OPEN ACCESS
Global Journal of Research in Medical Sciences
ISSN: 2583-3960 (Online)
Volume 06 | Issue 03 | May-June | 2026
Journal homepage: https://gjrpublication.com/gjrms/
Research Article

Bacteriological Assessment of Borehole Water and Associated Household Health Outcomes in Girie, Yola North, and Yola South, Adamawa State, Nigeria

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DOI: 10.5281/zenodo.20092422 **Submission Date: 30 March 2026 | Published Date: 09 May 2026**

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Abstract

Groundwater from boreholes serves as the primary drinking water source for many communities in Adamawa State, northeastern Nigeria. However, the bacteriological safety of these sources remains poorly characterized despite increasing concerns about waterborne diseases. This study assessed the bacteriological quality of borehole water from three locations, Girie, Yola North, and Yola South, and evaluated household water handling practices and self-reported health outcomes. A total of 253 water samples were collected from household storage tanks and analyzed for total heterotrophic bacteria, total coliforms, fecal coliforms, and Salmonella–Shigella counts using standard microbiological techniques. Bacterial isolates were identified through cultural and biochemical methods. Additionally, structured questionnaires were administered to 304 household heads to capture data on water handling practices, health outcomes, and knowledge, attitudes, and practices regarding waterborne diseases. Total heterotrophic bacterial counts ranged from 5.92 to 6.15 log CFU/mL, while total coliform and fecal coliform levels ranged from 2.34 to 2.60 log MPN/100 mL and 1.88 to 2.01 log MPN/100 mL, respectively, with no significant differences between locations ($p > 0.05$). Pseudomonas spp. (22.9–25.5%) and Escherichia coli (16.3–17.1%) were the most prevalent isolates. Salmonella spp. (8.6–10.2%), Shigella spp. (8.6–11.2%), Klebsiella spp. (10.2–11.4%), and Vibrio cholerae were also recovered. Household survey revealed water-related illness prevalence of 60.0–78.7%, with typhoid fever accounting for 66.7–86.5% of reported illnesses. Despite the highest awareness (95.7%) and training coverage (79.8%) in Girie, this location paradoxically recorded the worst health outcomes (78.7% illness prevalence). "Poor water source" was consistently identified as the primary challenge (40.0–41.5% of respondents). Borehole water sources across the study area are heavily contaminated with fecal indicator organisms and multiple enteric pathogens, rendering them unsafe for direct consumption. The uniformity of contamination suggests a region-wide sanitary crisis. The observed knowledge-behavior paradox indicates that structural interventions, including source water protection, routine chlorination, and improved sanitation infrastructure, are urgently needed alongside continued health education to reduce the high burden of waterborne diseases in these communities.

Keywords: *Bacteriological assessment, coliform contamination, groundwater quality, waterborne diseases, borehole water.*

INTRODUCTION

Groundwater is an essential source of drinking water worldwide, but its bacteriological quality depends on multiple interacting factors, some natural, others stemming directly from human activity. On the natural side, geological formations and soil layers can release various substances, including heavy metals, into groundwater through dissolution and leaching. Meanwhile, human actions present an equally significant concern. The heavy reliance on agrochemicals like nitrogen-based fertilizers, organophosphate insecticides, carbamate pesticides, and weed killers has introduced numerous synthetic chemicals into subsurface environments (Adeyemo and Ogunbanwo, 2024; Bamidele *et al.,*2025). These compounds do more than just change water chemistry; they also disturb the natural microbial communities living underground. Adding to this problem is poor sanitation infrastructure. Leaky septic tanks and uncovered latrines create direct pathways for disease-causing microbes and organic waste to enter shallow groundwater reserves (Chukwu and Ezeh, 2024; Okafor *et al.,*2025). What this means is straightforward: the safety of groundwater from a bacteriological standpoint reflects both how well the environment can naturally purify itself and how much pressure human activities place on it. This makes regular monitoring essential, especially where boreholes are the primary source of household water (Adebayo *et al.,* 2025; Nwachukwu and Idris, 2024).

The health consequences of consuming unsafe water remain severe across the globe, though low-income countries carry a much heavier burden of sickness and death. Germs that travel through water, bacteria, viruses, and parasites cause a range of gut-related illnesses. Diarrhea alone is responsible for a large portion of preventable deaths, hitting children below five years old particularly hard in places with limited resources (Eze and Oluwole, 2024; Ogunsanya *et al.,*2025). People often assume groundwater is cleaner than surface water because soil layers act as natural filters, trapping particles and removing some microorganisms. That assumption holds true to an extent, but it is not universally reliable (Ibrahim and Mohammed, 2025; Umar *et al.,*2024). Water can move quickly through cracks, large pores, or broken rock layers, carrying surface contaminants downward without going through the slow filtering process that finer soils provide. So, when communities depend on hand-pumped boreholes without conducting frequent, thorough bacteriological checks, they face a real but often overlooked health threat, particularly in rural and semi-urban settings (Akinwumi *et al.,*2024; Oyebamiji and Adeleke, 2025).

Standard approaches for evaluating water quality focus on detecting indicator bacteria. Total coliforms and fecal coliforms act as warning signs for fecal pollution and suggest that pathogens like disease-causing *Escherichia coli*, *Salmonella* species, *Shigella* species, or *Vibrio cholerae* might also be present (Obiora and Nwosu, 2024; Ugwu *et al.,*2025). The real danger from waterborne germs comes from drinking water tainted by human or animal waste; finding coliform bacteria signals that harmful organisms could be there, creating an immediate health concern (Ekwe and Nnabue, 2025; Ogunleye *et al.,*2024). Yet the range of microbial threats in groundwater goes beyond these traditional indicators. Opportunistic pathogens, including *Pseudomonas aeruginosa*, various *Klebsiella* and *Proteus* species, *Streptococcus*, and *Clostridium*, also turn up in water supplies. These organisms are especially dangerous for people with weakened immune systems, as well as for infants and older adults (Anyanwu and Okeke, 2024; Yusuf *et al.,*2025). It is also worth noting that individual immunity varies a great deal depending on age, gender, nutritional status, and living environment, all of which affect how susceptible someone is to water-related diseases. And for germs that spread through the fecal-oral route, drinking water is not the only pathway. Contaminated food, hands, eating utensils, and clothing all contribute significantly, especially where household sanitation and hygiene practices are lacking (Adeyinka and Lawal, 2025; Ezeigbo and Onwuka, 2024).

The time of year also makes a substantial difference in groundwater microbiology, thanks to shifts in rainfall amounts, groundwater table levels, and how quickly aquifers recharge. The wet season brings more rain, which increases surface runoff, washes contaminated soil into water bodies, and speeds up the movement of pathogen-filled water into unconfined or partly confined aquifers (Abubakar and Sani, 2024; Omodara *et al.,*2025). This hydrological connection usually leads to noticeably higher bacterial counts, more coliform bacteria, and more frequent detection of disease-causing species during rainy months relative to drier periods (Eniola and Odetoyin, 2025; Olaniyi and Fasasi, 2024). Dry season conditions, by contrast, involve less recharge and lower water tables, which often means fewer microbes overall. Still, contamination can linger in stagnant zones or within the aquifer material itself (Adamu and Bello, 2025; Nwankwoala and Amadi, 2024). Getting a handle on these seasonal effects is crucial for planning sampling efforts that truly represent conditions, making sense of long-term water quality data, and putting effective risk reduction measures, such as treating water at the point of use during high-risk months, into practice (Gbadebo and Taiwo, 2025; Onyekwere and Nwagwu, 2024).

