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Assessment of Microbiological Contaminants in Selected Wells in Agona Swedru Township, Ghana

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Abstract

Rapid global urbanization has intensified pressure on water resources, particularly groundwater, which serves about 4.1 billion people worldwide. Shallow aquifers near residential areas are vulnerable to contamination, particularly where sanitation systems are poorly managed. This study assessed microbiological contamination of well water and examined the association between contamination levels and distance from septic tanks in Agona Swedru Township. Ten cemented hand-dug wells were selected purposively and sampled once weekly for five consecutive weeks, generating 50 well-week observations. Microbiological assessment used membrane filtration and pour-plate culture methods with Harlequin agar to detect total coliforms and *Escherichia coli*. Descriptive statistics, Pearson correlation and multiple linear regression were used. For regression, the five weekly observations for each well were summarized as a well-level mean, giving an effective sample size of 10 independent wells; the regression models were therefore treated as exploratory. *E. coli* was detected in six of the ten wells (60%), while total coliforms were detected in seven wells (70%). No statistically significant association was observed between septic-tank distance and either *E. coli* or total coliform levels. Because well construction, drainage, soil characteristics, groundwater flow and septic-tank leakage were not directly measured, they are considered potential explanations rather than demonstrated determinants. The study recommends routine microbiological monitoring, improved protection of hand-dug wells, and further investigation of pathogenic bacteria, viruses and protozoa in groundwater used for domestic purposes.

Keywords

Microbiological Contamination, Groundwater, Agona Swedru Township, Septic Tanks

1. Introduction

Safely managed drinking water is a fundamental public-health requirement and a core Sustainable Development Goal. An estimated 1.8 billion people have been exposed to drinking water contaminated with faecal matter, increasing the risk of infection by pathogenic bacteria, viruses and protozoa [1]-[3]. Microbiological contamination poses particular risks to children, older adults and immune-compromised individuals [4] [5].

1.1. Microbiological Risks in Groundwater Systems

Groundwater is often perceived as microbiologically safer than surface water because of natural filtration through soil and geological formations [6]. However, shallow aquifers in rapidly urbanizing areas can be vulnerable to faecal contamination where sanitation infrastructure is inadequate [7] [8]. Poorly designed or poorly maintained sanitation systems can provide pathways through which microorganisms reach groundwater [9] [10]. In Ghana, groundwater is an important source of domestic water, and contamination of shallow wells can therefore have important public-health implications [11] [12].

1.2. Microbial Indicator Organisms

Because direct detection of every potential pathogen is technically demanding and costly, microbiological water-quality assessment commonly uses indicator organisms [3] [13]. Total coliforms are broad indicators of sanitary vulnerability, whereas *Escherichia coli* is a more specific indicator of recent faecal contamination [4] [14]. Indicator organisms do not, however, demonstrate the presence of every bacterial, viral or protozoan pathogen [14] [15].

1.3. Monitoring and Detection

International drinking-water guidelines emphasize the absence of *E. coli* in water intended for human consumption [4] [5]. Membrane filtration is widely used for microbiological water-quality assessment because a measured volume of water can be filtered and organisms subsequently enumerated on selective or differential media [16] [17]. In this study, microbiological indicators were used to assess the sanitary quality of selected hand-dug wells.

2. Materials and Methods

2.1. Description of Study Site

The study was conducted in Agona Swedru Township, the capital of the Agona West Municipality in Ghana's Central Region. The Municipality lies approximately between latitudes 5˚30' and 5˚50'N and longitudes 0˚35' and 0˚55'W and covers about 447 km^2 [18]. The area has a wet semi-equatorial climate with bimodal rainfall [18]. The study focused on selected cemented hand-dug wells used for domestic water supply (see **Figure 1**).

