

Bacteriological and Physicochemical Assessment of Groundwater Quality in Selected Villages around the Sokoto-Rima Basin

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Abstract

Groundwater remains an important source of domestic water supply in many rural and semi-urban communities within the region; however, poor sanitation practices, flooding, agricultural activities, and indiscriminate waste disposal increase the risk of microbial contamination and associated waterborne diseases. This study assessed the physicochemical properties and microbiological quality of groundwater in selected villages around the Sokoto-Rima Basin. A total of forty-eight (48) groundwater samples were collected from wells and boreholes across selected villages in Wamakko, Dange Shuni, and Sokoto South Local Government Areas. Physicochemical parameters, including temperature, pH, electrical conductivity, total dissolved solids, turbidity, dissolved oxygen, biochemical oxygen demand, nitrate, phosphate, hardness, salinity, and sulphate, were analyzed using standard American Public Health Association (APHA) methods. Microbial analysis was carried out using the spread-plate and Most Probable Number (MPN) techniques for bacterial enumeration and coliform detection. Isolates were identified using cultural, morphological, and biochemical methods. The results revealed variations in physicochemical parameters across sampling locations, with some samples exceeding World Health Organization (WHO) and National Agency for Food and Drug Administration and Control (NAFDAC) permissible limits, particularly for turbidity, dissolved oxygen, biochemical oxygen demand, and salinity. The microbiological analysis showed the presence of fecal and non-fecal coliforms in several water samples, indicating contamination from environmental and fecal sources. Predominant bacterial isolates included *Escherichia coli*, *Klebsiella pneumoniae*, *Enterobacter* spp., and *Pseudomonas aeruginosa*. Some groundwater sources around the Sokoto-Rima Basin were microbiologically unsafe for human consumption without



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appropriate treatment. These findings underscore the need for regular groundwater-quality monitoring, improved sanitation, public-health education, and effective water-treatment measures. The findings represent the sampling period and may not reflect seasonal variation.

Introduction

Water is one of the most essential natural resources required for the survival of humans, animals, and plants. It plays a fundamental role in domestic activities, agriculture, industrial production, environmental sustainability, and public health. Access to safe and adequate water is recognized as a basic human necessity because it directly influences health, food security, and socio-economic development. (WHO, 2022).

Groundwater, which refers to water stored beneath the Earth's surface within soil pores and rock formations, is one of the most important sources of freshwater worldwide. It serves as the primary source of drinking water for billions of people and supports agricultural and industrial activities, particularly in developing countries where access to treated municipal water is limited (Suhag, 2016). Contaminated groundwater poses serious public health challenges because it serves as a vehicle for the transmission of disease-causing microorganisms and harmful chemical substances. Pathogenic bacteria, viruses, and protozoa present in polluted groundwater can cause waterborne diseases such as cholera, typhoid fever, dysentery, and acute diarrhoea, particularly in communities lacking adequate sanitation and safe drinking water infrastructure (Forstinus et al., 2016; Pal et al., 2018). The Nigeria Centre for Disease Control (2021) has reported repeated outbreaks of cholera associated with unsafe drinking water and poor sanitation in several parts of the country. This study aimed to assess the physicochemical properties and microbiological quality of groundwater in selected villages around the Sokoto-Rima Basin.

Materials and Methods

Study Area

The study was conducted in the Sokoto–Rima Basin, located in north-western Nigeria between latitudes 13°8'45" to 13°5'45" North and longitudes

5°28'45" to 5°33'45" East, covering parts of Kebbi, Sokoto, Zamfara and Katsina, States. The basin is a major hydrological system that supports over 15 million people in the region, with rivers and streams serving as primary sources of water for domestic use, agriculture, and livestock production. Human activities within the basin are predominantly water-dependent and include intensive agricultural practices, livestock rearing, and expanding rural and peri-urban settlements. Irrigated and rain-fed farming of crops such as rice, millet, sorghum, and vegetables involves extensive use of fertilizers and agrochemicals.

Study Design

A cross-sectional study design was used. Groundwater samples were collected from selected wells and boreholes across different communities within the basin. The samples were subjected to laboratory analyses to determine physicochemical parameters, enumerate total coliform bacteria using the Most Probable Number (MPN) technique, and identify coliform bacteria through cultural, morphological, and biochemical methods (Bagudo et al., 2024).

Sampling Technique

A convenient sampling technique was employed in this study, which involves selecting sampling sites based on their accessibility, safety, and relevance to the research objectives. This non-probability method allowed the researcher to collect water samples from locations that are representative of the major groundwater sources used by the local population within the study area (Etikan et al., 2016). In practice, wells and boreholes that were frequently used for domestic purposes and were accessible within the selected villages around the Sokoto-Rima Basin were selected. No pond samples were included in the present study. This approach is particularly suitable for field-based environmental and microbiological studies where random sampling may be impractical due to

logistical or geographical constraints (WHO, 2022; APHA et al., 2017). Although convenient sampling does not ensure complete randomness, it provides a practical and efficient means of obtaining relevant data from multiple sites within limited time and resources while still reflecting the general water use patterns in the area.

Sample Collection

A total of 48 groundwater samples were collected from three Local Government Areas (LGAs): Wamakko, Dange Shuni, and Sokoto South to ensure adequate spatial coverage. From each LGA, four villages were selected, and two types of water sources (borehole and well) were sampled per village, giving 16 samples per LGA. Sampling sites included Baga, Barkeji, Girabchi, and Wajake (Wamakko); Amanawa, Dange Shuni, Gidan Gara, and Kwanar Kimba (Dange Shuni); and Gagi, Mabera Idi, Tudun Wada, and Mana (Sokoto South). Water samples (250 mL each) were aseptically collected in sterilized bottles, properly labeled, and immediately stored in ice-packed coolers at approximately 4°C to prevent microbial alteration during transit. All samples were transported to the Microbiology Laboratory of Abdullahi Fodio University of Science and Technology, Aliero, within three hours of collection for physicochemical and microbiological analysis (APHA et al., 2017; WHO, 2022; Erickson et al., 2012).