Borehole water is an inexpensive technological solution for household water supply in poorer nations, often viewed as a "safe option" as long as boreholes are sited correctly, built properly, and operated following accepted standards (Adekunle and Oyedeji, 2024; Nwosu and Okolo, 2025). However, contamination often happens not at the source but during collection, transport, storage, or pouring. Borehole operators are expected to provide safe, dependable drinking water without interruption, but this is not always achievable (Ezeh and Ugwuanyi, 2025; Ogunbiyi and Adebayo, 2024). When testing reveals coliforms or other bacteria, there is an immediate need to track down where the contamination originated. Meeting microbiological standards matters greatly because waterborne illnesses can spread rapidly through large populations (Akinola and Oluwo, 2025; Oni and Ogunwale, 2024). Actions that improve water quality and accessibility, enhance waste disposal systems, and raise overall hygiene levels all play important roles in cutting down disease transmission through the fecal-oral route (Arowolo and Fayemi, 2025; Obi and Eze, 2024). With this background, the present study set out to identify bacterial isolates present in borehole water drawn from several towns across Adamawa State, evaluate the water's bacteriological safety status, and pinpoint likely contamination sources. The ultimate goal is to provide useful information for public health interventions and for managing water safety more effectively in these communities (Danladi and Usman, 2025; Ibrahim and Haruna, 2024).

MATERIALS AND METHODS

Study Area and Design

A cross-sectional design was adopted for this study, which was carried out between March and December 2025 (representing both dry and wet seasons) across three distinct locations within Adamawa State, northeastern Nigeria: Girie, Yola North, and Yola South. This region experiences a tropical climate characterized by clearly demarcated wet and dry seasons. A total of 253 water samples were collected from household storage tanks across the three locations: 70 samples from Girie, 98 from Yola South, and 85 from Yola North. In parallel, a structured questionnaire was administered to 304 household heads (94 from Girie, 110 from Yola North, and 100 from Yola South) to gather information on demographic characteristics, water handling practices, self-reported health outcomes, and knowledge, attitudes, and practices relating to waterborne diseases.

Sample Collection and Processing

Water samples (500 mL each) were collected aseptically from household storage containers using sterile borosilicate glass bottles fitted with screw caps. Where residual chlorine was anticipated, sodium thiosulfate (0.1% w/v) was added to neutralize its antimicrobial effect. All samples were placed in coolers maintained at 4–8°C with ice packs and transported to the laboratory within six hours of collection. For each sampling location, samples were collected in quadruplicate to allow for comprehensive microbiological analysis.

Enumeration of Total Heterotrophic Bacteria

Total heterotrophic bacterial counts were determined using the standard pour plate technique. Briefly, 1 mL aliquots of serially diluted water samples (dilution factors ranging from 10^{-1} to 10^{-6}) were mixed with approximately 15 mL of molten Plate Count Agar cooled to 45°C. The mixture was poured into sterile Petri dishes and allowed to solidify. Plates were then incubated aerobically at 37°C for 48 hours. Colony counting was performed using a digital colony counter, and results were expressed as log colony-forming units per milliliter (log CFU/mL). Each dilution was plated in duplicate, and mean values were recorded (Yari *et al.,* 2018).

Enumeration of Total and Fecal Coliforms

The Most Probable Number (MPN) method was employed for the enumeration of both total and fecal coliforms. A five-tube, three-dilution series (10^{-1}, 10^{-2}, and 10^{-3}) was prepared using lauryl sulfate tryptose broth (LST, Oxoid, UK). Tubes were incubated at 37°C for 48 hours, and those showing turbidity accompanied by gas production were recorded as presumptive positive for total coliforms. To confirm the presence of fecal coliforms, positive LST tubes were sub-cultured into brilliant green lactose bile broth followed by incubation at 44.5°C for 48 hours. Gas production at this elevated temperature confirmed fecal coliforms. MPN values were derived from standard statistical tables and reported as log MPN per 100 mL (log MPN/100 mL) (Dahiru *et al.,* 2024).

Isolation and Enumeration of Salmonella and Shigella Species

For the enumeration of *Salmonella* and *Shigella* species, water samples underwent an initial enrichment step in selenite F broth (Oxoid, UK) at 37°C for 24 hours. Following enrichment, 0.1 mL aliquots were spread-plated onto Salmonella–Shigella agar supplemented with 0.1% sodium deoxycholate. Plates were incubated at 37°C for 24 to 48 hours. Presumptive *Salmonella* colonies appeared colorless with characteristic black centers (due to hydrogen sulfide production), while presumptive *Shigella* colonies appeared colorless without black centers. Counts were recorded and expressed as log CFU/mL (Abaka *et al.,* 2025).

Isolation and Identification of Bacterial Genera

To recover specific bacterial genera, water samples were spread-plated onto a panel of selective media. These included MacConkey agar for general Enterobacteriaceae, Eosin Methylene Blue (EMB) agar for *Escherichia coli*, Cetrimide agar for *Pseudomonas* spp., Mannitol Salt Agar (MSA) for *Staphylococcus aureus*, KF Streptococcus agar for *Enterococcus* spp., and Xylose Lysine Deoxycholate (XLD) agar for *Shigella* and *Salmonella* species. All plates were incubated at 37°C for 24 to 48 hours. Distinct colonies exhibiting characteristic morphological features were aseptically sub-cultured onto nutrient agar slants to obtain pure isolates, which were then stored at 4°C pending further biochemical characterization (Abaka *et al.,* 2024).

Biochemical Characterization

Presumptive bacterial isolates were subjected to a comprehensive panel of conventional biochemical tests following standard protocols. The tests performed included indole production (using Kovac's reagent), urease activity (on Christensen's urea agar), methyl red test, Voges–Proskauer test, hydrogen sulfide production (on triple sugar iron agar), and carbohydrate fermentation profiles using phenol red broth supplemented with sucrose, glucose, maltose, or lactose, each containing Durham tubes for gas detection. Test results were interpreted according to the taxonomic schemes outlined in Bergey's Manual of Systematic Bacteriology. From the total pool of isolates, eight representative isolates were selected for detailed biochemical profiling to confirm their presumptive identities as *Staphylococcus aureus*, *Escherichia coli*, *Pseudomonas aeruginosa*, *Salmonella typhi*, *Klebsiella pneumoniae*, *Vibrio cholerae*, *Proteus vulgaris*, and *Shigella flexneri* (Dominic *et al.,* 2025).

Household Survey and Data Collection

A pretested, structured questionnaire was administered through face-to-face interviews to 304 household heads (94 from Girie, 110 from Yola North, and 100 from Yola South). The questionnaire captured information across several domains: (i) sociodemographic characteristics (age, sex, marital status, educational attainment, occupation); (ii) water source and handling practices (primary drinking water source, frequency of water collection, frequency of tank cleaning, whether tanks were covered, primary uses of water); (iii) hygiene practices (handwashing before fetching water); (iv) health outcomes (self-reported water-related illness within the preceding three months, and among those reporting illness, specific diagnosis of typhoid fever); (v) health-seeking behavior (type of treatment sought); (vi) awareness and prior training (awareness of health risks associated with waterborne diseases, whether the respondent had received any prior training on water safety); (vii) sources of information (non-governmental organizations, health workers, etc.); (viii) perceived challenges related to water safety; and (ix) suggested solutions. Verbal informed consent was obtained from all participants before enrollment, and the voluntary nature of participation was emphasized.

Statistical Analysis

All microbiological analyses were performed in quadruplicate, and results were expressed as mean ± standard error of the mean (SEM). Data were analyzed using SPSS software. One-way analysis of variance (ANOVA) was employed to compare microbial densities across the three locations, with statistical significance set at a threshold of $p < 0.05$. Where significant differences were detected, Duncan's Multiple Range Test was applied for post-hoc pairwise comparisons. For categorical survey data, descriptive statistics (frequencies and percentages) were computed, and Chi-square tests were used where appropriate to assess associations between variables. Graphical representations and tables were generated using Microsoft Excel and GraphPad Prism (version 9.0) (Abaka *et al.,* 2025).

Ethical Considerations

Ethical clearance for this study was obtained from the Health Research Ethics Committee of the Adamawa State Ministry of Health (Approval Reference Number: ADHREC/2025/075). The study was conducted in full compliance with the ethical principles outlined in the Declaration of Helsinki. Participation was entirely voluntary, and all respondents were assured of the strict confidentiality of their responses. Participants were informed of their right to withdraw from the study at any point without fear of negative repercussions or loss of any benefits to which they might otherwise be entitled.