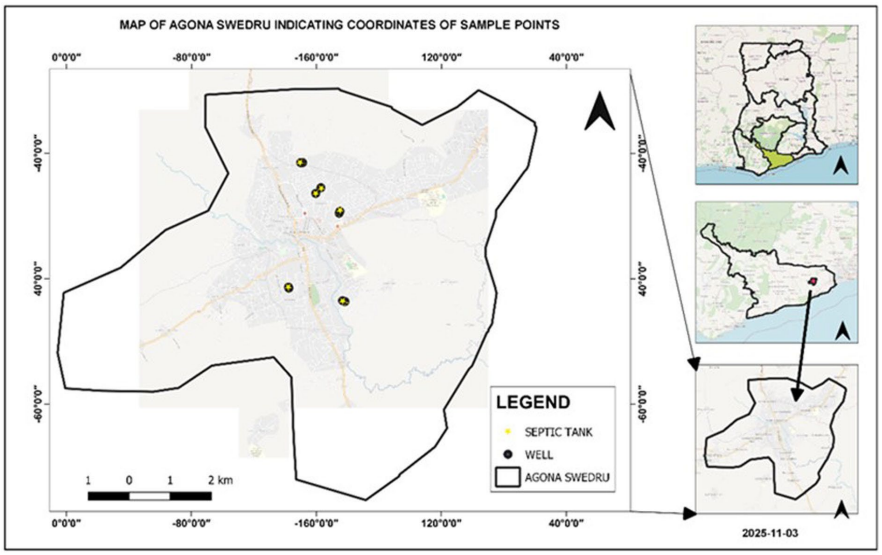

Figure 1. Geographical map of the study area showing the sampling locations.

2.2. Research Design and Sampling Strategy

A repeated-sampling observational design was used [19]. Ten cemented hand-dug wells were selected purposively and sampled once per week for five consecutive weeks. Thus, the dataset comprised 50 well-week observations. The measured distances between the wells and septic tanks ranged from 3.205 to 32.488 m. The five weekly measurements for each well were averaged to obtain one well-level mean for each physicochemical and microbiological outcome before the correlation and regression analyses (see Table 1). Consequently, the effective sample size for the regression models was 10 wells, not 50 observations. The regression models were treated as exploratory because four predictors were examined with only ten independent wells.

2.3. Sample Collection and Microbiological Data

Water samples were collected aseptically in sterile containers, transported under controlled conditions below 4˚C, and analyzed on the day of collection. A total of 50 sampling events were included in the five-week dataset. The study assessed total coliforms and *E. coli* using culture-based methods.

The total coliforms were cultivated on a medium that has lactose at 35˚C to 37˚C. They were tentatively determined by the production of acid and gasses due to the fermentation of the lactose. The microbiologically procedure involved the following steps [16] [17]:

- Before the experiment began, the whole bench was sterilized with methylated spirit.
- 100 mL of well water sample was poured into a glass filter holder with filter paper beneath while the valve was closed.
- The vacuum pump was turned on to filter the water through the membrane filter that retained the bacteria, while this process was ongoing, a harlequin

medium in a maccatini bottle was heated and poured into a petri dish.

- The filter paper was inoculated into the surface of the petri dish containing harlequin agar that is selective for the growth of specific organisms and distinguishes colonies of desired organism.
- The medium was allowed to solidify and incubated at 37˚C for 24 - 48 hours.
- After incubation, the colonies grown were counted and identified by the use of illuminated magnifier with a greenish-gold sheen with results were expressed as CFU/100 mL.

Three important controls (blanks, duplicates, and standards/reference controls) were put in place to determine whether the results were reliable and whether contamination occurred during sampling or laboratory analysis. These Quality Control measures strengthened the credibility of the laboratory results.

BLANKS: A sterile sample containing no well water was first used to detect contamination introduced from bottles, reagents, equipment, transport, or laboratory handling.

DUPLICATES: Two analytical portions from the same well sample were analyzed twice to check precision/reproducibility of sampling and laboratory analysis. Sample W1 was analyzed twice and compared the *E. coli* or total coliform counts.