Water samples from boreholes were allowed to flow for 2–3 minutes to remove stagnant water before collection. Samples were collected directly from the borehole outlet at reduced flow, leaving a small headspace in the bottles, and were immediately capped to avoid contamination. Each sample was labeled with its source, location, date, and time of collection, preserved in an ice-packed cooler at approximately 4°C, and transported to the laboratory within three hours for analysis (Erickson et al., 2012; APHA et al., 2017).

Water samples from wells were collected aseptically using a sterile cup to avoid external contamination. Each sample was carefully transferred into a sterile, labeled 250 mL polyethylene bottle through a sterile funnel to

ensure cleanliness and accuracy. The containers were properly sealed and labeled with details such as the sample code, location, date, and time of collection before being stored in an ice-packed cooler at approximately 4°C for transport to the laboratory (APHA et al., 2017; WHO, 2022).

Determination of Physicochemical Parameters

The physicochemical properties of the water samples was analyzed to evaluate their quality and suitability for domestic use. Parameters to be measured include temperature, pH, turbidity, electrical conductivity (EC), total dissolved solids (TDS), dissolved oxygen (DO), biological oxygen demand (BOD), chemical oxygen demand (COD), nitrate, phosphate, sulphate, hardness, and salinity. Temperature was measured on-site using a thermometer, while pH, EC, and TDS was determined with portable digital meters. Turbidity was measured using a nephelometric turbidity meter, and DO was determined using a DO meter following the Winkler method. BOD and COD was analyzed by standard incubation and reflux methods, respectively. Nutrient parameters (nitrate, phosphate, and sulphate) was determined spectrophotometrically, and hardness was measured by EDTA titration. All analyses followed the APHA (2012) standard methods to ensure reliability and accuracy.

Media preparation

Nutrient agar, SS Agar, Mannitol salt, Mueller-Hinton agar were prepared according to manufacturer's instructions 28g, 111g, 38g respectively were weighed and dissolved in 1 liter of distilled water and heated using hot plate for the media to completely dissolved which was then autoclaved at 121°C for 15 minutes.

Enumeration of Total Bacterial Counts

A series of test tubes containing 9 mL of sterile distilled water was corked with cotton wool, covered with aluminum foil, and sterilized by autoclaving at 121 °C for 15 minutes. Using a sterile pipette, 0.5 mL of the serially diluted water sample (10^{-3} dilution) was inoculated into Petri dishes containing nutrient agar medium. The inoculum will then be evenly spread across the agar surface using a sterile bent glass rod. Plates was incubated

at 37 °C for 24 hours, after which bacterial growth was observed (Olutiola, 2000). The resulting colonies were counted and expressed as colony-forming units per millilitre (cfu/mL). Each plate was divided into four quadrants, the colonies in each counted individually, and the mean value recorded as the final count (Erickson et al., 2012). Distinct colonies were sub-cultured on selective media using streak plate method and incubated at 37°C resulting colonies were sub-cultured on nutrient agar slant and stored at 4°C for further analysis.

Determination of Total Coliform Count Using Most Probable Number

Non-Fecal Coliform

Non-fecal coliforms are environmentally derived coliform bacteria commonly found in soil, vegetation, and surface water, and their presence in groundwater indicates environmental contamination rather than direct fecal pollution. These organisms, which include genera such as *Enterobacter*, *Klebsiella*, and *Citrobacter*, were detected using the Most Probable Number (MPN) technique, where positive presumptive tubes are subcultured onto Eosin Methylene Blue (EMB) agar. Colonies that do not display the metallic-green sheen typical of *E. coli* but exhibit general coliform morphology underwent confirmatory biochemical tests such as citrate utilization, urease activity, and indole testing to distinguish them from fecal coliforms and accurately classify them as non-fecal coliforms (Tambi et al., 2023).

Presumptive Test

For each water sample, MacConkey lactose broth was prepared in three double-strength and six single-strength test tubes, each containing 10 mL of broth and an inverted Durham tube to detect gas production (Microbiology-Branch, 2015). The three double-strength tubes each received 10 mL of the water sample (10–10 dilution), while three of the single-strength tubes will receive 1.0 mL (10 dilution) and the remaining three single-strength tubes will receive 0.1 mL (10 dilution). All tubes were incubated at 37 °C for 48 hours. Tubes showing acid and gas production within the Durham tubes were recorded as positive presumptive tests for

coliforms, while those showing no or doubtful gas formation were considered negative (Bhattacharya, 2025). All the test tubes were incubated at 37°C for 48 hours after which the tubes were observed for acid and gas production. Tubes showing visible gas formation occupying about one-tenth or more of the Durham tube's volume were recorded as positive presumptive tests for coliforms, while those showing no or only trace gas production after incubation at 37 °C for 48 hours were considered negative presumptive tests (Bhattacharya, 2025).

Confirmatory Test

One loopful of sample from each positive tube obtained from presumptive test was inoculated in respective tubes containing Brilliant green lactose bile broth and incubated at 24 hours at 37°C. Gas production 10% or more is recorded as positive while less than 10% is recorded as doubtful. Doubtful tubes are again incubated and the result is recorded. All the positive test tubes are now confirmed for presence of coliforms. (APHA, 2017; Cheesbrough, 2020).

Completed Test

This is a final test in which a loopful of sample from positive confirmatory tubes is streaked on Eosin methylene blue agar and incubated for 24 hours. After incubation, plates were examined for characteristic coliform colony morphology. Typical coliforms produce dark-centered colonies with a metallic green sheen, indicating *Escherichia coli*, while *Enterobacter* and *Klebsiella* species form large, mucoid pink to purple colonies without a metallic sheen. Colonies from Eosin methylene blue plate were then streaked onto nutrient agar slants, bottles, and incubated for subsequent phenotypic and biochemical identification (Tegegn, 2025).