Table 1: Microbial Density of Girie, Yola North, and Yola South

Location	Total Heterotrophic Bacteria (log CFU/mL)	Total Coliform (log MPN/100 mL)	Fecal Coliform (log MPN/100 mL)	Salmonella–Shigella (log CFU/mL)
Girie	5.92 ± 0.18^{ab}	2.34 ± 0.07^{b}	1.88 ± 0.09^{b}	2.21 ± 0.21^{a}
Yola North	6.15 ± 0.22^{b}	2.51 ± 0.10^{b}	1.95 ± 0.08^{b}	2.30 ± 0.18^{a}
Yola South	6.08 ± 0.31^{b}	2.60 ± 0.13^{b}	2.01 ± 0.10^{b}	2.18 ± 0.24^{a}

- Values are presented as mean ± standard error (SE), n = 4.
- Means within the same column bearing different superscript letters (a, b) are significantly different ($P < 0.05$) based on Duncan's Multiple Range Test (DMRT).
- CFU = Colony Forming Units; MPN = Most Probable Number.

Table 2: Prevalence of Bacterial Isolates in Water Samples from Girie, Yola South, and Yola North, Adamawa State

Bacterial Genus/Species	Girie (n = 70)		Yola South (n = 98)		Yola North (n =85)	
	n	%	n	%	n	%
Shigella spp.	6	8.6	11	11.2	9	10.6
Enterobacter spp.	7	10.0	10	10.2	8	9.4
Enterococcus spp.	5	7.1	8	8.2	7	8.2
Escherichia coli	12	17.1	16	16.3	14	16.5
Klebsiella spp.	8	11.4	10	10.2	9	10.6
Pseudomonas spp.	16	22.9	25	25.5	20	23.5
Staphylococcus aureus	5	7.1	8	8.2	7	8.2
Salmonella spp.	6	8.6	10	10.2	8	9.4
Proteus spp.	5	7.1	,	,	3	3.5

Table 3: Morphological and Biochemical Characteristics of Bacterial Isolates

Isolate	Indole	Urease	Methyl Red	Voges–Proskauer	H_2S	Sucrose	Glucose	Maltose	Lactose	Presumptive Identity
1	–	+	+	+	–	A	A	A	A	Staphylococcus aureus
2	+	–	+	–	–	A/G	A/G	A/G	A/G	Escherichia coli
3	–	–	–	–	–	–	–	–	–	Pseudomonas aeruginosa
4	–	–	+	–	+	–	A	A	–	Salmonella typhi
5	–	+	–	+	–	A/G	A/G	A/G	A/G	Klebsiella pneumoniae
6	+	–	+	–	–	A/G	A/G	A/G	–	Vibrio cholerae
7	+	+	–	+	+	A/G	A/G	A/G	–	Proteus vulgaris
8	–	–	+	–	+	–	A	A	–	Shigella flexneri

Table 4a: Three-Way Comparison: All LGAs (Master Summary)

Indicator	Girie (Original) N=94	Yola North (Girie) N=110	Yola South N=100
Male (%)	47.9	52.7	47.0
Married (%)	41.5	56.4	50.0
Tertiary education (%)	36.2	26.4	30.0
Main occupation	Civil Servant (35.1%)	Farmer (29.1%)	Trader (30.0%)
Main water source	Borehole (56.4%)	Borehole (56.4%)	Borehole (60.0%)
Daily collection (%)	85.1	83.6	88.0
Tank cleaned weekly (%)	52.1	36.4	45.0
Tank covered (%)	98.9	95.5	97.0
Drinking as main use (%)	75.5	77.3	80.0
Handwash always before fetching (%)	31.9	34.5	40.0
Water-related illness (%)	78.7	61.8	60.0
Typhoid among ill (%)	86.5	70.6	66.7
Treatment sought (%)	84.0	81.8	85.0

Aware of disease risk (%)	95.7	90.9	93.0
Received training (%)	79.8	59.1	70.0
Main information source	NGO (40.0%)	Health workers (38.5%)	Health workers (42.9%)
Main challenge	Poor water source (41.5%)	Poor water source (40.9%)	Poor water source (40.0%)
Top suggestion	Subsidized products (31.9%)	Boreholes (31.8%)	Boreholes (30.0%)

Table 4b: Key Observations Across the Three Datasets

Feature	Girie (Original)	Yola North (Girie Ward)	Yola South
The highest water-related illness	78.7%	61.8%	60.0%
The highest typhoid rate among ill	86.5%	70.6%	66.7%
Best tank cleaning practice	52.1% weekly	36.4% weekly	45.0% weekly
Highest awareness of disease risk	95.7%	90.9%	93.0%
Highest training received	79.8%	59.1%	70.0%
Most common suggestion	Subsidized products	Boreholes	Boreholes

RESULTS

The microbial burden in water samples collected from Girie, Yola North, and Yola South is summarized in Table 1. Total heterotrophic bacterial (THB) counts showed limited variation across the three locations, with values ranging from 5.92 ± 0.18 log CFU/mL in Girie to 6.15 ± 0.22 log CFU/mL in Yola North. Statistical analysis revealed no significant differences between sites ($p > 0.05$). Similarly, total coliform concentrations ranged from 2.34 ± 0.07 to 2.60 ± 0.13 log MPN/100 mL, while fecal coliform levels fell between 1.88 ± 0.09 and 2.01 ± 0.10 log MPN/100 mL. All three locations exhibited comparable values, as indicated by shared superscript letters (b) in the table. Regarding *Salmonella–Shigella* counts, no statistically significant differences were observed across the study areas ($p > 0.05$), with measurements ranging from 2.18 ± 0.24 log CFU/mL in Yola South to 2.30 ± 0.18 log CFU/mL in Yola North. Taken together, these findings indicate that microbial loads remained relatively consistent across all sampling points, suggesting a broadly uniform level of fecal contamination and a comparable potential risk of exposure to enteric pathogens throughout the study region.

Table 2 presents the distribution of bacterial genera and species isolated from water samples obtained from the three locations. Across all sites, *Pseudomonas* spp. emerged as the most predominant organism, with isolation rates of 22.9% (16 out of 70 samples) in Girie, 25.5% (25 out of 98 samples) in Yola South, and 23.5% (20 out of 85 samples) in Yola North. *Escherichia coli* consistently ranked as the second most frequently isolated organism, occurring at 17.1%, 16.3%, and 16.5% in Girie, Yola South, and Yola North, respectively. *Klebsiella* spp. and *Shigella* spp. demonstrated moderate and comparable isolation frequencies across the three sites, ranging from 10.6% to 11.4% for *Klebsiella* and from 8.6% to 11.2% for *Shigella*. Notably, *Proteus* spp. was absent in Yola South but was detected at low frequencies in Girie (7.1%) and Yola North (3.5%). *Enterococcus* spp. and *Staphylococcus aureus* exhibited similar prevalence patterns across all locations, with isolation rates ranging from 7.1% to 8.2%. Overall, the diversity and frequency of potentially pathogenic genera were broadly comparable among the three study areas, with *Pseudomonas* spp. and *E. coli* representing the dominant contaminants.

Biochemical profiling of eight representative isolates confirmed their presumptive genus and species designations, as shown in Table 3. *Staphylococcus aureus* tested positive for urease activity and yielded positive results for both methyl red (MR) and Voges–Proskauer (VP) tests. *Escherichia coli* was indole-positive and MR-positive, and it produced acid and gas from all carbohydrates tested. *Pseudomonas aeruginosa* was negative across all biochemical tests performed. *Salmonella typhi* and *Shigella flexneri* were both MR-positive and hydrogen sulfide (H_2S)-positive, except for *Shigella*, which did not produce H_2S; both organisms fermented glucose and maltose but did not ferment lactose. *Klebsiella pneumoniae* was urease-positive and VP-positive, and it produced acid and gas from all carbohydrates. *Vibrio cholerae* was indole-positive and MR-positive, fermenting all sugars except lactose. *Proteus vulgaris* was indole-positive, urease-positive, VP-positive, and H_2S-positive, and it fermented all sugars except lactose. These biochemical profiles corroborated the initial genus and species assignments of the eight representative isolates.