STANDARD/REFERENCE CONTROL: A sample or organism with a known expected response was used to confirm that the analytical method, media, reagents, and incubation conditions were effective.

2.4. Physicochemical Analysis

2.4.1. Conductivity and Total Dissolved Solids

Multi-parameter electrode was used to determine the conductivity and total concentration of the ions of the cations and the anions present in an aqueous solution. When chloride and sodium mix, cations like calcium and magnesium that gives its water sample its hardness is given away and also the anions like chlorides which combine with calcium/ magnesium or sodium to form different salts like NaCl. It is generally in micro milisiemens per centimetre (µs/cm or ms/cm).

The Total Dissolved solids contain inorganic salt, mainly calcium, magnesium, potassium, sodium, bicarbonate, chlorides, Sulphate and a small part of organic matter that were dissolved in water. TDS test is a qualitative measure of the quantity of dissolved ions and is an indicator test to establish the overall quality of water. The procedure involved [16] [17] [20]:

1) 50 mL of water was poured into the beaker.

2) The multi-parameter electrode probe was fully immersed in the water.

3) The readings of both conductivity and TDS were taken at the same time.

Blank: Deionized water was used to check for dissolved solids and excessive background conductivity.

Duplicate: The same well-water sample was measured twice for reproducibility. Similar readings were read indicating good precision.

Standard: A certified conductivity standard of known conductivity was used to calibrate or verify the conductivity meter.

2.4.2. Total Suspended Solids (TSS)

The spectrophotometer was used to measure total suspended solids. The spectrophotometer operates on the Beer lambert law: the amount of light absorbed or transmitted by a solution is proportional to the solution's molar absorptivity and the concentration of the solute. In the process of determining TSS [16] [17] [20]:

1) Distilled water was first used to zero the spectrophotometer.

2) Sample bottle was cleaned with well water.

3) Well water was poured into the sample bottle and insert into the spectrophotometer.

4) Readings were recorded.

BLANKS: A clean, known-quality water sample is processed through the entire filtration and drying procedure. The blank should have very little or no measurable residue.

DUPLICATE: The same well-water sample was filtered and analyzed twice for analytical precision.

STANDARD/REFERENCE: TSS was determined gravimetrically. Quality control included method blanks, duplicate samples, and verification of the analytical balance using certified calibration weights.

2.5. Statistical Analysis and Interpretation

Microbiological data were summarized using well-level means (see **Table 2**). Pearson correlation coefficients were used to describe linear associations among total coliforms, *E. coli*, distance, conductivity, TDS and TSS (see **Table 3**). Separate multiple linear regression models were fitted for total coliforms and *E. coli* using distance, conductivity, TDS and TSS as predictors (**Table 4**). Each model therefore contained four predictors and ten independent well-level observations. The models were considered exploratory because the number of independent wells was small relative to the number of predictors. Statistical significance was assessed at $\alpha = 0.05$.

3. Results and Discussion

3.1. Physicochemical and Microbiological Levels in Well Water

The well-level results showed variation in conductivity, TDS, TSS, total coliforms and *E. coli* concentrations among the sampled wells. These measurements were compared with the applicable drinking-water quality guidance and thresholds used in the study (see **Table 1**). The microbiological results were interpreted primarily using the presence or absence and concentration of indicator organisms, with particular attention to *E. coli* because drinking-water guidelines generally require its absence in a 100 mL sample intended for human consumption [4] [5].

Table 1. Laboratory analysis of well water for five consecutive weeks.