Gram Staining

Smears of the isolates were made on a clean grease-free glass slide, air-dried and heat-fixed and heat-fixed. The smears were flooded with crystal violet and kept for 30 seconds to 1 minute, then they were rinsed with water. The slides were flooded with dilute Lugol's iodine solution for one minute. This was rinsed with distilled water and the smears were decolorized with 95% alcohol for 30 seconds and rinsed off with distilled water. The smears were

counter stain with safranin solution for one minute. Finally, the slides was wash off with distilled water, air dried and observe under the microscope using x100 oil emersion lens (Al-Bayati et al., 2021)

Biochemical Characterization of Isolates

Indole test

The bacterial growths was inoculated into 5mls of peptone water and incubated at 37 °C for 24 hours. Three drops of Kovac's reagent was added and shaken gently. A positive reaction was indicated by the development of red or pink color in the reagent layer above the broth within one-minute, yellow color which indicate a negative reaction (Robert, 2022)

Methyl Red Test

Glucose broth was prepared and autoclaved at 121 °C for 30min. A medium was inoculated with a loop of the selected isolate's culture, then incubated at 37°C for 48 hrs. After incubation, methyl red was added as an indicator. The remaining red colour indicated the acidity of the medium as a result of fermenting the glucose and production of acids (Yahia et al., 2020)

Voges-Proskauer Test

Glucose phosphate broth was prepared and autoclaved at 121 °C for 30 min. A medium was inoculated with a loop of the selected isolate's culture, then incubated at 37°C for 48 hrs. After incubation, 1 ml of NaOH (1N) and 3 drops of Alpha-naphthol were added as an indicator solution. Formation of reddish-brown ring at the surface of the test tube after 15 to 20 min indicated the production of acetoin (Yahia et al., 2020)

Citrate test

Citrate utilisation test is used to check the ability of an organism to utilize sodium citrate as a sole carbon source and ammonium salts as a sole source of nitrogen. It is indicated by change in color of bromothymol blue indicator from green to blue. Inoculate and incubate the simmons citrate agar by touching colony that is 18-24 hours old with an inoculating loop (Ali et al., 2020)

Catalase Test

This test was used to differentiate bacteria that produce the enzyme catalase from non-catalase-producing bacteria. Catalase breaks down hydrogen peroxide into water and oxygen. A drop of 3% hydrogen peroxide was placed on a clean slide, and a colony from the nutrient-agar slant was emulsified in the drop using a sterile wire loop. Immediate bubble formation indicated a positive catalase reaction, whereas the absence of bubbles indicated a negative reaction (Cheesbrough, 2000).

Sugar Fermentation Test

The growth medium used was peptone water, the peptone water was prepared in a conical flask and the indicators; phenol red was added. The mixture was dispensed into test tubes containing Durham tubes which was then sterilized by autoclaving at 121°C for 15 minutes. A volume of 1% solution of the sugar was prepared and sterilized separately at 115°C for 10 minutes. This was then aseptically dispensed in 5ml volume into the tubes containing the peptone water and indicator. The tubes were inoculated with young culture of the isolates and incubated at 37°C. Acid and gas production or acid only were observed after about 24 hours of incubation. Acid production was indicated by the change of the medium from light green to yellow colour while gas production indicated by the presence of gas in the Durham's tubes (APHA, 1998).

Sub-culturing and Preservation of Pure Isolates

Sub-culturing was performed to obtain pure isolates of coliform bacteria for further analysis. Using a sterile wire loop, dip it into the broth to pick a small amount and streak it onto fresh Cetrimide agar plates. These plates was incubated at 37°C for 24 hours. After incubation, the plates was examined to confirm the presence of pure cultures, which should exhibit round, smooth, grape-like odor with blue-green pigmentation (pyocyanin) often mixed with yellow-green fluorescence (pyoverdine), giving a metallic sheen. The pure isolates was then stored on nutrient agar slants at 4 °C to preserve their viability for subsequent identification and testing (Shalaby et al., 2022).

Total Fecal Coliform

Total fecal coliforms are a subgroup of coliform bacteria that originate specifically from the intestines of warm-blooded animals, and their presence in water serves as a strong indicator of fecal contamination and the possible presence of pathogenic microorganisms. To determine total fecal coliforms in the collected water samples, the Most Probable Number (MPN) method was used. Positive presumptive tubes showing gas production was incubated at $44 \pm 0.5^\circ\text{C}$, a temperature selective for fecal coliform growth, and then subcultured onto Eosin Methylene Blue (EMB) agar. Colonies exhibiting a characteristic metallic-green sheen, typical of *Escherichia coli*, was identified as fecal coliforms and further confirmed through standard biochemical tests. This approach ensures accurate detection of fecal contamination and reflects the sanitary quality of the water samples (Bhattacharya, 2025).

Statistical Analysis

Data obtained from the microbiological and physicochemical analyses were analyzed using IBM SPSS Statistics version 25. Means, standard deviations, and ranges were calculated. A two-way analysis of variance (ANOVA) was used to test the effects of sampling area and water source (borehole versus well) on each water-quality parameter. Sampling area had four levels within each study area, while water source had two levels (borehole and well); the area-by-source interaction was also included in the model. Where appropriate, significant differences were interpreted at $p < 0.05$. Pearson's correlation coefficient (r) was used to assess relationships between physicochemical parameters and microbial counts. Results were presented in tables and figures (Hoorzook, 2022).

Results

The physicochemical parameters in wamako, sokoto south and dange study area is shown in Figure 1 and 2 with wamako recoding the highest and dange with the lowest concentrations. The heavy metal concentrations in wamako, dange and sokoto south study area is shown in Table 1, 2 and 3 with wamako recoding the highest and dange with the lowest concentrations. The bacterial

colony count in wamako, sokoto south and dange study area is shown in Table 4. With wamako recoding the highest and dange with the lowest concentrations. The gram staining and biochemical tests results of wamako, sokoto south and dange study area is shown in table 5, 6, and 7. The coliform count of samples collected from wamako, sokoto south and dange study area is shown in Table 8 with wamako recoding the highest no of positives and dange with the lowest. Correlation analysis result of wamako, sokoto south and dange study area is shown in Figure 3. The figure shows visual representation of these correlations, where red indicates positive correlation and blue indicates negative correlation.