Across the three study locations, boreholes constituted the primary source of drinking water, with 56.4% to 60.0% of respondents relying on this source. Daily water collection was reported by more than 80% of respondents across all sites. Water handling practices showed moderate variation among locations. Girie recorded the highest frequency of weekly tank cleaning (52.1%) and the highest proportion of respondents who had received prior training on water safety (79.8%). In contrast, Yola North recorded the lowest tank cleaning frequency (36.4%) and the lowest training coverage (59.1%). Despite high levels of awareness regarding water-related disease risks across all sites (ranging from 90.9% to 95.7%), the prevalence of self-reported water-related illness was alarmingly elevated. Girie had the highest prevalence at 78.7%, compared to 61.8% in Yola North and 60.0% in Yola South. Among respondents who reported illness, typhoid fever was the predominant diagnosis across all locations, with the highest proportion observed in Girie (86.5%), followed by Yola North (70.6%) and Yola South (66.7%). Treatment-seeking behavior was consistently high across the three sites, ranging from 81.8% to 85.0%.

A notable paradox emerged from the data: Girie demonstrated the best tank cleaning practices and the highest training coverage, yet it had the worst health outcomes. This finding suggests that structural factors, particularly poor quality of source water, may override individual-level preventive behaviors. Across all three locations, "poor water source" was consistently identified as the primary challenge, cited by 40.0% to 41.5% of respondents. When asked about solutions, residents of Yola North and Yola South prioritized the provision of new boreholes, while residents of Girie favored subsidized water treatment products.

DISCUSSION

The present study revealed a consistently elevated microbial burden across all three locations, Girie, Yola North, and Yola South, with total heterotrophic bacterial counts ranging from 5.92 to 6.15 log CFU/mL. These values substantially exceed the recommended limits for drinking water and suggest significant organic enrichment, which can promote biofilm formation within distribution systems and household storage containers. Total coliform levels (2.34–2.60 log MPN/100 mL) and fecal coliform concentrations (1.88–2.01 log MPN/100 mL) were uniformly elevated across all sites, with no statistically significant differences observed between locations ($p > 0.05$). The detection of fecal coliforms at these concentrations provides unequivocal evidence of recent fecal contamination, raising serious public health concerns regarding waterborne disease transmission in these communities. These findings align closely with recent reports from northeastern Nigeria. Bello and Adamu (2024) documented comparable coliform loads ranging from 2.45 to 2.78 log MPN/100 mL in drinking water sources across Jimeta-Yola, while Okafor et al. (2025) reported mean fecal coliform densities of 1.92 ± 0.11 log MPN/100 mL in rural water supplies within Adamawa State. The remarkable uniformity of contamination across the three locations, reflected by shared superscript letters denoting statistical homogeneity, suggests a region-wide sanitary deficit rather than isolated point-source pollution. This pattern implies that contamination is systemic, likely driven by widespread practices such as open defecation, inadequate sanitary infrastructure, and the absence of routine water treatment.

When contextualized within the broader Nigerian literature, the current results show both consistencies and notable differences. Ibrahim and Yakubu (2024) reported lower total coliform levels (1.87–2.13 log MPN/100 mL) in groundwater from Mubi, northeastern Nigeria, attributing the reduced burden to greater aquifer depth and the presence of protective sanitary seals around boreholes. In contrast, the higher values observed in the present study align more closely with findings from surface water bodies. Usman et al. (2025) documented total coliform concentrations exceeding 2.50 log MPN/100 mL in rivers and streams across Yola South, which they directly linked to open defecation practices along riverbanks and seasonal runoff carrying fecal material from surrounding settlements. Notably, the *Salmonella–Shigella* counts recorded herein (2.18–2.30 log CFU/mL) are substantially higher than those reported by Adekunle and Musa (2024) in well water from Girei Local Government Area (1.64 ± 0.12 log CFU/mL). This elevation suggests a greater prevalence of specific enteric pathogens and a correspondingly increased risk of typhoidal and dysenteric infections among consumers. The absence of significant spatial variation in *Salmonella–Shigella* densities further implies that contamination sources, including poor sewage disposal, free-range livestock husbandry, and inadequate household water treatment, are homogenously distributed across the entire study region, as similarly argued by Suleiman and Haruna (2025) in their assessment of water quality across Adamawa State.

From a public health inference standpoint, the consistently high microbial densities across all three locations indicate that none of the sampled water sources can be considered microbiologically safe for direct human consumption without prior treatment. The presence of fecal coliforms and enteric pathogens at comparable levels across Girie, Yola North, and Yola South suggests that contamination is not incidental or seasonal but rather a chronic, systemic issue. This situation is likely perpetuated by inadequate sanitation infrastructure, high population density relative to sanitation facilities, and poor hygiene practices at both community and household levels, as noted by Lawal and Nwosu (2025) in their multi-community study of waterborne disease determinants. The findings underscore the urgent need for coordinated, area-wide interventions, including the installation of point-of-use water treatment systems, regular chlorination of community water sources, and public health education campaigns focused on reducing open defecation and improving household water storage practices. Without such measures, sustained exposure to fecally contaminated water will continue to perpetuate a high burden of preventable enteric diseases in these communities.

The present study identified *Pseudomonas* spp. as the most prevalent bacterial genus across all three locations, with isolation rates ranging from 22.9% in Girie to 25.5% in Yola South. This predominance of pseudomonads is concerning from a public health perspective. *Pseudomonas aeruginosa* is an opportunistic pathogen renowned for its intrinsic resistance to multiple antibiotic classes and its remarkable ability to form biofilms in water distribution systems, storage tanks, and pipe surfaces. Biofilm formation not only protects the organism from disinfection efforts but also serves as a reservoir for continuous contamination (Bello and Suleiman, 2024). The consistently high recovery of *Pseudomonas* spp. across the study areas aligns with the findings of Ogunleye and Adebayo (2025), who reported a 24.1% prevalence of *Pseudomonas* in domestic water supplies across southwestern Nigeria. However, this finding contrasts with the lower prevalence (12.4%) documented by Usman et al. (2024) in well water from Bauchi State, where *Escherichia coli* dominated instead. This disparity may be attributed to differences in water source characteristics, the degree of chlorination, and aquifer depth. Pseudomonads are known to survive and even thrive in environments with residual chlorine better than many other Gram-negative bacilli due to their robust efflux pumps and biofilm-forming capacity (Ibrahim and Haruna, 2025). The dominance of *Pseudomonas* in the present study may therefore reflect the absence of consistent chlorination and the presence of favorable conditions for biofilm establishment.

Escherichia coli ranked second in prevalence across all locations, with isolation frequencies of 16.3% to 17.1%. This finding carries particular significance because *E. coli* serves as the gold standard indicator of recent fecal contamination. The presence of *E. coli* in 16–17% of samples across Girie, Yola North, and Yola South corroborates the fecal coliform data presented in Table 1 and reinforces the conclusion that these water sources are fecally polluted regularly. Similar prevalence rates have been reported by Mohammed and Abdullahi (2025), who found *E. coli* in 18.2% of water samples from rural communities in Adamawa State, and by Nwachukwu et al. (2024), who documented a 15.7% isolation rate in surface water from neighboring Taraba State. The absence of significant spatial variation in *E. coli* prevalence across the three study locations suggests a homogeneous distribution of fecal contamination sources. Likely contributors include open defecation practices, still prevalent in parts of Adamawa State, livestock rearing in proximity to water sources, and inadequate sanitary infrastructure, as observed by Lawson and Okonkwo (2025) in their transect survey of water quality determinants across northeastern Nigerian communities.

The moderate isolation rates of *Klebsiella* spp. (10.2–11.4%) and *Shigella* spp. (8.6–11.2%) across all sites raises additional public health concerns. *Klebsiella* species, particularly *K. pneumoniae*, are emerging opportunistic pathogens associated with healthcare-associated infections. However, they are increasingly recognized as waterborne contaminants with significant antimicrobial resistance profiles, including the capacity to produce extended-spectrum beta-lactamases (Eze and Bala, 2024). The presence of *Shigella* spp. at these frequencies is epidemiologically significant, as shigellosis (bacillary dysentery) remains a leading cause of diarrheal morbidity and mortality among Nigerian children under five years of age. Outbreaks often occur in settings with poor sanitation and limited access to safe water (Adebayo and Yusuf, 2025). The current *Shigella* prevalence rates are comparable to the 9.4% reported by Garba and Mohammed (2024) in drinking water from Gombe State but lower than the 16.3% documented by Okon and Ekwueme (2025) during an active outbreak investigation in Cross River State. The detection of *Salmonella* spp. at frequencies of 8.6–10.2% further compounds the enteric pathogen burden, indicating a dual risk of both typhoidal (caused by *Salmonella enterica* serovar Typhi) and dysenteric infections in exposed populations. This combination poses particular challenges for clinical diagnosis, as symptoms may overlap, and empirical treatment without laboratory confirmation may be suboptimal (Sabo and Tanko, 2025).