WELL	DISTANCE/M	PARAMETER	WEEK 1	WEEK 2	WEEK 3	WEEK 4	WEEK 5	MEANS	USEPA THRESHOLD
1	3.205	COND.	618	616	618	620	623	619	1000 µS/cm
		TDS	437	437	439	437	438	437.6	≤ 500 mg/L
		TSS	3	2	2	3	3	2.6	≤ 5 mg/L
		TC	99.0	101	113	98	100	102.2	ND cfu/mL
		E. coli	23.0	25	30	20	23	24.2	ND cfu/mL
2	17.92	COND.	384	384	390	377	380	383	1000 µS/cm
		TDS	274	270	280	268	270	272.4	≤ 500 mg/L
		TSS	48	47	48	48	48	47.8	≤ 5 mg/L
		TC	0.0	0.0	0.0	0.0	0.0	0	ND cfu/mL
		E. coli	0.0	0.0	0.0	0.0	0.0	0	ND cfu/mL
3	20.051	COND.	734	738	733	734	730	733.8	1000 µS/cm
		TDS	529	533	530	529	530	530.2	≤ 500 mg/L
		TSS	1	1	1	1	1	1.0	≤ 5 mg/L
		TC	0.0	0.0	0.0	0.0	0.0	0.0	ND cfu/mL
		E. coli	0.0	0.0	0.0	0.0	0.0	0.0	ND cfu/mL
4	4.436	COND	853	855	852	853	854	853.4	1000 µS/cm
		TDS	605	606	605	605	606	605.4	≤ 500 mg/L
		TSS	9	9	8	9	9	8.8	≤ 5 mg/L
		TC	128.0	128	127	130	128	128.2	ND cfu/mL
		E. coli	4.0	6.0	4.0	8.0	5.0	5.4	ND cfu/mL
5	10.164	COND	641	643	641	641	642	641.6	1000 µS/cm
		TDS	455	456	454	455	455	455	≤ 500 mg/L
		TSS	3	4	4	3	3	3.4	≤ 5 mg/L
		TC	325.0	325.0	327.0	326.0	328.0	326.2	ND cfu/mL
		E. coli	153.0	153.0	155.0	160.0	158.0	155.8	ND cfu/mL
6	3.90	COND	447	445	447	450	446	447	1000 µS/cm
		TDS	311	312	311	315	313	312.4	≤ 500 mg/L
		TSS	2	2	1	3	1	1.8	≤ 5 mg/L
		TC	46.0	48.0	46.0	50.0	46.0	47.2	ND cfu/mL
		E. coli	6.0	7.0	6.0	8.0	6.0	6.6	ND cfu/mL
7	4.411	COND	335	336	335	334	337	335.4	1000 µS/cm
		TDS	235	237	233	233	235	234.6	≤ 500 mg/L
		TSS	1	2	1	1	1	1.2	≤ 5 mg/L
		TC	2.0	2.0	2.0	3.0	1.0	2.0	ND cfu/mL
		E. coli	0.0	0.0	0.0	0.0	0.0	0.0	ND cfu/mL

Continued

		COND	352	353	355	352	351	352.6	1000 µS/cm
		TDS	249	247	250	246	249	248.2	≤ 500 mg/L
8	32.488	TSS	2	2	2	2	2	2.0	≤ 5 mg/L
		TC	0.0	0.0	0.0	0.0	0.0	0.0	ND cfu/mL
		E. coli	0.0	0.0	0.0	0.0	0.0	0.0	ND cfu/mL
		COND	478	479	477	478	479	478.2	1000 µS/cm
		TDS	345	345	346	344	348	345.6	≤ 500 mg/L
9	27.613	TSS	0	0	0	0	0	0.0	≤ 5 mg/L
		TC	32.0	35.0	33.0	32.0	31.0	32.6	ND cfu/mL
		E. coli	23.0	23.0	26.0	23.0	24.0	23.8	ND cfu/mL
		COND	572	572	573	572	572	572.2	1000 µS/cm
		TDS	408	409	410	408	408	408.6	≤ 500 mg/L
10	3.92	TSS	2	2	3	2	2	2.2	≤ 5 mg/L
		TC	56.0	56.0	58.0	55.0	56.0	56.2	ND cfu/mL
		E. coli	1.0	1.0	1.0	1.0	1.0		ND cfu/mL

*COND—CONDUCTIVITY; TDS—TOTAL DISSOLVED SOLIDS; TSS—TOTAL SUSPENDED SOLIDS; TC—TOTAL COLIFORM; ND—NOT DETECTED. *E. coli—Escherichia coli*; *A value of 0 indicates no colonies were recorded in the reported observation.