Discussion

The findings of this study showed the microbiological and physicochemical quality of groundwater in selected villages around the Sokoto Rima Basin. The result of physicochemical properties of groundwaters collected from villages around the Sokoto Rima Basin indicated that most parameters, including temperature, pH, and Total Dissolved Solids (TDS), were generally within the permissible limits set by the World Health Organization (WHO). However, significant correlations were observed between these parameters and the bacterial load.

The strong positive correlation (0.88) between Electrical Conductivity (E.C.) and TDS observed in this study is consistent with the findings of Wali (2022), who investigated groundwater quality in urban centers of the Sokoto Basin and noted that E.C. is a direct function of dissolved ions. Similarly, Hamidu et al. (2022) reported that the hydrogeochemical characterization of shallow aquifers in the Sokoto Rima floodplain showed a close relationship between mineralization and conductivity.

The moderate positive correlation (0.35) between Biological Oxygen Demand (BOD) and bacterial load suggests that organic matter serves as a substrate for microbial growth. This aligns with the research by Shuaibu (2023), who modeled the groundwater system in the Zamfara part of the

basin and found that organic pollutants significantly influence microbial proliferation

Furthermore, the negative correlation (-0.41) between pH and bacterial load observed in this study suggests that more alkaline conditions may

inhibit certain bacterial species. This is supported by Kaoje (2015), who found that the slightly acidic to neutral pH of groundwater in the southwestern Sokoto-Rima Basin was more conducive to the survival of coliforms compared to highly alkaline sources.

