of five (Odeyemi, 2015). According to studies, Nigerian drinking water sources are regularly contaminated with faecal germs and other diseases (Clasen and Bastable, 2003). The Bonny River is subject to pollution from oil spills and industrial activities, which may introduce harmful chemicals and pathogens into the water. Potential infections caused by bacterial pathogens could be found expressing resistance to antibiotics. Thus, this study is significant as it evaluates the bacteriological quality and antibiogram of bacteria isolated from different drinking water sources in Bonny Island.

Materials and Methods

Study Area and Sample Collection

The study area was the Bonny Island located in the heart of the Niger Delta of Nigeria. Water samples were collected from five (5) different drinking water sources located at Finima, Hospital Road, Oguede, Akiama, and By-Pass. These are public taps connected to the five water treatment facilities managed by the Bonny Utility Company (BUC) as the distributor. A total of seventy-five (75) water samples were aseptically collected using sterile polypropylene sample bottles as described by Huq *et al.*, (2012) from 15 public taps (water kiosks) monthly for a period of five months (September, 2022-January, 2023). The Map showing the locations of the water sources where the drinking water samples were collected are presented in Figure 1.

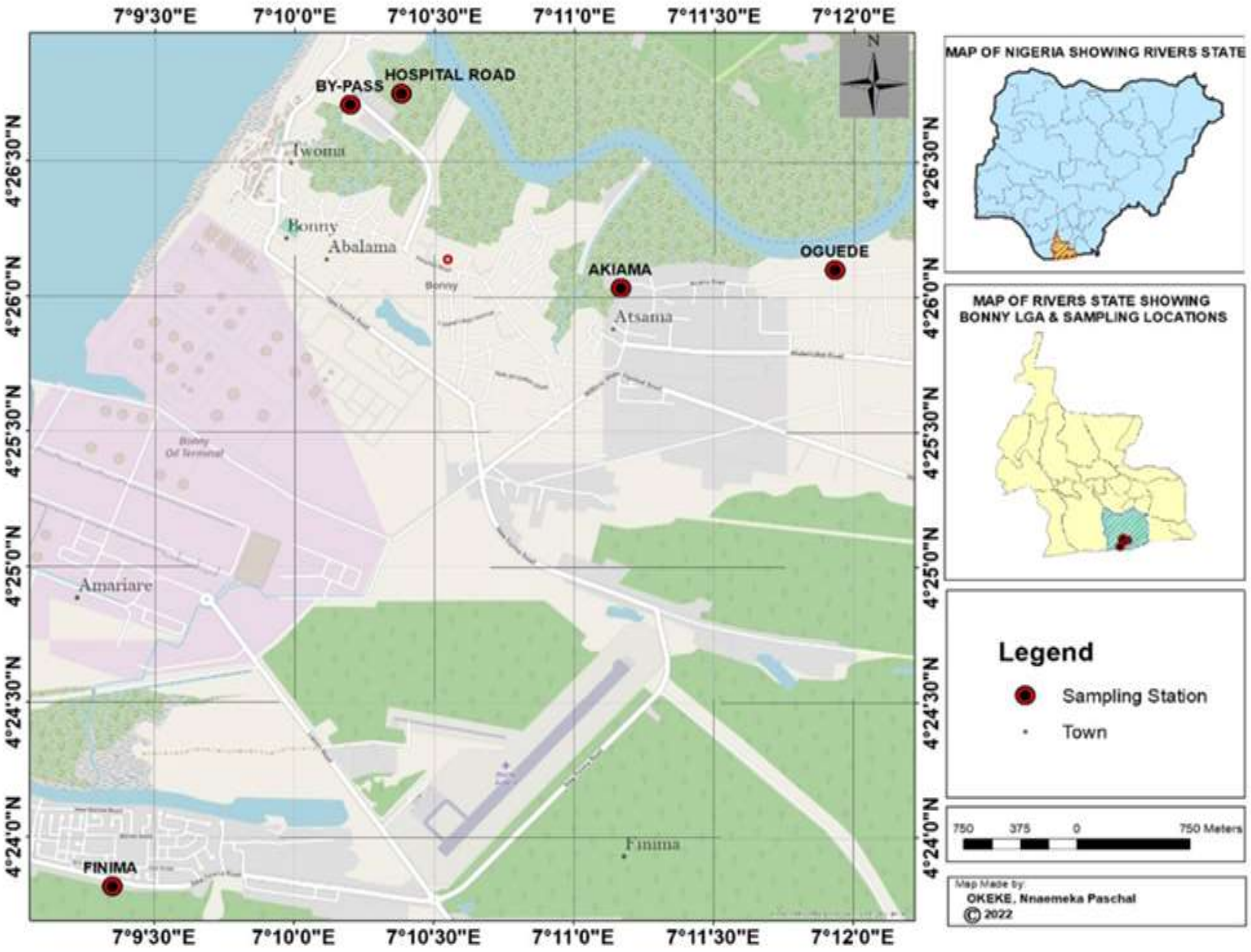

Fig. 1: Map showing location of drinking water sampled

Determination of Physicochemical Parameters

Physicochemical parameters such as pH, electrical conductivity, dissolved solid, hardness, salinity, manganese and iron were determined using the APHA method (APHA, 2017).