Table 2. Means of all parameters.

Samples	Distance/m	Cond. 1000	TDS ≤ 500	TSS ≤ 5	TC ND	*E. coli* ND
W_1	3.205	619	437.6	2.6	102.2	24.2
W_2	17.92	383	272.4	47.8	0.0	0.0
W_3	20.051	733.8	530.2	1	0.0	0.0
W_4	4.436	88.4	605.4	8.8	128.2	5.4
W_5	10.164	641.6	455	3.4	326.2	155.8
W_6	3.90	447	312.4	1.8	47.2	6.6
W_7	4.411	335.4	234.6	1.2	2.0	0.0
W_8	32.488	352.6	248.2	2.0	0.0	0.0
W_9	27.613	478.2	345.6	0.0	32.6	23.8
W_{10}	3.92	572.2	408.6	2.2	56.2	1.0

Source: Field Work, 2025. *Cond.—conductivity. *ND—NOT DETECTED.

3.2. Relationship between Total Coliform and Predictor Variables

Table 3. Pearson correlation matrix for total coliforms and predictor variables.

Parameter	TC	Distance	Conductivity	TDS	TSS
TC	1.000	−0.339	0.178	0.468	−0.167
Distance	−0.339	1.000	0.055	−0.297	0.096

Continued

Conductivity	0.178	0.055	1.000	0.114	−0.251
TDS	0.468	−0.297	0.114	1.000	−0.213
TSS	−0.167	0.096	−0.251	−0.213	1.000

Table 4. Multiple-regression coefficients for total coliforms (n = 10 wells).

Predictor	Standardized β	t	p-value	Interpretation
Distance	0.232	−0.582	0.586	Not statistically significant
Conductivity	0.140	0.357	0.736	Not statistically significant
TDS	0.377	0.931	0.394	Not statistically significant
TSS	−0.029	−0.074	0.944	Not statistically significant

The full model had R = 0.534 and R^2 = 0.285, meaning that the four predictors together accounted for 28.5% of the variation in well-level mean total coliform concentrations. The overall model was not statistically significant, F (4,5) = 0.498, p = 0.740. Distance was also not a statistically significant individual predictor (β = 0.232, t = −0.582, p = 0.586). The bivariate Pearson correlation between distance and total coliforms was r = −0.339. These statistics indicate that the small sample did not demonstrate a statistically significant association.

3.3. Relationship between *E. coli* and Predictor Variables

Table 5 shows that conductivity had the strongest positive correlation with *E. coli* concentration (r = 0.363), indicating that wells with higher conductivity tended to have higher *E. coli* levels, although the association was weak-to-moderate. Distance, TDS, and TSS showed very weak relationships with *E. coli*. The predictor variables were also weakly correlated with one another, with the strongest relationship being between distance and TDS (r = 0.297), suggesting little evidence of multicollinearity (see Table 5).

Consistent with this finding, Table 6 shows that conductivity had the largest standardized regression coefficient (β = 0.344), indicating a positive association with *E. coli* after controlling simultaneously for distance, TDS, and TSS. The similarity between the correlation and regression coefficients is consistent with the relatively low correlations among the predictors. However, the conductivity effect was not statistically significant (p = 0.455) (see Table 6). The overall findings of Table 5 and Table 6 indicate that none of the four predictors, distance, conductivity, TDS, or TSS was a statistically significant independent predictor of *E. coli* concentration in the 10 wells.

Table 5. Pearson correlation matrix for *E. coli* and predictor variables.