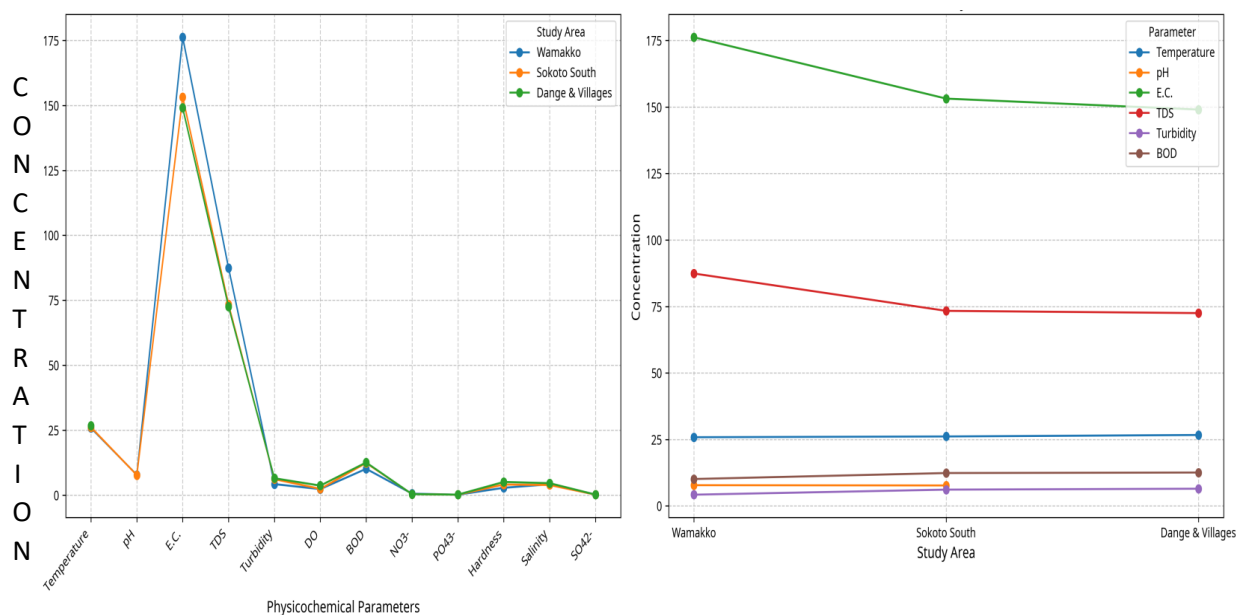


Figure 1. Physicochemical parameters of sampling sites

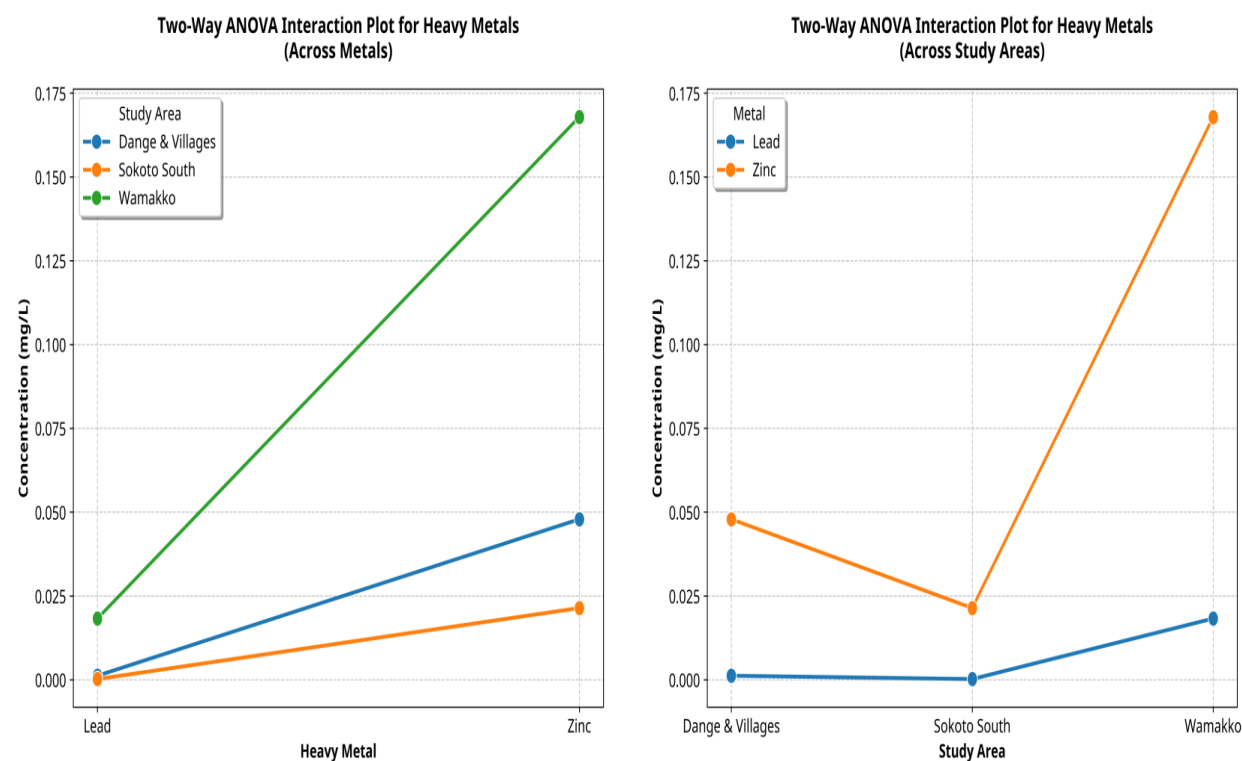


Figure 2. Interaction of study areas and heavy metal concentrations across sampling sites

Table 1: Heavy Metal Concentrations in Wamako study area

Sample ID	Zinc (Zn) Mean $\pm$ SD (mg/L)	Lead (Pb) Mean $\pm$ SD (mg/L)
WHO/NAFDAC Standard	3mg/L	0.01mg/L
WBB1	0.364 $\pm$ 0.009	0.000 $\pm$ 0.000
WBB2	0.193 $\pm$ 0.009	0.000 $\pm$ 0.000
WGB3	0.181 $\pm$ 0.004	0.000 $\pm$ 0.000
WGB4	0.198 $\pm$ 0.005	0.000 $\pm$ 0.000
WBW1	0.179 $\pm$ 0.005	0.020 $\pm$ 0.000
WBW2	0.202 $\pm$ 0.000	0.037 $\pm$ 0.000
WGW3	0.176 $\pm$ 0.008	0.053 $\pm$ 0.002
WGW4	0.139 $\pm$ 0.000	0.001 $\pm$ 0.000
WBW5	0.119 $\pm$ 0.001	0.000 $\pm$ 0.000
WBB5	0.156 $\pm$ 0.004	0.000 $\pm$ 0.000
WBW6	0.147 $\pm$ 0.005	0.000 $\pm$ 0.000
WBB6	0.148 $\pm$ 0.002	0.010 $\pm$ 0.000
WWW7	0.175 $\pm$ 0.000	0.083 $\pm$ 0.000
WWb7	0.101 $\pm$ 0.002	0.054 $\pm$ 0.000
WWW8	0.101 $\pm$ 0.004	0.026 $\pm$ 0.001
WWb8	0.107 $\pm$ 0.005	0.008 $\pm$ 0.000

Interpretation: WB = Wamako Baga, WG = Wamakko Girebshi, WB = Wamakko Barkeji WW= Wamakko Wajake

Table 2: Heavy Metal Concentrations in Study Area Dange and villages

Sample ID	Zinc (Zn) Mean $\pm$ SD (mg/L)	Lead (Pb) Mean $\pm$ SD (mg/L)
WHO/NAFDAC Standard	3mg/L	0.01mg/L
DSB9	0.113 $\pm$ 0.004	0.000 $\pm$ 0.000
DSW9	0.115 $\pm$ 0.005	0.000 $\pm$ 0.000
DSB10	0.047 $\pm$ 0.001	0.000 $\pm$ 0.000
DSW10	0.040 $\pm$ 0.002	0.003 $\pm$ 0.000
DAB11	0.037 $\pm$ 0.001	0.006 $\pm$ 0.000
DAW11	0.030 $\pm$ 0.000	0.000 $\pm$ 0.000
DAB12	0.024 $\pm$ 0.001	0.000 $\pm$ 0.000
DAW12	0.025 $\pm$ 0.001	0.000 $\pm$ 0.000
DGB13	0.027 $\pm$ 0.001	0.004 $\pm$ 0.000
DGW13	0.044 $\pm$ 0.002	0.000 $\pm$ 0.000
DGB14	0.044 $\pm$ 0.000	0.000 $\pm$ 0.000
DGW14	0.025 $\pm$ 0.001	0.000 $\pm$ 0.000
DKB15	0.035 $\pm$ 0.000	0.000 $\pm$ 0.000
DKW15	0.086 $\pm$ 0.001	0.006 $\pm$ 0.000
DKB16	0.033 $\pm$ 0.000	0.000 $\pm$ 0.000
DKW16	0.041 $\pm$ 0.001	0.000 $\pm$ 0.000

Interpretation: DA = Dange Amanawa, DS= Dange Shuni, DK= Dange Kwanar Kimba, DG = Dange Gindan Gara