Isolation and Enumeration of Bacteria

A ten-fold serial dilution was aseptically carried and aliquots (0.1mL) from the 10^{-2} dilution was transferred into dried surfaces of prepared nutrient agar, eosine methylene blue agar, Mac Conckey agar and Thio citrate bile sucrose agar plates in triplicates. The plates were incubated for 24-48 hours at 37℃ after plating (Aleruchi *et al.*, 2023). The different colonies that formed after incubation were identified based on morphological and biochemical characterization *(Ihechu et al.*, 2023)

Antibiotics Susceptibility Test

The antibiotics susceptibility test was conducted using the Kirby-Bauer disc diffusion method on Mueller-Hinton agar using already prepared commercial discs (Abtek discs). A turbid suspension of the bacterial isolates was prepared based on the 0.5McFarland standard. This was done by transferring colonies of the test bacterial isolates into sterile 4mL normal saline until the turbidity matched the 0.5McFarland used as reference (Okafor *et al.*, 2023). The standardized test isolates were inoculated on sterile Mueller-Hinton agar plates after which discs containing varying concentrations of different antibiotics were placed aseptically. Plates were incubated at 37ºC for 24 hours. Zones of inhibition were recorded and results interpreted based on the guidelines of the Clinical Laboratory Standard Institute (CLSI, 2019). The Multi antibiotics resistance indices were determined.

Statistical Analysis

Colony counts and physicochemical parameters were subjected into descriptive statistics to obtain mean and standard deviation. The analysis of variance was carried out to check for significant differences and means were separated using the Duncan multiple range test. The % of the antibiotic resistance and prevalence of bacterial isolates in the water supplies were also determined. All analyses were carried out on SPSS v27. The test for significance was accepted if $P<0.05$.

Results

Results of the physicochemical parameters of the various drinking water sources are depicted in Table 1. The pH values exhibited variations across the different locations, ranging from 7.16 to 7.30. The lowest pH value of 7.16 was recorded at the By-Pass location, while Akiama and Finima had the highest pH values of 7.30. The electrical conductivity values ranged from 252.5µS/cm to 275.2µS/cm across the locations. Finima displayed the highest conductivity of 275.2µS/cm, while the By-Pass location had the lowest conductivity of 252.5µS/cm. Compared to the other places, Finima had a larger concentration of dissolved salts or ions, however this difference was not statistically significant ($p > 0.05$). Total Dissolved Solids (TDS) values varied from 171.75mg/L to 192.0mg/L across the locations. The By-Pass location recorded the lowest TDS value of 171.75mg/L, whereas Finima exhibited the highest TDS value of 192.0mg/L. Salinity values ranged from 0.11ppt to 0.13ppt across the locations. The By-Pass location displayed the lowest salinity value of 0.11ppt, while Akiama, Finima, and Hospital Road exhibited the highest salinity values of 0.13ppt. By-Pass and Oguede locations' water was significantly ($P<0.05$) lower than the salinity values of Akiama, Finima, and Hospital Road. The hardness values ranged from 113.25mg/L to 123.0mg/L across the locations. The By-Pass location exhibited the lowest hardness value of 113.25mg/L, while Hospital Road recorded the highest hardness value of 123.0mg/L. These findings suggest that the water at Hospital Road contained a higher concentration of minerals, specifically calcium and magnesium ions, compared to the other locations. Iron content values varied from 0.10mg/L to 0.13mg/L across the locations. The lowest iron content was observed at Finima and Oguede (0.10mg/L), whereas Akiama, Hospital Road, and Oguede exhibited the highest iron content (0.13mg/L). The iron concentration varied significantly ($p< 0.05$) among all the locations. Manganese content values ranged from 0.08mg/L to 0.13mg/L across the locations. The By-Pass location displayed the lowest manganese content of 0.08mg/L, while Akiama, Hospital Road, and Oguede exhibited the highest manganese content of 0.13mg/L. The samples from the By-Pass and Finima locations differed significantly (p 0.05) from those from Akiama, Hospital Road, and Oguede, indicating that the latter three had water with a higher concentration of manganese than the By-Pass location did.

