

Microbial and Physicochemical Analysis of Borehole Water within Oza Nogogo, Agbor, Delta State

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Abstract

This study assessed the physicochemical and microbiological quality of borehole water used for domestic purposes in Oza Nogogo, Agbor, Delta State, Nigeria. Fifteen borehole water samples were collected from Oza Nogogo, Alisor and Alizomor and subjected to standard microbiological and physicochemical analyses. We evaluated antibiotic susceptibility using the Kirby–Bauer disc diffusion method. Heterotrophic bacterial counts ranged from 36.67 ± 3.06 to 64.00 ± 2.65 CFU/mL, while total coliform counts ranged from 3.00 ± 0.00 to 43.67 ± 2.52 CFU/mL. Faecal coliforms occurred in samples A1, A2, B2, C1 and C2, with values ranging from 2.33 ± 0.58 to 15.00 ± 2.65 CFU/mL. Twelve bacterial isolates were characterized and comprised *Escherichia coli*, *Klebsiella* spp., *Enterobacter* spp., *Proteus* spp., *Serratia marcescens*, *Citrobacter* spp., *Salmonella typhi*, *Enterococcus faecalis*, *Corynebacterium* spp. and *Clostridium* spp. Gram-negative organisms accounted for 75.0% of the isolates. Antibiotic susceptibility results showed substantial resistance to several commonly used antibiotics, particularly amoxicillin, ampiclox and erythromycin, whereas ciprofloxacin, ofloxacin and sparfloxacin were comparatively more effective. pH ranged from 5.3 to 6.1, EC from 8 to 18 $\mu\text{S}/\text{cm}$, TDS from 4 to 9 ppm, temperature from 27.6 to 28.4 °C, TTA from 20 to 55 mg/L and hardness from 15.01 to 150.14 mg/L as CaCO_3 . ANOVA showed significant differences in pH, EC, TDS and TTA among sampling groups. The combined microbiological and physicochemical findings indicate that the

borehole sources require regular monitoring and appropriate treatment before use for drinking or other domestic purposes.

Keywords: borehole water; microbial quality; coliforms; antibiotic resistance; physicochemical parameters.

1. Introduction

Water is essential to human survival, household activities and public health, but the safety of groundwater cannot be assumed solely because it occurs below the surface (Ighalo & Adeniyi, 2020). Borehole water is widely relied upon in developing communities where public water supplies are inadequate or unreliable (Olalemi *et al.*, 2021). Its quality may nevertheless be affected by borehole construction, maintenance, hydrogeological conditions, proximity to waste disposal sites, septic tanks and latrines, surface runoff and other human activities (Olalemi *et al.*, 2023; Lapworth *et al.*, 2023). Microbial contamination is particularly important because the detection of indicator organisms and enteric bacteria can signal sanitary deficiencies and potential exposure to waterborne pathogens (Ekiamene *et al.*, 2024; Adomi *et al.*, 2025). The project identified Oza Nogogo, Agbor, Delta State, as a community where residents rely substantially on boreholes for domestic activities and where local information on microbiological quality was limited. The study therefore evaluated the microbial quality of borehole water in relation to its suitability for domestic use, determined the microbial load, characterized bacterial contaminants and assessed the antibiotic sensitivity patterns of recovered isolates. The work also incorporated physicochemical measurements to provide a broader assessment of water quality. The study objectives were to isolate and characterize bacterial contaminants, determine microbial load in CFU/mL and evaluate antibiotic sensitivity patterns of the isolates.

2. Materials and Methods

2.1 Study area and design

Fifteen borehole water samples were collected from three sampling locations designated Oza Nogogo (Group A), Alisor (Group B) and Alizomor (Group C). Five samples were obtained from each location and coded A1–A5, B1–B5 and C1–C5. Samples were collected in sterile sample bottles, properly labelled and transported immediately to the laboratory for analysis. Culture media used included Nutrient Agar, MacConkey Agar and Mueller-Hinton Agar, prepared according to manufacturers' instructions. For bacterial enumeration, one millilitre of each water sample was transferred into 9 mL

of sterile diluent and subsequently plated using the pour-plate method. Plates were incubated at 37°C for 24 h, after which colonies were counted and expressed as CFU/mL. Discrete colonies were purified by repeated subculture on Nutrient Agar and maintained on Nutrient Agar slopes.