Table 3: Heavy Metal Concentrations in Study Area Sokoto south

Sample ID	Zinc (Zn) Mean $\pm$ SD (mg/L)	Lead (Pb) Mean $\pm$ SD (mg/L)
WHO/ NAFDAC Standard	3mg/L	0.01mg/L
SGB17	0.023 $\pm$ 0.000	0.000 $\pm$ 0.000
SGB18	0.024 $\pm$ 0.000	0.000 $\pm$ 0.000
SGW17	0.038 $\pm$ 0.000	0.001 $\pm$ 0.000
SGW18	0.018 $\pm$ 0.001	0.000 $\pm$ 0.000
SmB23	0.019 $\pm$ 0.000	0.000 $\pm$ 0.000
SmB24	0.022 $\pm$ 0.000	0.000 $\pm$ 0.000
SmiB19	0.019 $\pm$ 0.001	0.000 $\pm$ 0.000
SmiB20	0.020 $\pm$ 0.000	0.000 $\pm$ 0.000
SmiW19	0.021 $\pm$ 0.000	0.000 $\pm$ 0.000
SmiW20	0.014 $\pm$ 0.000	0.000 $\pm$ 0.000
SmW23	0.028 $\pm$ 0.000	0.001 $\pm$ 0.000
SmW24	0.017 $\pm$ 0.001	0.000 $\pm$ 0.000
STB21	0.016 $\pm$ 0.000	0.000 $\pm$ 0.000
STB22	0.022 $\pm$ 0.000	0.000 $\pm$ 0.000
STW21	0.020 $\pm$ 0.001	0.000 $\pm$ 0.000
STW22	0.021 $\pm$ 0.000	0.000 $\pm$ 0.000

ST = Sokoto-South Tudun Wada, SM = Sokoto-South Mana, SMI = Sokoto-South Mabera Idi, SG = Sokoto-South Gagi

Table 4: Bacterial Colony Count

Study Area	Location	Mean $\pm$ SD (log ₁₀ CFU/mL)
DA	Location B	2.4085 $\pm$ 1.9090
DA	Location W	2.1032 $\pm$ 1.8133
DG	Location B	2.0231 $\pm$ 1.8444
DG	Location W	2.7795 $\pm$ 1.3031
DK	Location B	2.1110 $\pm$ 1.8472
DK	Location W	2.0284 $\pm$ 1.8956
DS	Location B	2.4059 $\pm$ 1.9040
DS	Location W	1.8845 $\pm$ 2.1974
SG	Location B	2.2444 $\pm$ 2.1222
SG	Location W	1.3657 $\pm$ 1.6959
SM	Location I B	2.1731 $\pm$ 2.1704
SM	Location I W	2.7592 $\pm$ 1.1338
SM	Location B	3.2904 $\pm$ 1.6483
SM	Location W	2.5233 $\pm$ 1.2322
ST	Location B	1.5338 $\pm$ 1.9361
ST	Location W	1.0505 $\pm$ 1.2939
WB	Location B	1.7631 $\pm$ 1.8222
WB	Location W	1.4333 $\pm$ 1.5913
WB	Location b B	3.0824 $\pm$ 1.3619
WB	Location b W	1.9731 $\pm$ 1.7704
WG	Location B	2.1650 $\pm$ 2.0586
WG	Location W	1.7080 $\pm$ 1.8160
WW	Location B	2.6277 $\pm$ 1.8380
WW	Location W	2.0029 $\pm$ 1.8133

Table 5: Gram Staining and Biochemical Tests Wamakko Study Area

Sample ID	Organism	Gram	Shape	Cat	Cit	In	Ur	MR	VP	Gl	La	Su	TSI	H2S/ Gas
WBb1	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
WBb2	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
	<i>E. coli</i>	-ve	Rod	+	-	+	-	+	-	+	+	-	Y/Y	-/+
WBW1	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
WBW2	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
WGB3	<i>E. coli</i>	-ve	Rod	+	-	+	-	+	-	+	+	-	Y/Y	-/+
	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
WGB4	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
WGW3	<i>K. oxytoca</i>	-ve	Rod	+	+	+	+	-	+	+	+	+	Y/Y	-/+
	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
	<i>B. cereus</i>	+ve	Rod	+	+	-	+	+	+	+	-	-	R/Y	-/+
WGW4	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
WBB5	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
WBB6	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
WBW5	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
	<i>E. coli</i>	-ve	Rod	+	-	+	-	+	-	+	+	-	Y/Y	-/+
WBW6	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
WWB7	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
WWB8	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
WWW7	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
WWW8	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
	<i>B. cereus</i>	+ve	Rod	+	+	-	+	+	+	+	-	-	R/Y	-/+
	<i>K. oxytoca</i>	-ve	Rod	+	+	+	+	-	+	+	+	+	Y/Y	-/+

Interpretation: WB = Wamako Baga, WG = Wamakko Girebshi, WB = Wamakko Barkeji WW= Wamakko Wajake

Table 6: Gram Staining and Biochemical Tests of Sokoto South Study Area

Sample ID	Organism	Gram	Shape	Cat	Cit	In	Ur	MR	VP	Gl	La	Su	TSI	H2S/ Gas
SGB17	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
SGB18	<i>K. oxytoca</i>	-ve	Rod	+	+	+	+	-	+	+	+	+	Y/Y	-/+
	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
SGW17	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
	<i>K. pneumonia</i>	-ve	Rod	+	+	-	+	-	+	+	+	+	Y/Y	-/+
SGW18	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
SmiB19	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>K. oxytoca</i>	-ve	Rod	+	+	+	+	-	+	+	+	+	Y/Y	-/+
SmiB20	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>E. coli</i>	-ve	Rod	+	-	+	-	+	-	+	+	-	Y/Y	-/+
	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
SmiW19	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
SmiW20	<i>B. cereus</i>	+ve	Rod	+	+	-	+	+	+	+	-	-	R/Y	-/+
	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
STB21	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>B. cereus</i>	+ve	Rod	+	+	-	+	+	+	+	-	-	R/Y	-/+
STB22	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
STW21	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>B. cereus</i>	+ve	Rod	+	+	-	+	+	+	+	-	-	R/Y	-/+
STW22	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
	<i>E. coli</i>	-ve	Rod	+	-	+	-	+	-	+	+	-	Y/Y	-/+
SmB23	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
	<i>S. flexneri</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	-/-
SmB24	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
	<i>E. coli</i>	-ve	Rod	+	-	+	-	+	-	+	+	-	Y/Y	-/+
SmW23	<i>K. pneumonia</i>	-ve	Rod	+	+	-	+	-	+	+	+	+	Y/Y	-/+
	<i>B. cereus</i>	+ve	Rod	+	+	-	+	+	+	+	-	-	R/Y	-/+
SmW24	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-