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Table 1: Mean values of Physicochemical constituents of various drinking water sources in Bonny Island

Location	**Physicochemical constituents of various drinking water**						
	pH	**Conductivity (µS/cm)**	**TDS (mg/L)**	**Salinity (ppt)**	**Hardness (mg/L)**	**Iron (mg/L)**	**Mn (mg/L)**
Akiama	7.30±0.04^{b}	259.25±32.5^{a}	181.0±25.8^{a}	0.13±0.0^{c}	117.5±1.0^{a}	0.13±0.0^{c}	0.87±0.0^{ab}
By-Pass	7.16±0.07^{a}	252.5±24.5^{a}	171.75±11.1^{a}	0.11±0.0^{b}	113.25±3.9^{a}	0.11±0.01^{abc}	0.08±0.0^{a}
Finima	7.29±0.06^{b}	275.25±8.5^{a}	192.0±12.8^{a}	0.13±0.0^{c}	116.5±1.0^{a}	0.10±0.01^{a}	0.09±0.0^{b}
Hospital Road	7.30±0.05^{b}	257.0±25.4^{a}	180±20.5^{a}	0.13±0.0^{c}	123.0±13.4^{a}	0.13±0.0^{c}	0.83±0.0^{ab}
Oguede	7.26±0.07^{b}	258.0±31.1^{a}	182.25±22.9^{a}	0.10±0.0^{a}	116.7±1.5^{a}	0.11±0.0^{ab}	0.85±0.0^{ab}

*Means with similar superscript along the column showed no significant difference ($P>0.05$)
Key: TDS – Total Dissolved Solids, Mn – Manganese.

Results of the mean values of bacterial counts of the water samples are presented in Table 2. The mean and standard deviation counts (THB x 10^{4} CFU/ml) of the respective water sources exhibited variations, ranging from 5.8±2.2^{a} to 6.2±5.0^{a} x 10^{4} CFU/ml. When compared to other places, Finima and Hospital Road exhibited a significant difference (P 0.05). It is worth noting that the FCC and TVC (x 10^{2}CFU/ml) consistently maintained a count of 0 across all locations, making any analysis or comparison impossible. In terms of the TCC, the counts ranged from 3.9±2.5^{b} to 4.5±4.1^{a} x 10^{2} CFU/ml, Finima was significantly different ($p<0.05$). In regard to the TSC (x 10^{2} CFU/ml), the counts ranged from 1.6±3.2^{a} to 2.5±3.6^{b}. Specifically, Oguede, By-Pass and Akiama displayed significant difference ($P<0.05$) compared to other locations. The distribution of bacterial isolates in the various drinking water sources in Bonny Island is shown in Table 3. Result of the tentative characteristics of the bacterial isolates after subjecting them to series of biochemical and morphological tests showed that they belonged to seven genera: *Bacillus*, *Pseudomonas*, *Serratia*, *Shigella*, *Staphylococcus*, *Enterococcus*, and *Erythrobacter*. Results of the bacterial distribution in the water sources showed that seven genera were isolated from the different drinking water sources.

Results of the percentage occurrence of bacterial isolates in drinking water sources are shown in Fig. 2. The result revealed that *Erythrobacter*, *Pseudomonas*, *Shigella* and *Staphylococcus* spp were the most prevalent bacterial isolates recording 18.2% each while *Bacillus*, *Enterococcus* and *Serratia* sp were the least with a percentage occurrence of 9.1%.

Table 2: Bacterial Count (CFU/ml) of various drinking water sources in Bonny Island

Location of drinking water kiosk	**Bacterial Population (CFU/ml)**				
	THB ($x10^{4}$)	**FCC ($x10^{2}$)**	**TCC ($x10^{2}$)**	**TSC ($x10^{2}$)**	**TVC ($x10^{2}$)**
Akiama	5.8±2.2^{a}	0	4.4±4.3^{a}	1.7±2.2^{a}	0
By-Pass	6.2±5.0^{a}	0	4.3±4.4^{a}	1.7±3.5^{a}	0
Finima	5.4±3.9^{b}	0	3.9±2.5^{b}	2.5±3.6^{b}	0
Hospital Road	5.5±2.8^{b}	0	4.5±4.1^{a}	2.0±2.8^{b}	0
Oguede	6.1±3.9^{a}	0	4.2±4.4^{a}	1.6±3.2^{a}	0
P. value	0.0427		0.0238	0.0379	

*Means with similar superscript along the column showed no significant difference ($P>0.05$); **Keys:** THB – total heterotrophic bacteria; FCC – faecal coliform; TCC – total coliform count, TSC – total staphylococci count; TVC – total *Vibrio* count