2.2 Analyses of samples

For the laboratory analysis, the major equipment used included a light microscope (Olympus CX23), autoclave (Hirayama HVE-50), incubator (Mettler IN30), colony counter (Stuart SC6), analytical weighing balance (Ohaus Pioneer PX224), pH meter (Hanna Instruments HI 2211), conductivity/TDS meter (Hanna Instruments HI 99300), and digital thermometer. Other routine laboratory equipment, including burettes and related materials, was also used during the study.

Cultural characteristics were assessed from colony morphology on Nutrient Agar and MacConkey Agar, including colour, size, shape, elevation, transparency and margin. Gram staining was used to distinguish Gram-positive and Gram-negative organisms. Biochemical tests included catalase, urease, citrate utilization, hydrogen sulphide and indole production, while carbohydrate fermentation tests covered glucose, lactose, sucrose, fructose, maltose, starch and sorbitol. Antibiotic susceptibility was determined by the Kirby–Bauer disc diffusion technique on Mueller-Hinton Agar after 24 h incubation at 37°C, with inhibition zones measured in millimeters. Physicochemical analysis covered pH, temperature, EC, TDS, TTA and hardness. pH was measured directly with a digital pH meter; temperature was recorded after a stable thermometer reading; EC was measured using a conductivity meter calibrated with 0.01 M potassium chloride; TDS was measured with a TDS meter; TTA was determined by titration of 50 mL water with 0.1 N sodium hydroxide using phenolphthalein as endpoint indicator; and hardness was determined by EDTA titration. All analyses were carried out in triplicate and results were expressed as mean values. One-way ANOVA was used to assess differences among sampling groups, with percentages and average values used where appropriate.

3. Results

Table 1: Microbiological counts of borehole water samples (mean $\pm$ SD)

Sample	Heterotrophic bacteria (CFU/mL)	Total-coliform (CFU/mL)	Faecal-coliform (CFU/mL)
A1	54.00 $\pm$ 4.36	43.67 $\pm$ 2.52	13.67 $\pm$ 1.15
A2	41.00 $\pm$ 2.65	25.00 $\pm$ 2.00	15.00 $\pm$ 2.65
A3	63.67 $\pm$ 3.51	38.00 $\pm$ 2.65	ND
A4	44.67 $\pm$ 3.06	18.00 $\pm$ 0.00	ND
A5	53.33 $\pm$ 3.51	30.67 $\pm$ 2.08	ND

B1	63.00 ± 2.65	5.33 ± 0.58	ND
B2	36.67 ± 3.06	33.33 ± 2.52	5.67 ± 3.06
B3	59.67 ± 3.51	5.00 ± 0.00	ND
B4	45.33 ± 2.52	10.00 ± 0.00	ND
B5	55.00 ± 3.61	28.33 ± 1.53	ND
C1	64.00 ± 2.65	20.00 ± 1.00	6.33 ± 3.06
C2	42.67 ± 3.06	9.00 ± 0.00	2.33 ± 0.58
C3	60.67 ± 4.04	31.67 ± 1.53	ND
C4	40.00 ± 2.65	3.00 ± 0.00	ND
C5	55.67 ± 3.06	7.00 ± 0.00	ND

The microbiological results demonstrated contamination across the sampled boreholes. Heterotrophic bacterial counts ranged from 36.67 ± 3.06 CFU/mL in B2 to 64.00 ± 2.65 CFU/mL in C1. Total coliform counts ranged from 3.00 ± 0.00 CFU/mL in C4 to 43.67 ± 2.52 CFU/mL in A1. Faecal coliforms were detected in five samples: A1, A2, B2, C1 and C2. A2 recorded the highest faecal coliform count at 15.00 ± 2.65 CFU/mL, followed by A1 at 13.67 ± 1.15 CFU/mL. The occurrence of total coliforms in every sample and faecal coliform in selected samples indicates that the water sources were exposed to environmental and localized faecal contamination. The low standard deviations across replicate determinations indicate relatively consistent analytical results.