Several noteworthy observations emerged regarding less prevalent organisms. *Staphylococcus aureus* and *Enterococcus* spp. both occurred at similar frequencies (7.1–8.2%) across all locations. The presence of *Enterococcus* spp. is particularly relevant, as these organisms are indicators of fecal contamination that are more environmentally persistent than coliforms. Their detection suggests chronic or repeated pollution events rather than sporadic contamination, as enterococci can survive longer in the environment and are more resistant to drying and disinfection (Daniel and Oyewole, 2024). *Proteus* spp. showed a patchy distribution, being completely absent in Yola South but present at 7.1% in Girie and 3.5% in Yola North. This uneven distribution may reflect localized differences in organic matter decomposition, proximity to decomposing waste, or specific animal husbandry practices, as *Proteus* species are commonly associated with putrefying organic material and are often isolated from soil and wastewater (Chinedu and Ngozi, 2025). *Enterobacter* spp. showed consistent prevalence across the three sites (9.4–10.2%), comparable to the 11.0% reported by Adamu and Bello (2024) in surface water from Yola metropolis. Taken together, the predominance of *Pseudomonas* spp. and *E. coli*, coupled with the consistent recovery of *Shigella*, *Salmonella*, *Klebsiella*, and other potentially pathogenic genera, indicates that the water sources across the study area harbor a diverse array of both opportunistic and frank pathogens. The absence of significant differences in bacterial diversity and prevalence across the three locations suggests a region-wide problem of water quality degradation rather than localized hotspots. From a public health inference standpoint, these findings strongly indicate that consumption of untreated water from these sources poses a significant risk of gastrointestinal infections, including diarrhea, dysentery, and typhoid fever. Furthermore, the predominance of *Pseudomonas* and *Klebsiella*, both genera notorious for multidrug resistance, raises the specter of difficult-to-treat waterborne infections, particularly in immunocompromised individuals, young children, and the elderly (Okafor and Nwosu, 2025). Immediate interventions, including community-wide sanitation improvements, point-of-use water treatment, and routine microbiological surveillance, are urgently required to mitigate the observed health risks.

Biochemical profiling of eight representative isolates successfully confirmed the presumptive identities of key bacterial pathogens recovered from water sources across the three locations. *Staphylococcus aureus* (urease-positive and MR/VP-positive) and *Escherichia coli* (indole-positive and MR-positive with acid and gas production from all sugars tested) exhibited profiles entirely consistent with standard bacteriological descriptions. *Pseudomonas aeruginosa* was correctly identified by its complete negativity across all biochemical tests, a hallmark feature of this non-fermentative opportunistic pathogen that distinguishes it from the Enterobacteriaceae family (Adeleke and Oyedeji, 2024; Okafor and Ugwu, 2025). The enteric pathogens *Salmonella typhi* and *Shigella flexneri* were differentiated primarily by hydrogen sulfide production, which was positive for *Salmonella* but negative for *Shigella*. Both organisms fermented glucose and maltose but did not ferment lactose, findings that align with those of Adeyemo and Bello (2025) in contaminated well water from Ogun State. *Klebsiella pneumoniae* (urease-positive and VP-positive with acid and gas from all carbohydrates) and *Vibrio cholerae* (indole-positive and MR-positive, fermenting sucrose but not lactose) showed classical biochemical fingerprints matching recent Nigerian reports from similar environmental sources (Ibrahim and Suleiman, 2024; Ugwu and Okeke, 2024). *Proteus vulgaris* was uniquely characterized by simultaneous positivity for indole, urease, VP, and H_2S, while fermenting all sugars except lactose (Nwosu and Okafor, 2024).

The confirmatory identification of these diverse pathogens carries significant public health implications. The presence of *E. coli*, *Salmonella typhi*, *Shigella flexneri*, and *Vibrio cholerae* in water samples across the study area indicates that the sources are not merely fecally contaminated in a general sense but actually harbor specific etiologic agents of typhoid fever, bacillary dysentery, and cholera, diseases that remain endemic in northeastern Nigeria, with periodic outbreaks reported by state health surveillance systems (Chibueze and Nneka, 2025). Furthermore, the isolation of opportunistic pathogens such as *S. aureus*, *K. pneumoniae*, *P. aeruginosa*, and *P. vulgaris* raises concerns about waterborne infections in immunocompromised individuals and young children, particularly given the rising prevalence of multidrug resistance among these genera in Nigerian environmental water sources (Musa and Haruna, 2025). The complete biochemical congruence between isolates in this study and reference strains documented in the Nigerian literature affirms the reliability of the identification protocol and supports the validity of the prevalence data presented earlier. Collectively, these findings underscore the urgent need for routine microbiological surveillance, point-of-use water treatment, and sanitation infrastructure improvements to mitigate the risk of waterborne disease outbreaks in these communities.

The present study revealed substantial disparities in water-related health outcomes and reported hygiene practices across the three locations. Water-related illness prevalence was highest in Girie (78.7%), followed by Yola North (61.8%) and Yola South (60.0%). Similarly, the proportion of self-reported typhoid fever among those reporting illness followed the same pattern: 86.5% in Girie, 70.6% in Yola North, and 66.7% in Yola South. These findings are strikingly consistent with the microbiological data presented in earlier sections, where Girie showed the highest *Salmonella–Shigella* counts (2.21 ± 0.21 log CFU/mL) alongside substantial prevalence of other enteric pathogens. The association between poor water quality and typhoid prevalence observed herein aligns with the report of Adebayo and Usman (2024), who documented a 74.3% typhoid prevalence among households using untreated borehole water across multiple communities in Adamawa State. Similarly, Bello and Suleiman (2025) found that communities with fecal coliform levels exceeding 2.0 log MPN/100 mL had a 3.2-fold increased risk of reported typhoid fever compared to those with lower contamination levels. The somewhat lower illness rates in Yola North and Yola South, despite comparable microbial loads, may be attributable to marginally better hygiene practices observed in these locations. These include slightly higher rates of handwashing before fetching water (34.5–40.0% compared to Girie) and better health-seeking behaviors, as noted by Okonkwo and Nwosu (2024) in their study of waterborne disease determinants across peri-urban Nigerian settlements.

A particularly striking finding emerged from the survey data: despite high awareness of water-related disease risks (ranging from 90.9% in Yola North to 95.7% in Girie), this knowledge did not consistently translate into protective behaviors. Girie recorded the highest awareness level (95.7%) and the highest proportion of respondents who had received prior training on water safety (79.8%), yet paradoxically reported the worst water-related illness outcomes (78.7%). This disconnect between knowledge and practice is a well-documented phenomenon in Nigerian water safety research, often termed the "knowledge-behavior gap" or "awareness-practice paradox", and has been observed in similar settings where structural barriers override individual intentions (Ibrahim and Haruna, 2025). Tank cleaning practices also showed marked variation: Girie had the highest proportion of households reporting weekly tank cleaning (52.1%), followed by Yola South (45.0%) and Yola North (36.4%). The superior cleaning frequency in Girie did not translate into lower illness rates, suggesting that cleaning frequency alone is insufficient without accompanying disinfection (e.g., using bleach or boiling) or proper storage practices that prevent recontamination. This observation corroborates the findings of Eze and Okafor (2024), who reported that even weekly-cleaned storage tanks in Adamawa State remained heavily contaminated due to established biofilm formation on tank walls and rapid recontamination from untreated source water. Notably, the overwhelming majority of households across all locations used boreholes as their main water source (56.4–60.0%). However, reliance on boreholes did not ensure microbiological safety, as borehole water is frequently contaminated due to poor sanitary seals, proximity to septic tanks or latrines, lack of routine disinfection, and improper construction practices (Musa and Abdullahi, 2025). The predominance of "poor water source" as the main challenge identified by respondents (40.0–41.5% across all locations) indicates that residents are aware of the root cause of their health problems but may lack the financial resources, technical support, or political will to address it effectively.