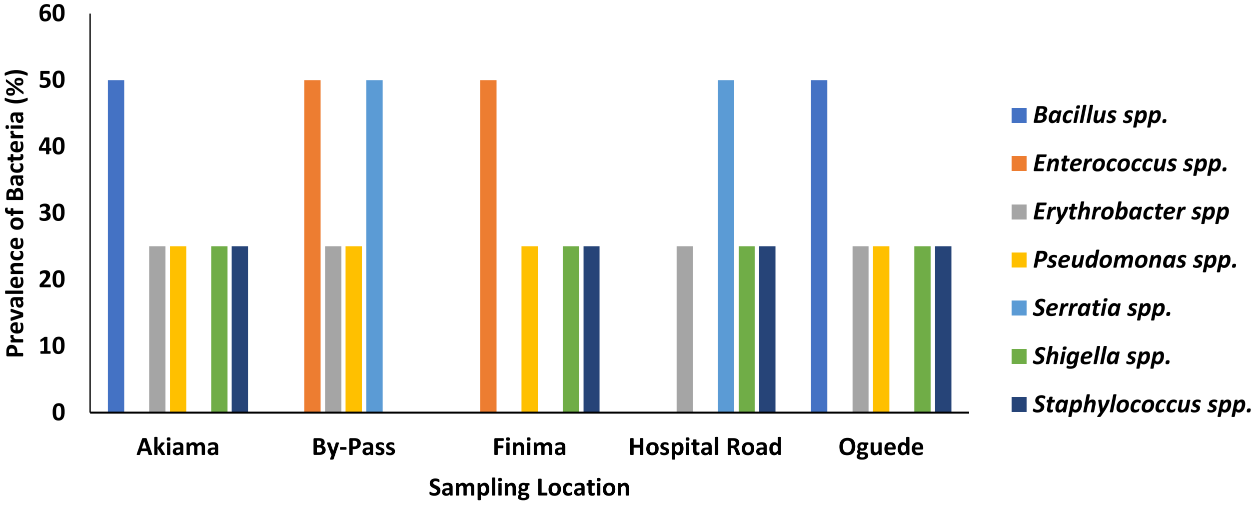

Fig. 2: Prevalence of bacterial isolates in drinking water sources from various locations in Bonny Island

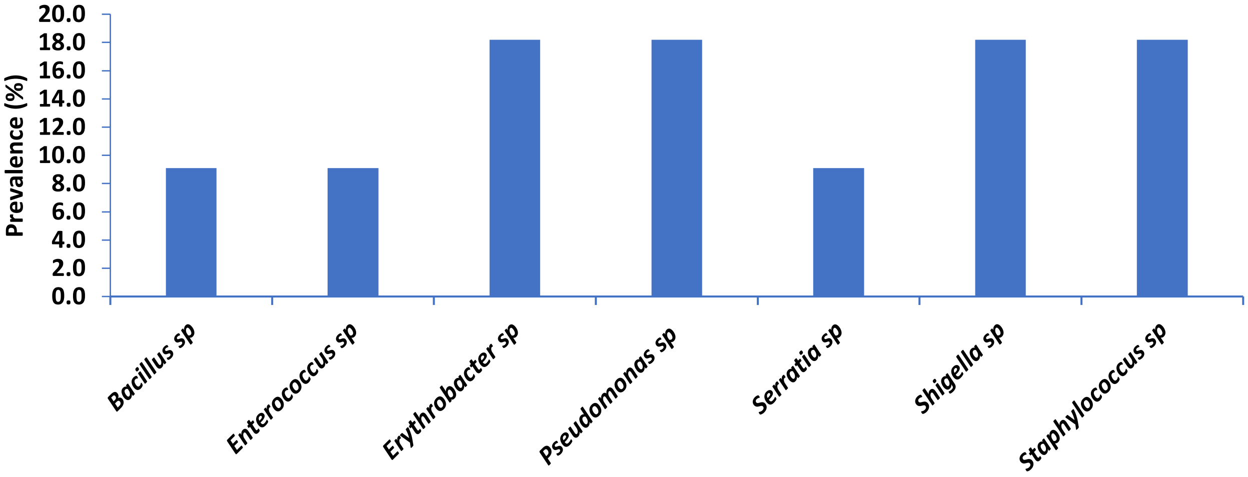

Fig. 3: Cumulative prevalence of bacterial isolates of the water sources studied in Bonny Island

Results of the antibiotics susceptibility test of Gram-positive bacterial isolates is presented in Table 4. Results showed that Ampicillin susceptibility was observed in 50% of the isolates, while the remaining 50% showed resistance. All (100%) isolates showed meropenem susceptibility. Tetracycline had mixed results, with 50% intermediate response and 50% resistance. Cotrimoxazole showed 50% susceptibility and 50% intermediate response. Complete (100%) resistance to Cefuroxime was observed. Gentamicin had a split response, with 50% susceptibility and 50% resistance. Ciprofloxacin had no susceptibility but exhibited intermediate response. Augmentin showed complete resistance. Vancomycin had a divided response, with 50% susceptibility and 50% resistance. All isolates were resistant to ceftazidime. Cephalexin showed a mixed response, with 50% susceptibility and 50% resistance among the isolates. The susceptibility of *Staphylococcus* sp to different antibiotics showed that Ampicillin and Ceftazidime displayed 100% resistance across all isolates tested. Meropenem and Ciprofloxacin exhibited susceptibility in 66.7% of the isolates, an intermediate response in 33.3%, and no resistance. Erythromycin showed an intermediate response in 100% of the isolates. Tetracycline demonstrated susceptibility in 33.3% of the isolates, an intermediate response in 66.7%, and no resistance.