Interpretation: ST = Sokoto-South Tudun Wada, SM = Sokoto-South Mana, SMI = Sokoto-South Mabera
Idi, SG = Sokoto-South Gagi

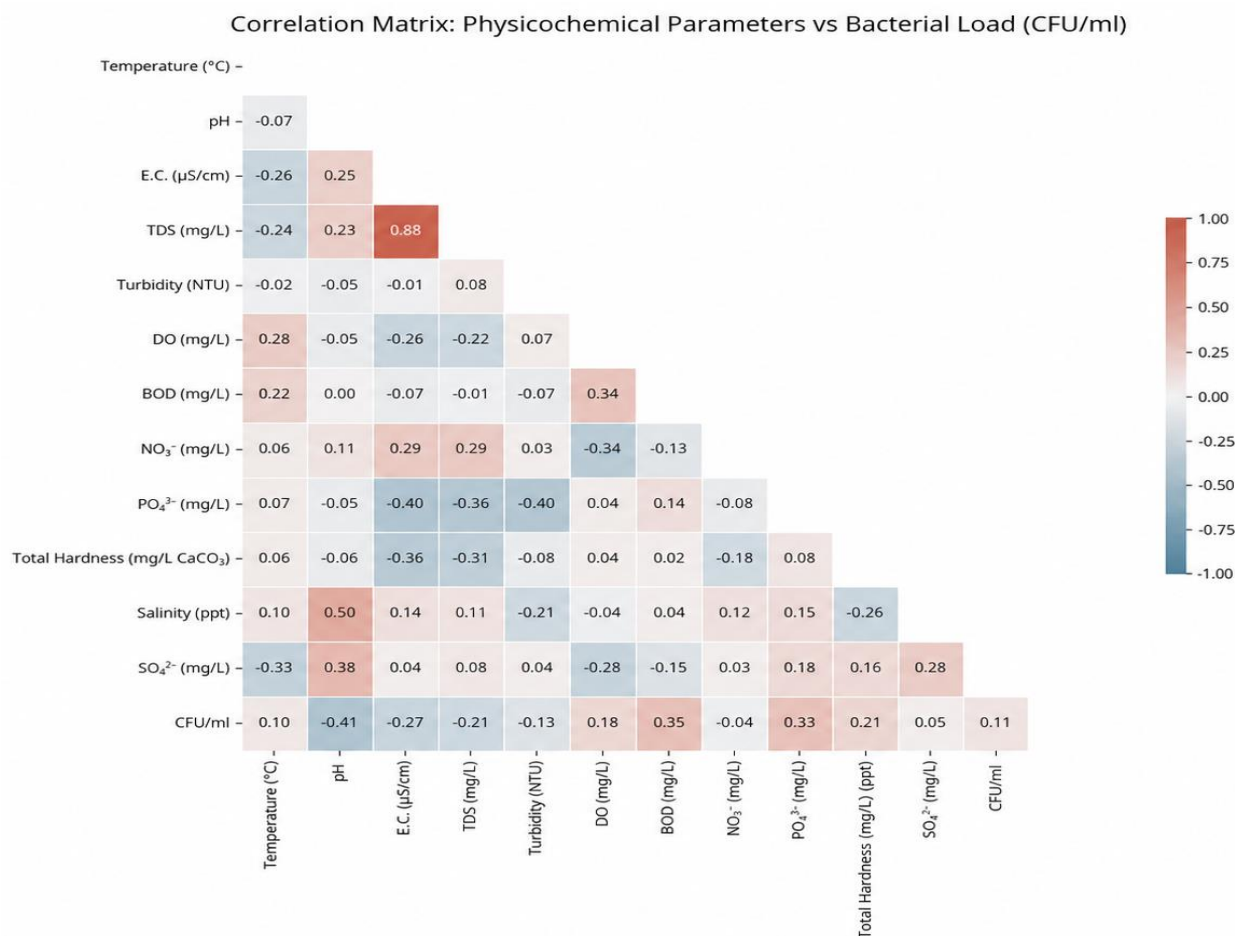
Table 7: Gram Staining and Biochemical Tests of Dange & Villages Study Area

Sample ID	Organism	Gram	Shape	Cat	Cit	In	Ur	MR	VP	Gl	La	Su	TSI	H2S/ Gas
DSB9	<i>B. cereus</i>	+ve	Rod	+	+	-	+	+	+	+	-	-	R/Y	-/+
	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
DSB10	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>E. coli</i>	-ve	Rod	+	-	+	-	+	-	+	+	-	Y/Y	-/+
DSW9	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
DSW10	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
DAB11	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
DAB12	<i>K. pneumonia</i>	-ve	Rod	+	+	-	+	-	+	+	+	+	Y/Y	-/+
	<i>E. coli</i>	-ve	Rod	+	-	+	-	+	-	+	+	-	Y/Y	-/+
DAW11	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
	<i>K. oxytoca</i>	-ve	Rod	+	+	+	+	-	+	+	+	+	Y/Y	-/+
DAW12	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
	<i>K. pneumonia</i>	-ve	Rod	+	+	-	+	-	+	+	+	+	Y/Y	-/+
	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
DGB13	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
DGB14	<i>S. aureus</i>	+ve	Cocci	+	-	-	-	+	+	+	+	+	Y/Y	-/-
	<i>E. coli</i>	-ve	Rod	+	-	+	-	+	-	+	+	-	Y/Y	-/+
DGW13	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>S. Typhimurium</i>	-ve	Rod	+	+	-	-	+	-	+	-	-	R/Y	+/+
DGW14	<i>S. Typhi</i>	-ve	Rod	+	-	-	-	+	-	+	-	-	R/Y	+/-
	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
DKB15	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>E. faecalis</i>	+ve	Cocci	-	-	-	-	+	-	+	+	+	Y/Y	-/-
	<i>K. pneumonia</i>	-ve	Rod	+	+	-	+	-	+	+	+	+	Y/Y	-/+
DKB16	<i>K. oxytoca</i>	-ve	Rod	+	+	+	+	-	+	+	+	+	Y/Y	-/+
	<i>C. freundii</i>	-ve	Rod	+	+	-	-	+	-	+	+	+	Y/Y	+/+
	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
DKW15	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>B. subtilis</i>	+ve	Rod	+	+	-	-	-	+	+	-	+	Y/Y	-/-
DKW16	<i>P. aeruginosa</i>	-ve	Rod	+	+	-	-	-	-	-	-	-	R/R	-/-
	<i>K. pneumonia</i>	-ve	Rod	+	+	-	+	-	+	+	+	+	Y/Y	-/+
DKW16	<i>B. cereus</i>	+ve	Rod	+	+	-	+	+	+	+	-	-	R/Y	-/+