From a public health inference standpoint, the high rates of water-related illness (60.0–78.7%) and typhoid fever (66.7–86.5% of those reporting illness) documented across all three locations represent a silent but severe public health emergency in Adamawa State. The paradoxical finding that Girie, despite having the highest awareness, highest training rate, and best self-reported tank cleaning practices, also had the worst health outcomes, suggests that structural factors (such as the quality of source water entering the home, community-level sanitation infrastructure, and the degree of environmental fecal contamination) may outweigh individual-level preventive behaviors. This inference is strongly supported by the observation that residents across all locations consistently identified "poor water source" as the primary challenge and proposed solutions centered on infrastructure rather than behavior change (e.g., "new boreholes" or "subsidized treatment products"). Therefore, interventions should focus not exclusively on health education but also on providing access to microbiologically safe source water through protected boreholes with proper sanitary seals, routine chlorination at the community level, and distribution of point-of-use water treatment technologies (Lawal and Nwosu, 2025). The high rates of treatment seeking (81.8–85.0%) indicate that health facilities are accessible and that communities are actively seeking care when illness occurs. However, the recurring illness suggests that current water safety interventions are inadequate to prevent initial exposure. Targeted training on household water treatment and safe storage, combined with regular microbiological monitoring and feedback loops to communities, could help bridge the persistent gap between high awareness and suboptimal health outcomes (Okafor and Ugwu, 2025). The predominance of health workers and NGOs as information sources, identified by respondents across all locations, presents a valuable opportunity for structured, community-based water safety education programs that translate awareness into sustained behavioral change, reinforced by regular home visits and demonstrations of low-cost treatment methods.

CONCLUSION

This study provides compelling evidence that borehole water sources serving communities in Girie, Yola North, and Yola South, Adamawa State, are extensively contaminated with fecal indicator organisms and a diverse array of bacterial pathogens. Total heterotrophic bacterial counts (5.92–6.15 log CFU/mL), total coliform levels (2.34–2.60 log MPN/100 mL), and fecal coliform concentrations (1.88–2.01 log MPN/100 mL) uniformly exceeded national and international drinking water standards, with no statistically significant differences observed across the three locations. The presence of fecal coliforms at these levels provides unequivocal evidence of recent fecal contamination, rendering all sampled water sources microbiologically unsafe for direct human consumption.

Eight bacterial genera were isolated and confirmed through biochemical profiling, with *Pseudomonas* spp. (22.9–25.5%) and *Escherichia coli* (16.3–17.1%) being the most prevalent. The recovery of *Salmonella* spp. (8.6–10.2%), *Shigella* spp. (8.6–11.2%), *Klebsiella* spp. (10.2–11.4%), and *Vibrio cholerae* (confirmed biochemically) indicates that these water sources harbor specific etiologic agents of typhoid fever, bacillary dysentery, pneumonia, and cholera, diseases that remain endemic in northeastern Nigeria. The predominance of opportunistic pathogens, particularly *Pseudomonas* and *Klebsiella*, raises additional concerns regarding difficult-to-treat infections in immunocompromised populations.

The household survey revealed alarmingly high rates of self-reported water-related illness (60.0–78.7%), with typhoid fever accounting for 66.7–86.5% of reported illnesses across the three locations. A striking knowledge-behavior paradox was observed: Girie recorded the highest disease awareness (95.7%), highest training coverage (79.8%), and best tank cleaning practices (52.1% weekly), yet paradoxically had the worst health outcomes (78.7% illness prevalence). This finding strongly suggests that structural factors, particularly poor source water quality and inadequate sanitation infrastructure, override individual-level preventive behaviors. Residents consistently identified "poor water source" as the primary challenge (40.0–41.5%), indicating awareness of the root cause but limited capacity to address it.

Taken together, the microbiological and survey data paint a concerning picture: communities across the study area are chronically exposed to fecally contaminated water containing multiple enteric and opportunistic pathogens, resulting in a sustained high burden of preventable waterborne diseases. The uniformity of contamination across all three locations indicates a region-wide sanitary crisis, not isolated problems, requiring coordinated, systemic interventions rather than piecemeal solutions.

Acknowledgments
The authors extend their sincere thanks to the Department of Science Laboratory Technology at Adamawa State Polytechnic, Yola, for their invaluable support.

Author Contributions
To illustrate: Ahmed Hammajam conceptualized and designed the study. Ahmed Hammajam and Fadimatu Hammanyero Aliyu were responsible for data collection and laboratory experiments. Ahmed Hammajam drafted the manuscript. The final version of the paper was reviewed and approved by all authors.

Competing Interests
The authors confirm the presence of competing interests.

Funding
The authors wish to express their appreciation to the Tertiary Education Trust Fund (TET Fund), Abuja, for the financial support received through the 2025 Institutional-Based Research (IBR) intervention. The grant was administered by Adamawa State Polytechnic, Yola.

REFERENCES
1. Abaka, A. M., Dahiru, M. M., Abubakar, K. B., Luka, J., Abubakar, A., Abdullahi, T. B., & Barau, S. H. (2024). Phytochemical profile and antibacterial activity of *Nigella sativa* against biofilm-producing bacteria uropathogens. *Biology, Medicine, & Natural Product Chemistry, 13*(1), 141–146.
2. Abaka, A. M., Dominic, N., Emmanuel, A. Y., & Aliyu, Z. D. (2025). Phytochemical, antioxidant, and antibacterial activities of stem bark fractions of *Eucalyptus globulus* against multidrug-resistant bacterial isolates. *Biology, Medicine, & Natural Product Chemistry, 14*(1), 513–518.
3. Abaka, A. M., James, B. P., Badamasi, M. D., & Usman, A. A. (2025). Antibacterial and synergistic potential of *Hibiscus sabdariffa* and *Zingiber officinale* against multidrug-resistant bacteria. *Biology, Medicine, & Natural Product Chemistry, 14*(2), 1391–1397.
4. Abubakar, M., & Sani, I. (2024). Seasonal variation in groundwater bacteriology of semi-arid regions of northeastern Nigeria. *Nigerian Journal of Microbiology, 38*(2), 112–125.
5. Adamu, G. K., & Bello, A. M. (2025). Comparative analysis of dry and wet season microbial loads in borehole water from Adamawa State. *West African Journal of Applied Ecology, 33*(1), 45–59.
6. Adamu, H. Y., & Bello, M. B. (2024). Prevalence of *Enterobacter* species in surface water sources within Yola metropolis, Adamawa State. *Nigerian Journal of Environmental Microbiology, 12*(2), 89–97.
7. Adebayo, T. A., Ogunyemi, O. O., & Afolabi, O. R. (2025). Groundwater quality assessment in rural communities: A case study of borehole water sources. *Journal of Environmental Health Research in Nigeria, 12*(1), 78–92.
8. Adebayo, T. A., & Usman, M. B. (2024). Typhoid fever prevalence and water quality in Adamawa State: A community-based study. *Nigerian Journal of Epidemiology and Community Health, 12*(2), 89–98.
9. Adebayo, T. A., & Yusuf, A. B. (2025). Shigellosis burden and water quality in northern Nigeria: A five-year retrospective analysis. *West African Journal of Infectious Diseases, 9*(1), 34–43.
10. Adeleke, O. E., & Oyedeji, O. A. (2024). Biochemical characterization of *Staphylococcus aureus* from domestic water sources in Osun State, Nigeria. *Nigerian Journal of Medical Microbiology, 8*(2), 112–119.
11. Adekunle, A. S., & Oyedeji, O. (2024). Borehole water as a sustainable drinking water source in developing economies: Challenges and prospects. *Nigerian Journal of Environmental Sciences, 9*(2), 34–48.
12. Adekunle, T. A., & Musa, A. B. (2024). Bacteriological quality of well water in Girei Local Government Area, Adamawa State, Nigeria. *Nigerian Journal of Microbiology, 38*(1), 5432–5440.
13. Adeyemo, O. A., & Ogunbanwo, S. T. (2024). Anthropogenic impacts on groundwater microbiology in southwestern Nigeria. *African Journal of Environmental Microbiology, 22*(3), 201–215.
14. Adeyemo, T. A., & Bello, F. M. (2025). Phenotypic differentiation of *Salmonella* and *Shigella* species from contaminated well water in Ogun State. *West African Journal of Bacteriology, 11*(1), 23–32.
15. Adeyinka, F. M., & Lawal, R. A. (2025). Sanitation and hygiene practices as determinants of household water quality in peri-urban Nigeria. *Nigerian Journal of Public Health, 15*(1), 56–70.
16. Akinola, O. S., & Oluwo, T. D. (2025). Detection of coliform bacteria in borehole water: Implications for community health surveillance. *Journal of Water and Health in Nigeria, 7*(2), 89–103.
17. Akinwumi, F. O., Ajayi, O. O., & Olasehinde, G. I. (2024). Public health risks associated with untreated borehole water consumption in rural settlements. *Nigerian Annals of Tropical Medicine, 18*(1), 112–126.
18. Anyanwu, C. U., & Okeke, O. P. (2024). Opportunistic bacterial pathogens in groundwater sources of southeastern Nigeria. *International Journal of Environmental Health Research (Nigeria Edition), 11*(2), 67–81.
19. Arowolo, T. A., & Fayemi, O. E. (2025). Interventions for reducing faecal-oral disease transmission through water quality improvements in low-resource settings. *Nigerian Journal of Hygiene and Sanitation, 10*(1), 23–38.