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Cotrimoxazole and Gentamicin showed susceptibility in 100% of the isolates, with no intermediate response or resistance observed. Cefuroxime demonstrated susceptibility in 33.3% of the isolates, an intermediate response in 33.3%, and resistance in one isolate (33.3%). Augmentin displayed an intermediate response in 33.3% of the isolates and resistance in 66.7%. Vancomycin exhibited susceptibility in 66.7% of the isolates, with no intermediate response observed, and resistance in 33.3%. Cephalexin demonstrated an intermediate response in 66.7% of the isolates and resistance in 33.3%. The patterns of tested antibiotic susceptibility of *Enterococcus* sp showed that Ampicillin and Vancomycin exhibited 100% susceptibility across all *Enterococcus* sp. Cotrimoxazole resulted in a split response, with 50% of isolates showing intermediate response, while the other 50% exhibited resistance. Ciprofloxacin, Gentamicin, and Cephalexin showed mixed responses, with 50% susceptible and 50% exhibiting intermediate responses. Conversely, Erythromycin, Augmentin, Meropenem, Tetracycline, Cefuroxime, and Ceftazidime demonstrated complete resistance (100%) in all tested *Enterococcus species.*

The susceptibility patterns of the Gram-negative bacterial isolates are presented in Table 5. Results showed that *Erythrobacter* species demonstrated 25% susceptibility to Tetracycline while 75% displayed resistance. The isolates exhibited a distribution of susceptibility, intermediate response, and resistance, with 50%, 25%, and 25% respectively to Gentamicin, Cotrimoxazole, and Chloramphenicol. Conversely, all isolates showed complete resistance to Cefuroxime, without any showing susceptibility or an intermediate response. Ceftriaxone resulted in 75% of isolates displaying an intermediate response, while 25% were resistant. For Cefotaxime, 25% of isolates showed an intermediate response, and 75% were resistant. Ciprofloxacin, Amikacin, and Vancomycin demonstrated a similar pattern, with 25% of isolates being susceptible, 50% showing an intermediate response, and 25% being resistant. Ceftazidime showed a resistance prevalence of 75% among isolates, with 25% showing an intermediate response. Lastly, 25% of isolates were susceptible, 50% showed an intermediate response, and 25% were resistant to Meropenem. *Pseudomonas* sp susceptibility to antibiotics showed no susceptibility to Tetracycline with 50% intermediate response and 50% resistance. Cotrimoxazole had no susceptibility (0%), with 75% resistance and 25% intermediate response. Gentamicin had 75% susceptibility and 25% resistance. Cefuroxime showed complete resistance (100%). Chloramphenicol had 50% resistance and 50% intermediate response. Ceftriaxone and Cefotaxime both exhibited full resistance (100%). Ciprofloxacin had 75% resistance, 25% intermediate response, and 25% susceptibility.

Amikacin showed balanced susceptibility (50%) and resistance (50%). Vancomycin had 25% susceptibility, 50% intermediate response, and 25% resistance. Ceftazidime showed 50% susceptibility, 50% resistance, and no intermediate response. Meropenem had 75% resistance and 25% intermediate response.

The susceptibility of *Serratia* sp to various antibiotics at different concentrations showed that Tetracycline and Gentamicin demonstrated complete susceptibility, as all (100%) *Serratia* sp were susceptible, and there were no isolates showing an intermediate response or resistance to this antibiotic. Cotrimoxazole, on the other hand, showed no susceptibility among the *Serratia species*, with 50% of the isolates exhibiting an intermediate response and the remaining 50% displaying resistance. For Cefuroxime, Ceftriaxone, Ciprofloxacin, Amikacin, Vancomycin, Ceftazidime, Chloramphenicol, and Meropenem, none of the *Serratia* species were found to be susceptible. Among these antibiotics, 50% of the isolates showed an intermediate response, indicating reduced effectiveness while the remaining 50% exhibited resistance.

The susceptibility of *Shigella* sp to different antibiotics at varying concentrations showed that 25% of the isolates were susceptible to Tetracycline, Vancomycin, Meropenem, and Ceftazidime, 25% exhibited an intermediate response, and 50% were resistant. For Ciprofloxacin, no isolates were susceptible, 75% displayed an intermediate response, and 25% were resistant.