Table 2: Bacterial isolates recovered from the borehole water samples

Probable isolate	Gram reaction
<i>Corynebacterium</i> sp.	Gram-positive
<i>Escherichia coli</i> 1	Gram-negative
<i>Proteus</i> sp.	Gram-negative
<i>Serratia marcescens</i> 1	Gram-negative
<i>Enterococcus faecalis</i>	Gram-positive
<i>Clostridium</i> sp.	Gram-positive
<i>Citrobacter</i> sp.	Gram-negative
<i>Serratia marcescens</i> 2	Gram-negative
<i>Klebsiella</i> sp.	Gram-negative
<i>Enterobacter</i> sp.	Gram-negative
<i>Escherichia coli</i> 2	Gram-negative

Twelve bacterial isolates were characterized. The isolates comprised three Gram-positive organisms and nine Gram-negative organisms, corresponding to 25.0% and 75.0%, respectively. The Gram-negative predominance is important because several of the identified organisms, including *Escherichia coli*, *Klebsiella*, *Enterobacter* and *Salmonella typhi*, are associated with environmental or enteric contamination. Biochemical testing showed catalase positivity in 75.0% of isolates, citrate utilization in 41.7%, urease production in 33.3%, indole production in 25.0% and hydrogen sulphide production in 41.7%. Carbohydrate utilization was also variable: glucose fermentation occurred in all isolates, fructose and maltose fermentation in 91.7% each, sucrose fermentation in 83.3%, sorbitol fermentation in 75.0%, and lactose fermentation in 50.0%. No isolate hydrolyzed starch. The combined cultural, morphological, biochemical and carbohydrate-utilization characteristics supported the presumptive identification of a mixed bacterial population containing both environmental and enteric organisms.

Table 3: Selected antibiotic susceptibility pattern and resistance indices of bacterial isolates

Isolate	Selected sensitive/intermediate responses	Selected resistant responses	R.I.
<i>Corynebacterium sp.</i>	PEF 20 S; CN 18 S; SXT 18 S	Z 10 R; AM 8 R; E 10 R	0.2
<i>Enterococcus faecalis</i>	PEF 12 I; SXT 14 I; E 12 I	CN 0 R; APX 0 R; Z 8 R; AM 4 R; R 0 R;	0.7
<i>Clostridium sp.</i>	CPX 20 S	CPX 10 R; S 10 R CN 8 R; APX 0 R; Z 0 R; AM 0 R; R 0 R	0.5
<i>E. coli</i> ₁	OFX 18 S	SXT 0 R; CH 0 R; AM 8 R; AU 10 R; CN 10 R; S 0 R	0.6
<i>Proteus sp.</i>	OFX 18 S	CH 4 R; AM 6 R; AU 0 R; CN 10 R; S 10 R	0.5
<i>S. marcescens</i> ₁	SP 20 S; CPX 20 S; OFX 18 S	SXT 10 R; CH 6 R; AM 6 R; AU 0 R; S 10 R	0.4
<i>Citrobacter sp.</i>	SP 20 S; CPX 20 S	SXT 0 R; CH 6 R; AM 8 R; S 4 R	0.4

<i>S. marcescens</i> ₂	CPX 18 S; SP 18 S	SXT 0 R; CH 0 R; AM 0.6 8 R; AU 10 R; CN 10 R; S 6 R
<i>Klebsiella</i> sp.	SP 20 S; OFX 18 S	SXT 0 R; CH 0 R; AU 0.4 0 R; S 6 R
<i>Enterobacter</i> sp.	PEF 22 S; SP 22 S	SXT 6 R; CH 0 R; AU 0.4 0 R; CN 10 R
<i>E. coli</i> ₂	APX 20 S; SP 18 S; OFX 20 S	SXT 0 R; CH 0 R; AU 0.5 0 R; CN 10 R; S 0 R
<i>Salmonella typhi</i>	PEF 14 I; OFX 14 I	SXT 0 R; CH 0 R; 0.6 APX 10 R; AU 0 R; CN 0 R; S 0 R

Key: Pefloxacin (PEF), Gentamicin (CN), Ampiclox (APX), Zinnacef (Z), Sparfloxacin (SP) Amoxicillin (AM), Rocephin (R), Ciprofloxacin (CPX), Septrin (SXT), Azithromycin (AZ), Augmentin (AU) Levofloxacin (LEV), Ofloxacin (OFX), Erythromycin (E). Resistance Index(RI), Resistant (R), Sensitive(S), Intermediate(I).