Parameter	*E. coli*	Distance	Conductivity	TDS	TSS
E. coli	1.000	−0.085	0.363	0.223	−0.140
Distance	−0.085	1.000	0.055	−0.297	0.096

Continued

Conductivity	0.363	0.055	1.000	0.114	−0.251
TDS	0.223	−0.297	0.114	1.000	−0.213
TSS	−0.140	0.096	−0.251	−0.213	1.000

Table 6. Multiple-regression coefficients for *E. coli* (n = 10 wells).

Predictor	Standardized β	t	p-value	Interpretation
Distance	−0.054	−0.126	0.905	Not statistically significant
Conductivity	0.344	0.810	0.455	Not statistically significant
TDS	0.165	0.377	0.722	Not statistically significant
TSS	−0.014	−0.032	0.976	Not statistically significant

The standard error of the estimate was calculated from the reported R^2 and the variance of the ten well-level mean outcomes, using residual degrees of freedom of 5. The *E. coli* model produced a negative adjusted R^2 (−0.498), indicating poor model performance after accounting for the four-predictor model complexity (see Table 7).

Table 7. Model summary for exploratory multiple regression.

Outcome	R	R^2	Adjusted R^2	F (4, 5)	Overall p	SE estimate
Total coliform	0.534	0.285	−0.287	0.498	0.740	114.38
E. coli	0.410	0.168	−0.498	0.252	0.897	58.83

3.4. Microbiological Contamination and Well Water Quality

Mean total coliform concentrations ranged from 0 to 326.2 CFU/100 mL, while mean *E. coli* concentrations ranged from 0 to 155.8 CFU/100 mL. W5 had the highest mean concentrations for both indicators (326.2 CFU/100 mL total coliforms and 155.8 CFU/100 mL *E. coli*). *E. coli* was detected in six wells, indicating faecal contamination in those wells. The presence of total coliforms in seven wells further indicates microbiological vulnerability of the water sources.

The observed contamination is important because drinking-water guidelines generally require the absence of *E. coli* in a 100-mL drinking-water sample [4] [5]. However, the present study did not directly test for specific pathogenic bacteria, viruses or protozoa. Therefore, the results demonstrate faecal-indicator contamination rather than confirmed occurrence of specific pathogens.

Distances between wells and septic tanks ranged from 3.205 to 32.488 m. The relationship between distance and microbiological contamination was not uniform. W3 and W8, which had distances of 20.051 m and 32.488 m respectively, had no detected total coliforms or *E. coli*. Conversely, W5 and W9, at 10.164 m and 27.613 m, had relatively high *E. coli* means. W4, W6, W7 and W10 had shorter distances but comparatively lower *E. coli* means. This variability is consistent with

the non-significant regression results.

Previous studies have reported relationships between sanitation-source proximity and groundwater contamination. Ngasala, Masten and Phanikumar (2019), for example, investigated domestic wells and hydrogeological conditions in peri-urban Dares Salaam and reported widespread *E. coli* contamination [21]. Such evidence supports the plausibility of sanitation-related groundwater contamination but does not establish that the same mechanism explains the variation observed in Agona Swedru.

3.5. Study Limitations

1) Only ten wells were investigated, resulting in low statistical power and a high risk of over-fitting when four predictors were included in the regression models.

2) The wells were selected through non-probability purposive sampling, limiting generalizability beyond the sampled wells and study area.

3) Each well was sampled repeatedly over five weeks. The regression analysis used well-level means to avoid treating repeated observations from the same well as independent; consequently, temporal variation was not modelled explicitly.

4) The geographical scope was limited to selected wells in Agona Swedru Township.

5) Specific pathogenic bacteria, viruses and protozoa were not directly tested.

6) Detailed hydrogeological characteristics, groundwater flow and septic-tank leakage were not directly assessed.

7) Detailed analytical quality-control information for the microbiological and physicochemical procedures was not available in the study record used for this revision.