Gentamicin, Cefuroxime, and Ceftriaxone showed 50% sensitivity to the isolates, and 50% were resistant. None of the isolates were susceptible to Chloramphenicol, 25% showed an intermediate response, and 75% were resistant. All isolates were resistant to Cefotaxime while 50% of the isolates were susceptible to Amikacin and 25% were resistant.

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Table 4: Antibiotics Susceptibility Pattern of Gram-positive bacteria isolates from drinking water sources in Bonny Island

Antibiotics	**Conc. (μg)**	***Bacillus* species**			***Enterococcus***			***Staphylococcus* sp**		
		S	**I**	**R**	**S**	**I**	**R**	**S**	**I**	**R**
Ampicillin	10	2(100)	0	0	2(100)	0	0	0	0	3(100)
Meropenem	10	2(100)	0	0	0	0	2(100)	2(66.7)	1(33.3)	0
Erythromycin	5	0	2(100)	0	0	0	2(100)	0	3(100)	0
Tetracycline	30	0	2(100)	0	0	0	2(100)	1(33.3)	2(66.7)	0
Cotrimoxazole	25	2(100)	0	0	0	1(50)	1(50)	3(100)	0	0
Cefuroxime	10	0	1(50)	1(50)	0	0	2(100)	1(33.3)	1(33.3)	1(33.3)
Gentamicin	10	1(50)	1(50)	0	1(50)	0	1(50)	3(100)	0	0
Ciprofloxacin	5	0	2(100)	0	1(50)	1(50)	0	2(66.7)	1(33.3)	0
Augmentin	30	0	0	2(100)	0	0	2(100)	0	1(33.3)	2(66.7)
Vancomycin	30	2(100)	0	0	2(100)	0	0	2(66.7)	0	1(33.3)
Ceftazidime	10	0	0	2(100)	0	0	2(100)	0	0	3(100)
Cephalexin	1.5	1(50)	1(50)	0	1(50)	1(50)	0	0	2(66.7)	1(33.3)

Key: S – susceptible; I – intermediate; R – resistance

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Table 5: Susceptibility Pattern of Gram-negative bacteria isolates from drinking water sources in Bonny Island

Antibiotics	**Conc. (µg)**	***Erythrobacter* sp**			***Pseudomonas***			***Serratia* sp**			***Shigella* sp**		
		S	**I**	**R**	**S**	**I**	**R**	**S**	**I**	**R**	**S**	**I**	**R**
Tetracycline	10	1(25)	0	3(75)	0	2(50)	2(50)	2(100)	0	0	1(25)	1(25)	2(50)
Cotrimoxazole	25	2(50)	1(25)	1(25)	0	3(75)	1(25)	0	1(50)	1(50)	0	3(75)	1(25)
Gentamicin	10	2(50)	1(25)	1(25)	3(75)	0	1(25)	2(100)	0	0	2(50)	0	2(50)
Cefuroxime	30	0	0	4(100)	0	0	4(100)	0	0	2(100)	2(50)	0	2(50)
Chloramphenicol	10	2(50)	1(25)	1(25)	0	2(50)	2(50)	0	1(50)	1(50)	0	1(25)	3(75)
Ceftriaxone	30	0	3(75)	1(25)	0	0	4(100)	0	1(50)	1(50)	2(50)	0	2(50)
Cefotaxime	30	0	1(25)	3(75)	0	0	4(100)	0	0	2(100)	0	0	4(100)
Ciprofloxacin	5	1(25)	2(50)	1(25)	0	1(25)	3(75)	0	1(50)	1(50)	0	3(75)	1(25)
Amikacin	30	1(25)	2(50)	1(25)	2(50)	0	2(50)	2(100)	0	0	2(50)	1(25)	1(25)
Vancomycin	30	1(25)	2(50)	1(25)	1(25)	2(50)	1(25)	1(50)	1(50)	0	1(25)	1(25)	2(50)
Ceftazidime	30	3(75)	1(25)	0	2(50)	0	2(50)	0	1(50)	1(50)	0	1(25)	3(75)
Meropenem	10	1(25)	2(50)	1(25)	0	1(25)	3(75)	0	1(50)	1(50)	0	2(50)	2(50)

Key: S – susceptible; I – intermediate; R – resistance

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Results of the MAR indices for the bacterial isolates are presented in Table 5. By analysing the MAR index values, the bacterial species within each genus can be classified into distinct levels of antibiotic resistance. Notably, the following categorizations emerged: 100% of *Bacillus* spp. demonstrate MAR indices of 0.2 and above, while 100% of *Enterococcus* spp., exhibited MAR indices above 0.2. 100%. *Staphylococcus* spp. displayed MAR indices of 0.2 and above while 75% *Erythrobacter* spp. indicated varying degrees of resistance with MAR indices of above 0.2. One hundred percent (100%) of the *Pseudomonas* spp. Isolated exhibited high level of resistance with MAR indices of above 0.2. Similarly, 75% *Shigella* spp. high level of resistance with MAR indices of above 0.2. Additionally, 100% *Serratia* spp. showcased MAR indices of 0.2 and above