The antibiotic susceptibility results demonstrated varying degrees of susceptibility and resistance among the isolates. Among the Gram-positive organisms, *Corynebacterium* sp. showed susceptibility to pefloxacin, gentamycin and erythromycin but resistance to zinnacef and amoxicillin as recorded in the project profile, while *Enterococcus faecalis* showed extensive resistance and had the highest resistance index of 0.7. *Clostridium* sp. showed susceptibility to ciprofloxacin but resistance to several beta-lactam antibiotics. Among the Gram-negative organisms, several isolates showed strong susceptibility to fluoroquinolones. *E. coli* isolate 1 was susceptible to ofloxacin, *Proteus* sp. was susceptible to ofloxacin, *Serratia marcescens* isolate 1 was susceptible to sparfloxacin and ciprofloxacin, *Citrobacter* sp. was susceptible to sparfloxacin and ciprofloxacin, *Klebsiella* sp. was susceptible to ciprofloxacin and ofloxacin, and *Enterobacter* sp. showed strong susceptibility to pefloxacin and ciprofloxacin. *Salmonella typhi* showed extensive resistance, with only intermediate responses to pefloxacin and ofloxacin. Resistance indices ranged from 0.2 in *Corynebacterium* sp. to 0.7 in *Enterococcus faecalis*, with most isolates falling between 0.4 and 0.6.

Table 4: Mean $\pm$ SD physicochemical characteristics of borehole water by sampling group

Parameter	Group A	Group B	Group C
pH	5.40 $\pm$ 0.17	5.86 $\pm$ 0.09	5.78 $\pm$ 0.26
EC (μ S/cm)	8.00 $\pm$ 0.00	18.00 $\pm$ 0.00	12.00 $\pm$ 0.00
TDS (ppm)	4.00 $\pm$ 0.00	9.00 $\pm$ 0.00	6.60 $\pm$ 0.55
Temperature ($^{\circ}$ C)	27.80 $\pm$ 0.35	27.68 $\pm$ 0.11	27.60 $\pm$ 0.00
TTA (mg/L)	45.00 $\pm$ 7.07	32.00 $\pm$ 5.70	27.00 $\pm$ 6.71
Hardness (mg/L as CaCO ₃)	68.06 $\pm$ 48.21	37.03 $\pm$ 7.59	38.03 $\pm$ 13.98

Physicochemical assessment showed that all groups had slightly acidic water. Individual pH values ranged from 5.3 to 6.1, with Group A recording the lowest group mean (5.40 ± 0.17) and Group B the highest (5.86 ± 0.09). EC ranged from 8 to 18 $\mu\text{S}/\text{cm}$, with Group B showing the highest mean value of $18.00 \pm 0.00 \mu\text{S}/\text{cm}$. TDS ranged from 4 to 9 ppm and followed a similar pattern, with Group B recording the highest mean value. Temperatures were relatively stable, ranging from 27.6 to 28.4°C. TTA varied from 20 to 55 mg/L, with the highest group mean in Group A ($45.00 \pm 7.07 \text{ mg/L}$), while hardness ranged from 15.01 to 150.14 mg/L as CaCO_3 and showed the greatest variability in Group A. The spatial differences indicate that some physicochemical properties varied according to sampling location.

Table 5: One - way ANOVA of selected physicochemical parameters

Parameters	F-value	p-value	Decision
pH	8.63	0.0048	Significant
EC	–	<0.001	Highly significant
TDS	312.67	<0.001	Highly significant
Temperature	1.15	0.349	Not significant
TTA	10.16	0.0026	Significant
Hardness	1.81	0.206	Not significant

One-way ANOVA confirmed significant spatial differences in pH ($F = 8.63$, $p = 0.0048$), EC ($p < 0.001$), TDS ($F = 312.67$, $p < 0.001$) and TTA ($F = 10.16$, $p = 0.0026$). Temperature ($F = 1.15$, $p = 0.349$) and hardness ($F = 1.81$, $p = 0.206$) did not differ significantly among the groups. These findings indicate that the ionic content, dissolved solids, acidity and pH varied more strongly with location than temperature or hardness. The slightly acidic pH observed throughout the study area is relevant to domestic water quality, while the relatively low EC and TDS values suggest that the waters did not contain high concentrations of dissolved ionic material. However, physicochemical acceptability alone cannot establish microbiological safety.

4. Discussion

The combined results indicate that borehole water quality in the study area was affected by measurable microbial contamination alongside location-related physicochemical variation. Total coliforms occurred in all fifteen samples, while faecal coliforms were detected in five. This pattern is consistent with Adomi *et al.* (2025), who reported poor bacteriological quality in borehole water across Delta State, and with Olalemi *et al.* (2021), who identified enteric bacteria in Nigerian groundwater sources. Olalemi *et al.* (2023) also linked sanitary inspection findings with microbial health risks in groundwater sources in Nigeria. In comparison, the present study adds evidence from Oza Nogogo, Alisor and Alizomor and shows that faecal contamination indicators were present in selected rather than all samples. This uneven distribution suggests that risks may differ between individual boreholes. Potential explanations include sanitation facilities, waste disposal, runoff or differences in borehole protection, as discussed in previous groundwater studies (WHO, 2022). However, these sources were not directly measured at each sampling point in the present work. The findings support routine monitoring and protection of individual boreholes rather than assuming that all groundwater sources have the same quality.