8) The negative adjusted R^2 for the *E. coli* model demonstrates poor predictive performance after accounting for model complexity.

4. Conclusions

This study identified microbiological contamination in selected hand-dug wells in Agona Swedru Township. Total coliforms were detected in seven of the ten wells (70%), while *Escherichia coli* (*E. coli*) was detected in six of the ten wells (60%). Mean concentrations varied substantially among the sampled wells, with W5 recording the highest mean concentrations of both indicator organisms. These findings indicate that several of the investigated wells were microbiologically contaminated and may pose a potential public-health concern, particularly where the water is used for domestic purposes without adequate treatment [4] [5].

Septic-tank distance from the wells ranged from 3.205 to 32.488 m and was not a statistically significant predictor of either total coliform or *E. coli* concentrations in the exploratory regression models. However, this finding should not be interpreted as evidence that septic-tank distance has no influence on well-water contamination. Rather, the small sample size, limited statistical power, and inclusion of multiple predictors mean that the present study did not provide sufficient sta-

tistical evidence of an independent association between septic-tank distance and the measured microbiological indicators.

Factors such as well construction and protection, soil characteristics, drainage conditions, groundwater flow, and potential wastewater or septic-system influence may contribute to microbial transport to groundwater [9] [10] [22]. However, these factors were not directly measured or modelled in the present study and therefore cannot be established as causes of the observed contamination. The findings should consequently be interpreted within the context of the study design, sampling approach, and small number of wells investigated.

Routine microbiological monitoring of hand-dug wells, improved protection and maintenance of well structures, appropriate household water treatment, and improved sanitary management around groundwater sources are recommended [3] [23]. Future studies should include larger and preferably probabilistically selected samples of wells, longer monitoring periods, detailed hydrogeological and sanitary-risk assessments, and direct investigation of relevant pathogenic microorganisms and potential contamination pathways.

Author Contributions

Gifty Nyarko Kwakye: Conceptualization, methodology, investigation, data collection, microbiological analysis, data curation, statistical analysis, interpretation of results, writing-original draft, review and editing.

Worlanyo Kwabena Agbosu: Supervision, methodology, investigation, microbiological analysis, data validation, statistical analysis, interpretation of results, writing- review and editing and critical review of the manuscript.

Felix Tetteh Kabutey: Methodology, investigation, microbiological analysis, data validation, interpretation of results, writing- review and editing.

All authors contributed to the study and manuscript development, reviewed the manuscript critically, approved the final version and agreed to be accountable for all aspects of the work.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

References

[1] Bain, R., Cronk, R., Hossain, R., Bonjour, S., Onda, K., Wright, J., *et al.* (2014) Global Assessment of Exposure to Faecal Contamination through Drinking Water Based on a Systematic Review. *Tropical Medicine & International Health*, **19**, 917-927. https://doi.org/10.1111/tmi.12334

[2] Bain, R., Johnston, R., Mitis, F., Chatterley, C. and Slaymaker, T. (2018) Establishing Sustainable Development Goal Baselines for Household Drinking Water, Sanitation and Hygiene Services. *Water*, **10**, Article 1711. https://doi.org/10.3390/w10121711

[3] World Health Organization (2014) Preventing Diarrhea through Better Water, Sanitation and Hygiene: Exposures and Impacts in Low- and Middle-Income Countries. WHO Press.

[4] World Health Organization (2022) Guidelines for Drinking-Water Quality: Fourth Edition Incorporating the First and Second Addenda. World Health Organization.

[5] World Health Organization (2017) Guidelines for Drinking-Water Quality. 4th Edition, World Health Organization.

[6] Magara, Y. (1993) The Significance of the Revised Drinking Water Quality Standard. *Japanese Journal of Public Health*, **40**, 350-352.

[7] Kothari, C.R. (2004) Research Methodology: Methods and Techniques. New Age International.