Cat: Catalase, Cit: Citrate, In: Indole, Ur: Urease, MR: Methyl Red, VP: Voges-Proskauer, Gl: Glucose, La: Lactose, Su: Sucrose, TSI: Triple Sugar Iron, H2S: Hydrogen Sulfide, Gas: Gas production; Y/Y (Yellow/Yellow, Acid/Acid), R/Y (Red/Yellow, Alkaline/Acid), R/R (Red/Red, Alkaline/Alkaline); DA = Dange Amanawa, DS= Dange Shuni, DK= Dange Kwanar Kimba, DG = Dange Gindan Gara

Table 8: Coliform Count

Study Site	Positive sample	Min MPN/100ml	Max MPN/100ml	Mean MPN/100ml	Median MPN/100ml
Wamakko	14	3	1100	126.21	9.0
Sokoto South	13	3	1100	213.38	11.0
Dange & Villages	12	3	150	29.33	11.0

**Figure 3: Correlation analysis for physicochemical parameters and bacterial load**

In a broader Nigerian context, Taiwo et al. (2015) observed that rural groundwater sources often exhibit higher variability in physicochemical parameters due to localized pollution, which was also evident in the varying concentrations across the study sites in this research, with Dange & Villages (DK) showing the highest concentrations. Finally, Popoola et al. (2019) emphasized that while physicochemical parameters might meet standards, they do not guarantee microbiological safety, a trend clearly reflected in this study where

acceptable chemical levels coincided with high bacterial contamination.

This study also shows that total fecal and non-fecal coliforms associated with the groundwater samples revealed a high detection of coliform bacteria, with *Escherichia coli* being the most frequent isolate (28.12%), followed by *Salmonella Typhimurium* (25.00%).

The high frequency of *E. coli* is an indicator of fecal contamination. This finding is in agreement with Opara et al. (2024), who assessed coliform bacteria

in the Sokoto Metropolis public water supply and identified *E. coli* and *Salmonella* spp. as major contaminants. Bashir et al. (2018) also reported significant bacterial contamination in borehole water in Wamakko Local Government, with coliform counts exceeding WHO standards, mirroring the high MPN values (up to 1100 MPN/100ml) found in this study for Wamakko and Sokoto South.

The presence of *Salmonella* and *Shigella* species in the samples poses a severe public health risk. Kaoje et al. (2019) noted that wells in the Sokoto-Rima Basin are frequently contaminated with these enteric pathogens due to poor sanitation and proximity to pit latrines. Lawal et al. (2024) further highlighted that the recurrent outbreaks of waterborne diseases in Northern Nigeria are directly linked to the consumption of groundwater contaminated with such fecal coliforms. Raji and Ibrahim (2011) found similar patterns in Zaria, where unprotected wells showed higher coliform counts than boreholes, a trend partially observed in this study where well water (W) often showed higher mean counts than boreholes (B) in several locations.

Lastly, Ibe and Okplenye (2005) emphasized that the presence of non-fecal coliforms like *Enterobacter* and *Klebsiella* also indicates environmental contamination and poor well maintenance. Statistical differences among locations should not be interpreted as evidence of guideline exceedance; conversely, a parameter may exceed a WHO or NAFDAC limit even when differences among locations are not statistically significant. The reported lead (Pb) concentrations, particularly values above the applicable 0.01 mg/L guideline, warrant attention because of potential chronic health risks. Possible sources include corroded plumbing, contaminated soil, waste disposal, and runoff, although source attribution was beyond the scope of this study. The findings represent the sampling period and may not capture seasonal variation in groundwater quality.

Conclusion

This study assessed the microbiological and physicochemical quality of groundwater in

selected villages around the Sokoto-Rima Basin. Most physicochemical parameters, including pH, TDS, and temperature, were within WHO guideline values, although variations and exceedances were observed for selected parameters. Higher BOD and site-specific environmental conditions, particularly in the Dange Shuni area, were associated with higher microbial counts. The occurrence of fecal and non-fecal coliforms indicates that some sources were unsafe for direct consumption and has implications for groundwater quality, public health, and environmental management. These findings apply to the sampling period and may not represent seasonal variation.

The research identified a high prevalence of fecal and non-fecal coliforms, with *Escherichia coli* (28.12%) and *Salmonella Typhimurium* (25.00%) being the most dominant. The high MPN values in Wamakko and Sokoto South indicate that some water sources were bacteriologically unsafe for drinking. Because antimicrobial-susceptibility testing and molecular confirmation were not described or reported in the present manuscript, no conclusions are drawn about antimicrobial resistance or PCR-based identification.

Recommendations

Residents in the affected villages should be strongly advised to treat their water through boiling or chlorination before consumption and local authorities should enforce strict guidelines on the siting of wells and boreholes, ensuring they are located at least 30 meters away from septic tanks and pit latrines to prevent the infiltration of fecal matter.

Author contributor

AIB supervised the work as major supervisor, GGJ supervised the work as second supervisor and HL carried out the work.

Conflict of Interest

There is no conflict of interest

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