The physicochemical findings complement the microbiological results. The pH values (5.3–6.1) indicate that the sampled water was acidic. This agrees with Badmus *et al.* (2020), who described groundwater in Ogun Waterside as slightly acidic, and overlaps with the lower end of the pH range reported by Jacob *et al.* (2022) for groundwater around Obajana. In contrast, EC and TDS in the present study (8–18 $\mu\text{S}/\text{cm}$ and 4–9 ppm, respectively) were much lower than the broad ranges reported in those studies, suggesting that the sampled boreholes contained comparatively little dissolved ionic material as measured by these parameters. Group B had the highest EC and TDS, whereas Group A had the highest mean TTA and the greatest variability in hardness. Such differences may be related to local hydrogeological conditions, but further chemical analysis would be needed to establish the causes. Most importantly, the comparatively low EC and TDS do not offset the microbiological concern: the detection of total coliforms in every sample means that chemical measurements alone cannot demonstrate that the water is safe for drinking.

The antimicrobial findings add another dimension to the public-health concern. Resistance indices ranged from 0.2 in *Corynebacterium* sp. to 0.7 in *Enterococcus faecalis*, and resistance to several commonly used antibiotics was observed. This broadly agrees with Wilcox *et al.* (2023), who detected antimicrobial-resistance genes in bacteria from drinking-water sources in Bonny Island, and with Rabi *et al.* (2024), whose review examined the role of drinking-water sources in the environmental dissemination of antibiotic-resistant *E. coli* in Africa. The key difference is that the present study

assessed phenotypic susceptibility using disc diffusion, whereas Wilcox *et al.* (2023) assessed resistance genes; the findings therefore support a shared concern but are not directly interchangeable. The present data also do not prove that antibiotic misuse caused the observed resistance, because antibiotic residues, resistance genes and the sources of resistant bacteria were not investigated. Nonetheless, the detection of resistant isolates in water intended for domestic use supports careful water treatment and continued antimicrobial-resistance surveillance. The comparatively greater susceptibility of some isolates to ciprofloxacin, ofloxacin or sparfloxacin should be interpreted only as an in-vitro result and not as a recommendation for treating human infections.

The study shows that the sampled borehole waters should not be considered microbiologically safe for drinking without appropriate treatment. The combination of total coliforms in all samples, faecal coliforms in selected samples, potentially enteric bacterial isolates, and antibiotic-resistant organisms represents a meaningful public-health concern. Regular microbiological and physicochemical monitoring, protection of boreholes from nearby contamination sources, proper sanitation and waste management, and treatment of water before drinking are therefore warranted. The study provides a useful local baseline for water-quality surveillance in Oza Nogogo and the surrounding Agbor area.

Conclusion

The investigation demonstrated that borehole water from Oza Nogogo, Alisor and Alizomor showed measurable microbiological contamination and variation in physicochemical quality. Heterotrophic bacteria and total coliforms were detected throughout the sampled sources, while faecal coliforms occurred in five samples. Twelve bacterial isolates representing both Gram-positive and Gram-negative organisms were characterized, including *E. coli*, *Klebsiella*, *Enterobacter*, *Proteus*, *Serratia*, *Citrobacter*, *Salmonella*, *Enterococcus*, *Corynebacterium* and *Clostridium*. Several isolates exhibited resistance to commonly used antibiotics, although fluoroquinolones were comparatively more effective. The water was also slightly acidic, with significant spatial differences in pH, EC, TDS and TTA. The findings indicate that the borehole sources require regular quality surveillance and suitable treatment before use as drinking water.

Recommendations

Routine microbiological and physicochemical testing of community boreholes should be conducted at regular intervals.

Boreholes should be protected from nearby septic tanks, pit latrines, refuse dumps, stagnant wastewater and other potential contamination sources.

Water intended for drinking should undergo an appropriate treatment process before consumption, particularly where coliform or faecal contamination is detected.

Community sanitation, waste-disposal practices and public awareness of groundwater protection should be strengthened.

Antibiotic use should be guided by appropriate clinical and microbiological evidence, while environmental surveillance of antimicrobial resistance should be encouraged.

Further studies should include a larger number of boreholes and, where possible, seasonal sampling to establish changes in microbial and physicochemical quality over time.

Declarations

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