Table 5: Multiple Antibiotic Resistant (MAR) Index of bacterial isolates from drinking water sources in Bonny Island

MAR Index	**Bacterial isolates**						
	***Bacillus* spp. 2(%)**	***Enterococcus* spp. 2(%)**	***Staphylococcus* spp. 3(%)**	***Erythrobacter* spp. 4(%)**	***Pseudomonas* spp. 4(%)**	***Serratia* spp. 2(%)**	***Shigella* spp. 4(%)**
0							
0.1				1(25)			1(25)
0.2	1(50)		1(33.3)			1(50)	
0.3	1(50)		1(33.3)	2(50)	1(25)		1(25)
0.4					1(25)		
0.5		1(50)	1(33.3)				
0.6							
0.7		1(50)				1(50)	
0.8					1(25)		1(25)
0.9				1(25)			
1					1(25)		1(25)

Discussion

The physicochemical parameters of the different water sources fluctuated from one water source to the other. The physicochemical parameters of water play a crucial role in assessing its quality and suitability for human consumption (Smith *et al.*, 2018).The pH of the water sources was slightly neutral but within the 6.5-8.5 pH range based on the World Health Organization standard (WHO, 2020). Maintaining the appropriate pH level is crucial as it affects chemical reactions and the behavior of substances in water (Smith and Johnson, 2016). Deviations from the recommended pH range can impact taste, odor, and the effectiveness of water treatment processes.

The conductivity values across the different showed that Finima displayed the highest conductivity value of 275.25µS/cm, while the By-Pass location had the lowest conductivity value of 252.5µS/cm. Although Finima exhibited a higher concentration of dissolved salts or ions compared to the other locations, this difference was not found to be statistically significant ($p > 0.05$) and differed from reports by Smith *et al.* (2019). The Total Dissolved Solids (TDS) values, they varied across the locations such that the By-Pass location recorded the lowest TDS value of 171.75mg/L, whereas Finima exhibited the highest TDS value of 192.0mg/L. The high TDS in the water at Finima implied that there was greater concentration of dissolved substances compared to the By-Pass location (Jones and Brown, 2020). In terms of salinity values ranged from 0.11ppt to 0.13ppt across the locations (Johnson *et al.*, 2018). The hardness values across the various locations showed that the By-Pass location demonstrated the lowest hardness value of 113.25mg/L, while Hospital Road exhibited the highest hardness value of 123.0mg/L. This implied that the water at Hospital Road contained a higher concentration of minerals, specifically calcium and magnesium ions, compared to the other locations (Anderson *et al.*, 2023). Hardness indicates the concentration of minerals, specifically calcium and magnesium ions, in water (Jones and Brown, 2019).

High hardness levels can lead to scaling issues, affecting water taste, appearance, and functionality. Iron and manganese concentrations are also important indicators, as excessive amounts can cause aesthetic and operational problems, impacting water quality and distribution systems (Chen *et al.*, 2017).

The Total Heterotrophic Bacterial Counts (THB), coliform and faecal coliform counts serves as a widely accepted method for evaluating the overall microbiological safety of drinking water.

Drinking water quality standards set by various organizations globally recommend specific THB limits, typically ranging from 100 to 500 Colony-Forming Units per milliliter (CFU/ml), < 3 cfu/ml for coliforms and zero (0) for faecal coliform (WHO, 2008). The findings in the present study showed that the drinking water sources do not meet the bacteriological standard for water quality despite having zero (0) faecal counts.

The high bacterial counts in the present study agreed with results of previous studies (Ezekiel-Hart *et al.*, 2012). Conversely, the absence of faecal Coliform Count (FCC) could suggest that the drinking water samples are likely devoid of pathogenic microorganisms due to treatment of the water using chlorination, especially since the faecal coliforms are indicators of contamination of pathogens or microorganisms from faecal routes (Prescott *et al.*, 2011). High bacterial counts in surface water and spring water has been reported in previous studies and human activities have been attributed as the reason behind the high bacterial load (Obire *et al*., 2005, 2014; Obire and Stephanie, 2016).