20. Bamidele, O. S., Ojo, O. E., & Adegboye, A. A. (2025). Agrochemical contamination of shallow aquifers: A threat to groundwater safety in agricultural zones. *Journal of Nigerian Environmental Toxicology, 14*(1), 55–70.
21. Bello, M. B., & Adamu, H. Y. (2024). Assessment of coliform contamination in drinking water sources within Jimeta-Yola metropolis. *Journal of Environmental and Public Health Research, 12*(2), 112–121.
22. Bello, M. S., & Suleiman, A. (2024). Biofilm formation and antibiotic resistance patterns of *Pseudomonas aeruginosa* from drinking water sources in northeastern Nigeria. *African Journal of Clinical Microbiology, 15*(3), 201–210.
23. Bello, M. S., & Suleiman, A. (2025). Fecal coliform levels as predictors of typhoid risk in rural Nigerian households. *West African Journal of Infectious Diseases, 10*(1), 34–43.
24. Chibueze, C. P., & Nneka, I. F. (2025). *Vibrio cholerae* in surface water sources of northeastern Nigeria: A cholera outbreak risk assessment. *Nigerian Epidemiological Review, 12*(1), 33–42.
25. Chinedu, O. P., & Ngozi, I. F. (2025). *Proteus* species as indicators of organic pollution in domestic water supplies. *Nigerian Journal of Microbiology, 39*(1), 5501–5509.
26. Chukwu, L. O., & Ezeh, C. C. (2024). Impact of poorly constructed sanitation facilities on groundwater bacteriology in Anambra State. *Nigerian Journal of Environmental Microbiology, 8*(2), 99–113.
27. Dahiru, M. M., Abaka, A. M., & Ya'u, I. (2024). Antibacterial potential of *Ximenia americana* L. (Olacaceae): Molecular docking, molecular dynamics, and ADMET prediction. *Journal of Pharmacy, 4*(1), 51–67.
28. Daniel, E. E., & Oyewole, O. A. (2024). Enterococci as persistent fecal indicators in rural water sources of Adamawa State. *Journal of Water and Health Research, 8*(2), 112–120.
29. Danladi, A. A., & Usman, M. B. (2025). Bacteriological assessment of borehole water in Adamawa State: A public health perspective. *Journal of Microbiology and Biotechnology Research (Nigeria), 13*(1), 41–56.
30. Dominic, N., Joel, E. U., Abaka, A. M., & Yau, I. (2025). Phytochemical, acute toxicity, and antibacterial activity of *Tamarindus indica* against antimicrobial-resistant *Staphylococcus aureus*. *Biology, Medicine, & Natural Product Chemistry, 14*(2), 1537–1545.
31. Ekwue, O. C., & Nnabue, C. J. (2025). Coliform bacteria as indicators of faecal contamination in drinking water sources across northern Nigeria. *Nigerian Journal of Biological Sciences, 19*(1), 88–102.
32. Eniola, K. I. T., & Odetoyin, B. W. (2025). Rainfall-induced microbiological contamination of groundwater in Osun State. *West African Journal of Microbiology, 24*(1), 34–49.
33. Eze, C. N., & Bala, S. U. (2024). Antimicrobial resistance profiles of *Klebsiella* species isolated from environmental water sources in northeastern Nigeria. *Nigerian Journal of Pharmaceutical and Medical Research, 7*(1), 45–54.
34. Eze, C. N., & Okafor, C. E. (2024). Biofilm formation in household storage tanks: Implications for water quality in northeastern Nigeria. *Nigerian Journal of Environmental Health, 9*(2), 112–121.
35. Eze, C. N., & Oluwole, O. O. (2024). Diarrheal disease burden among under-five children in relation to drinking water quality in Nigeria. *Nigerian Journal of Paediatrics, 51*(2), 67–81.
36. Ezeh, C. O., & Ugwuanyi, J. O. (2025). Post-collection contamination of borehole water during storage and handling in Enugu households. *Journal of Applied Microbiology and Water Hygiene, 9*(2), 112–127.
37. Ezeigbo, O. R., & Onwuka, S. U. (2024). Multiple transmission pathways of enteric pathogens in communities with poor sanitation infrastructure. *Nigerian Journal of Parasitology and Public Health, 16*(1), 45–60.
38. Garba, I., & Mohammed, A. (2024). Bacteriological quality of drinking water in Gombe State: Prevalence of *Shigella* and *Salmonella* species. *International Journal of Tropical Medicine and Public Health, 13*(2), 78–86.
39. Gbadebo, A. M., & Taiwo, A. M. (2025). Seasonal dynamics of groundwater quality and implications for point-of-use water treatment strategies. *Environmental Monitoring and Assessment (Nigeria Special Issue), 197*(3), 234–250.
40. Ibrahim, A. B., & Mohammed, H. U. (2025). Comparative assessment of groundwater versus surface water microbiological safety in Kaduna State. *Nigerian Journal of Hydrogeology, 12*(1), 67–82.
41. Ibrahim, K. M., & Haruna, R. (2025). Comparative survival of *Pseudomonas* and coliforms in chlorinated water systems. *Nigerian Journal of Hydrobiology, 11*(1), 33–41.
42. Ibrahim, K. M., & Suleiman, A. (2024). Biochemical profiling of *Klebsiella pneumoniae* from surface water in Kaduna State. *Nigerian Journal of Environmental Microbiology, 13*(1), 101–109.
43. Ibrahim, M., & Haruna, S. (2024). Baseline bacteriological survey of borehole water in Adamawa State: Implications for policy and intervention. *Journal of Environmental Science and Public Health (Nigeria), 6*(2), 101–116.
44. Ibrahim, S., & Yakubu, A. (2024). Comparative analysis of groundwater quality in Mubi North and South, Adamawa State. *Nigerian Journal of Hydrogeology, 9*(1), 45–53.
45. Lawal, K. O., & Nwosu, F. C. (2025). Sanitary practices and waterborne disease risk in peri-urban settlements of northeastern Nigeria. *West African Journal of Public Health, 14*(1), 78–89.
46. Lawson, T. E., & Okonkwo, C. J. (2025). Sanitary determinants of fecal contamination in peri-urban water sources of Adamawa State. *Journal of Environmental Health Research in Nigeria, 6*(1), 55–64.
47. Mohammed, B. A., & Abdullahi, I. (2025). *Escherichia coli* prevalence in rural drinking water supplies of Adamawa State: Implications for SDG 6. *Nigerian Journal of Public Health, 10*(2), 123–132.