[8] Obiri-Danso, K., Adjei, B., Stanley, K.N. and Jones, K. (2009) Microbiological Quality and Metal Levels in wells and Boreholes Water in Some Peri-Urban Communities in Kumasi, Ghana. *African Journal of Environmental Science and Technology*, **3**, 59-66.

[9] Selvam, S., Magesh, N.S., Chidambaram, S., Rajamanickam, M. and Sashikkumar, M.C. (2014) A GIS Based Identification of Groundwater Recharge Potential Zones Using RS and IF Technique: A Case Study in Ottapidaram Taluk, Tuticorin District, Tamil Nadu. *Environmental Earth Sciences*, **73**, 3785-3799. https://doi.org/10.1007/s12665-014-3664-0

[10] United States Environmental Protection Agency (2023) Groundwater and Drinking Water: Sources of Contamination. EPA Report. United States Environmental Protection Agency.

[11] Oyelude, E.O., Densu, A.E., Yankey, E. and Olajide, E. (2013) Quality of Groundwater in Kassena-Nankana District, Ghana and Its Health Implications. *Advances in Applied Science Research*, **4**, 442-448.

[12] Risebro, H.L., Breton, L., Aird, H., Hooper, A. and Hunter, P.R. (2012) Contaminated Small Drinking Water Supplies and Risk of Infectious Intestinal Disease: A Prospective Cohort Study. *PLOS ONE*, **7**, e42762. https://doi.org/10.1371/journal.pone.0042762

[13] Meays, C.L., Broersma, K., Nordin, R. and Mazumder, A. (2004) Source Tracking Fecal Bacteria in Water: A Critical Review of Current Methods. *Journal of Environmental Management*, **73**, 71-79. https://doi.org/10.1016/j.jenvman.2004.06.001

[14] Harwood, V.J., Levine, A.D., Scott, T.M., Chivukula, V., Lukasik, J., Farrah, S.R., *et al.* (2005) Validity of the Indicator Organism Paradigm for Pathogen Reduction in Reclaimed Water and Public Health Protection. *Applied and Environmental Microbiology*, **71**, 3163-3170. https://doi.org/10.1128/aem.71.6.3163-3170.2005

[15] Sinclair, R.G., Jones, E.L. and Gerba, C.P. (2009) Viruses in Recreational Water-Borne Disease Outbreaks: A Review. *Journal of Applied Microbiology*, **107**, 1769-1780. https://doi.org/10.1111/j.1365-2672.2009.04367.x

[16] Lipps, W.C., Braun-Howland, E.B. and Baxter, T.E. (2023) Standard Methods for the Examination of Water and Wastewater. 24th Edition, American Public Health Association, American Water Works Association, & Water Environment Federation.

[17] American Public Health Association (1998) Standard Methods for the Examination of Water and Wastewater. 20th Edition, American Public Health Association, American Water Works Association, and Water Environment Federation.

[18] Ghana Statistical Service (2020) 2020 Population and Housing Census: Regional Analytical Report, Central Region.

[19] Creswell, J.W. (2014) Research Design: Qualitative, Quantitative and Mixed Methods Approaches. Sage Publications.

[20] United States Environmental Protection Agency (2019) Field and Laboratory Meth-

ods for Investigating Drinking Water Contamination. EPA Report. United States Environmental Protection Agency.

[21] Ngasala, T.M., Masten, S.J. and Phanikumar, M.S. (2019) Impact of Domestic Wells and Hydrogeologic Setting on Water Quality in Peri-Urban Dar Es Salaam, Tanzania. *Science of the Total Environment*, **686**, 1238-1250. https://doi.org/10.1016/j.scitotenv.2019.05.202

[22] Fetter, C.W. (2001) Applied Hydrogeology. 4th Edition, Prentice Hall.

[23] Centers for Disease Control and Prevention (2020) Water, Sanitation, & Hygiene (WASH) and Health. U.S. Department of Health and Human Services.