The bacterial isolates in the present study with the exception of *Erythrobacter* sp have been reported in drinking water sources by previous studies. Onuorah *et al*. (2019) isolated *Klebsiella, Vibrio, Enterobacter* and *Staphylococcus* spp from the borehole water they examined in Ogbaru Community, Anambra State, Nigeria while Abdullahi *et al*. (2013) isolated *Klebsiella* from the Staff school, Science Department and female hostel boreholes in Niger State Polytechnic, Zungeru campus. Ngele *et al*. (2014) isolated *Enterobacter* spp in selected borehole samples in Amike-Aba, Abakaliki while Olujuba and Ogunika (2014) isolated *Klebsiella* and *Staphylococcus* spp from borehole samples from Akungba-Akoko, Ondo State, Nigeria. In addition, Josiah *et al*. (2014) isolated *Staphylococcus* spp from drinking water and water used for domestic purposes in Okada Town, Edo State, Nigeria while Ayandele *et al*. (2019) reported the presence of *Staphylococcus, Vibrio* and *Klebsiella* spp isolated from surface drinking water in Ogbomoso. Antibiotic resistance is an escalating global concern, underscoring the importance of continuously monitoring bacterial susceptibility patterns to inform clinical decisions, from the study, antibiotic susceptibility results emphasize the need for prudent antibiotic selection and personalized treatment strategies to address antibiotic resistance effectively.

Among Gram-positive bacteria, ampicillin exhibited a dual response, with a 50% susceptibility rate and 50% resistance rate. This suggests that ampicillin may not consistently combat Gram-positive infections, aligning with existing literature on ampicillin's decreasing efficacy (Charalambous *et al*., 2003). Conversely, meropenem demonstrated remarkable efficacy, with 100% susceptibility among all Gram-positive isolates. This is in line with previous research highlighting meropenem's potency against Gram-positive pathogens (Jones *et al*., 2005).

Tetracycline and cotrimoxazole both displayed mixed responses, each with 50% susceptibility and 50% intermediate response. These findings underscore the complexity of antibiotic selection for Gram-positive infections, with tetracycline resistance concerns corroborating prior studies (Murray *et al.*, 2018). Cefuroxime exhibited complete resistance (100%) among Gram-positive isolates, limiting its clinical utility in this context, consistent with previous reports (Brogden *et al*., 2012). Gentamicin showed a divided response, with 50% susceptibility and 50% resistance, underlining the need to consider bacterial strains and resistance mechanisms when prescribing gentamicin (Naparatek *et al*, 2014).

Furthermore, the study explains the Multiple Antibiotic Resistance (MAR) index values of the isolated bacterial *species* and their respective percentages. By analysing the MAR index values, the bacterial species within each genus can be classified into distinct levels of antibiotic resistance. Notably, the following categorizations emerge: 100% of *Bacillus species* demonstrated MAR indices of above 0.2, while 100% of *Enterococcus species* exhibited MAR indices above 0.2. Moderate resistance: 75% *Erythrobacter species* indicated high level of resistance with a MAR indices of above 0.2. 100% *Pseudomonas species* exhibited varying degrees of resistance, with MAR indices of up to 1. Similarly, 100% *Shigella* and *Serratia species* showcased MAR indices of above 0.2. Additionally, 100% *Staphylococcus species* displayed MAR indices of above 0.2.

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This analysis highlights the prevalence of antibiotic resistance among these bacterial genera and underscores the importance of addressing the challenges posed by such resistance patterns. Findings from a study by Boccella *et al.*, (2021) agrees with findings from this study that *Enterococcus species* showed multiple antibiotic resistance to the antibiotics used in the study. Also, a study by Bottery *et al.*, (2021) had findings similar to those from this study. By examining the MAR index values, it becomes possible to classify bacterial species within each genus into distinct levels of antibiotic resistance. Overall, this study contributes to the understanding of antibiotic resistant bacteria in drinking water, highlighting the significance of disinfection practices and the potential implications for antibiotic resistance development (Tiwari *et al.*, 2022). A MAR index greater than 0.2 indicates a significant level of antibiotic resistance within the tested bacterial population. This is concerning as it signifies that these bacteria are not only resistant to one type of antibiotic but are capable of resisting multiple antibiotics concurrently. This highlights the ongoing challenge of antibiotic resistance as a global health issue (Carlet, 2014).

This present study underscores the critical role of antibiotic susceptibility testing in guiding clinical practice. The results emphasize the need for tailored treatment strategies, antibiotic stewardship efforts, and continued research to combat antibiotic resistance effectively. By considering bacterial species and susceptibility profiles, clinicians can make informed antibiotic choices, optimizing patient care and mitigating the growing challenge of antibiotic resistance.

In conclusion, the combination of bacteriological assessment and antibiogram analysis highlights the challenges faced in maintaining safe drinking water supplies in Bonny Island, Rivers State, Nigeria. Addressing these challenges requires a holistic approach, including improved water treatment, source protection, and antibiotic stewardship, to safeguard public health and enhance the overall quality of life for the residents of Bonny Island.

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