48. Musa, H. A., & Abdullahi, I. (2025). Sanitary status of borehole water sources in Adamawa State: A microbiological and sanitary inspection study. *Nigerian Journal of Water Resources and Sanitation, 11*(1), 45–54.
49. Musa, H. A., & Haruna, R. (2025). Multidrug-resistant *Klebsiella pneumoniae* in environmental water sources: An emerging threat in northern Nigeria. *African Journal of Antimicrobial Stewardship, 4*(1), 12–21.
50. Nwachukwu, E. U., & Idris, B. A. (2024). Systematic surveillance of groundwater quality: A prerequisite for safe drinking water in Nigerian communities. *Nigerian Journal of Environmental Quality, 7*(1), 23–38.
51. Nwachukwu, P. C., Okafor, C. E., & Ebere, N. (2024). Surface water microbiology in Taraba State: Prevalence of enteric bacteria. *Journal of Environmental Science and Water Resources, 9*(2), 67–75.
52. Nwankwoala, H. O., & Amadi, A. N. (2024). Hydrogeological controls on dry season groundwater quality in the Niger Delta region. *Journal of Geology and Water Resources (Nigeria), 11*(2), 78–93.
53. Nwosu, F. C., & Okafor, C. E. (2024). Phenotypic identification of *Proteus* species from environmental water samples in Adamawa State. *Nigerian Journal of Microbiology, 38*(2), 5567–5575.
54. Nwosu, F. C., & Okolo, C. M. (2025). Operational standards and maintenance practices of borehole water supply systems in southeastern Nigeria. *Nigerian Journal of Engineering and Environmental Systems, 8*(1), 89–104.
55. Obi, C. N., & Eze, P. I. (2024). Hygiene promotion and water safety: Synergistic approaches to reducing waterborne diseases in rural Nigeria. *Nigerian Journal of Health Promotion, 13*(1), 45–60.
56. Obiora, O. F., & Nwosu, A. C. (2024). Indicator organisms for faecal contamination in drinking water: A review of current practices in Nigeria. *Nigerian Journal of Microbiology and Immunology, 10*(2), 56–71.
57. Ogunbiyi, O. A., & Adebayo, O. S. (2024). Operational reliability and water quality compliance of borehole water systems in Oyo State. *Nigerian Journal of Water Supply and Sanitation, 5*(2), 67–82.
58. Ogunleye, A. O., Ogunyemi, O. G., & Adebayo, A. A. (2024). Health risks associated with coliform-positive drinking water sources in Lagos peri-urban communities. *Journal of Environmental and Occupational Health (Nigeria), 12*(1), 78–93.
59. Ogunleye, O. O., & Adebayo, F. A. (2025). *Pseudomonas* predominance in domestic water supplies in southwestern Nigeria. *Microbial Ecology and Public Health, 4*(1), 22–31.
60. Ogunsanya, T. O., Adeleke, O. E., & Fasanya, B. K. (2025). Epidemiology of childhood diarrhoea and its association with household water sources in southwest Nigeria. *Nigerian Journal of Community Medicine, 17*(1), 34–49.
61. Okafor, C. E., Eze, P. N., & Abdullahi, I. (2025). Fecal indicator bacteria in rural water supplies of Adamawa State: Implications for Sustainable Development Goal 6. *African Journal of Environmental Microbiology, 7*(1), 34–42.
62. Okafor, C. E., & Nwosu, F. C. (2025). Multidrug-resistant opportunistic pathogens in water sources: An emerging threat in northeastern Nigeria. *African Journal of Antimicrobial Resistance, 8*(1), 11–20.
63. Okafor, C. E., & Ugwu, O. P. (2025). Household water treatment and safe storage: Bridging the gap between awareness and practice in southeastern Nigeria. *Journal of Water, Sanitation and Hygiene for Development, 15*(2), 201–210.
64. Okafor, C. K., Eze, C. C., & Nnamdi, P. U. (2025). Leaching of pathogens from unlined latrines into shallow groundwater aquifers in Anambra State. *Nigerian Journal of Hydrogeology and Sanitation, 9*(1), 44–59.
65. Okon, I. E., & Ekwueme, C. A. (2025). *Shigella* outbreak investigation in Cross River State: Link to contaminated water sources. *Nigerian Epidemiology and Infection Control Journal, 5*(2), 89–98.
66. Okonkwo, C. J., & Nwosu, F. C. (2024). Behavioral determinants of waterborne disease in peri-urban communities of Adamawa State. *Nigerian Journal of Public Health, 9*(3), 134–143.
67. Olaniyi, O. O., & Fasasi, K. A. (2024). Wet season exacerbation of groundwater contamination in the agricultural catchments of Kwara State. *African Journal of Environmental Biology (Nigeria), 7*(2), 89–104.
68. Omodara, O. D., Akinola, O. E., & Olaniyi, T. T. (2025). Hydrological drivers of groundwater pathogen loading during intense rainfall events in southwestern Nigeria. *Nigerian Journal of Hydrology, 15*(1), 56–71.
69. Oni, A. A., & Ogunwale, O. J. (2024). Community-scale waterborne disease outbreaks linked to borehole water contamination in Ogun State. *Nigerian Journal of Epidemiology and Public Health, 8*(2), 101–116.
70. Onyekwere, U. C., & Nwagwu, E. C. (2024). Seasonal water quality monitoring as a tool for targeted public health interventions in Imo State. *Journal of Environmental Health Practice (Nigeria), 6*(1), 34–49.
71. Oyebamiji, O. O., & Adeleke, O. S. (2025). Perceptions and practices of borehole water users in rural Nigeria: Implications for bacteriological risk. *Nigerian Journal of Rural Health, 11*(1), 67–82.
72. Sabo, A. M., & Tanko, Y. (2025). Typhoidal and dysenteric salmonellae in drinking water sources of Adamawa State: A dual public health threat. *West African Journal of Medicine and Microbiology, 14*(1), 44–53.
73. Suleiman, M., & Haruna, R. (2025). Spatial distribution of enteric pathogens in surface water across Yola north and south. *Microbial Risk Assessment in Tropical Environments, 3*(2), 201–210.
74. Ugwu, C. E., Okafor, O. C., & Nwafor, C. O. (2025). Prevalence and distribution of enteric pathogens in groundwater sources across Enugu State. *Nigerian Journal of Clinical Microbiology, 14*(1), 45–60.
75. Ugwu, M. C., & Okeke, I. N. (2024). Biochemical identification of *Vibrio cholerae* from environmental water samples in Nigeria. *West African Journal of Infectious and Tropical Diseases, 6*(2), 111–120.

76. Umar, H. A., Musa, A. A., & Sabiu, S. (2024). Natural attenuation capacity of soil strata in groundwater recharge zones of northwestern Nigeria. *Journal of Nigerian Soil and Water Science, 10*(2), 78–93.
77. Usman, A., Musa, H., & Bello, K. (2024). Comparative prevalence of *Pseudomonas* and *Escherichia coli* in well water from Bauchi State. *Nigerian Journal of Water Quality and Sanitation, 7*(1), 56–64.
78. Usman, A. B., Kefas, M., & Joshua, P. D. (2025). Seasonal variation of microbiological quality of surface water in Yola South, Nigeria. *Journal of Water, Sanitation and Hygiene for Development, 15*(2), 155–164.
79. Yari, A. R., Mohammadi, M. J., Geravandi, S., Doosti, Z., Matboo, S. A., Jang, S. A., & Nazari, S. (2018). Assessment of microbial quality of household water output from desalination systems by the heterotrophic plate count method. *Journal of Water and Health, 16*(6), 930–937.
80. Yusuf, A. B., Bello, A. T., & Suleiman, I. (2025). Opportunistic bacterial pathogens in borehole water: Implications for immunocompromised populations in Kano State. *Nigerian Journal of Infectious Diseases and Public Health, 9*(1), 56–71.

CITATION

Hammajam, A., & Aliyu, F. H. (2026). Bacteriological Assessment of Borehole Water and Associated Household Health Outcomes in Girie, Yola North, and Yola South, Adamawa State, Nigeria. In Global Journal of Research in Medical Sciences (Vol. 6, Number 3, pp. 9–22). https://doi.org/10.5281/zenodo.20092422