Bacteriological quality of household drinking water and cholera risk in the Greater Accra Region, Ghana

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Abstract

Background: The bacteriological quality of drinking water plays a critical role in preventing waterborne diseases. In Ghana, there is water scarcity and many communities depend on contaminated water sources for their domestic use. This study aimed to assess the microbiological quality of household drinking water in both cholera endemic and non-endemic areas in Greater Accra Region.

Methods: A community-based cross-sectional survey was conducted among 432 randomly selected households. A total of 432 water samples were collected in both the wet and dry seasons from the households and an additional 48 from other water sources within the area studied. The membrane filtration technique was used for the quantification of total coliform counts, faecal coliform counts and *vibrio* counts. The bacteria were further identified and characterized. The Kruskal Wallis rank test was used to determine any significant variations in the means of the log-transformed bacteria counts among specific factor variables.

Results: Household drinking water samples were contaminated with coliform counts exceeding the recommended zero colony-forming units per 100 ml standard in most communities across the cholera endemic and non-endemic areas. *Vibrio* counts were detected in all household water stored in vessels. Further characterization identified predominantly *Klebsiella penumoniae* and *Escherichia coli*. The coliform contamination levels were significantly higher in water stored in vessels compared to water directly obtained from the source. The contamination levels were generally higher during the wet season than the dry season.

Conclusion: The household stored drinking and direct source water were highly contaminated with coliform bacteria and a risk for transmission of pathogenic waterborne diseases. Therefore, the need to implement an effective water treatment strategy to improve on the quality of drinking water.

Keywords: Household water, contamination, coliform, cholera-risk, water source

Introduction

Water is a necessity for sustaining life and maintaining health. Access to safe and clean drinking water is a fundamental human right, yet billions of people globally, particularly in developing countries, are still deprived of this necessity [1, 2]. Among those who have access to water, millions drink from water sources which are contaminated with excreta [1], which increases the risk of contracting waterborne illnesses, such as cholera, which is still a serious public health concern in many parts of the world [3].

Cholera, is caused by the *Vibrio cholerae*, an acute diarrheal disease that can lead to severe dehydration and even death if left untreated. The disease is primarily transmitted through the consumption of contaminated water or food, with contaminated water being the most significant source of infection. Cholera outbreaks are known to occur in regions where sanitation and hygiene practices are suboptimal and access to safe drinking water is limited [3, 4].

The Greater Accra Region, located in southern-most part in Ghana, is a densely populated area with rapid urbanization and inadequate water and sanitation infrastructure. The region has experienced recurrent cholera outbreaks over the years, resulting in significant number of deaths [5, 6]. The lack of access to safe drinking water, coupled with poor sanitation practices, makes the population vulnerable to cholera infection.

Understanding the bacteriological quality of household drinking water is crucial in assessing the risk of cholera transmission within communities. Bacteriological analysis provides insights into the presence and levels of indicator microorganisms, such as faecal coliforms and *Escherichia coli (E. coli),* which serve as markers for faecal contamination [7]. High

levels of these indicator bacteria indicate the potential presence of pathogens, including *V. cholerae* [7].

Several factors can contribute to the deterioration of drinking water quality, such as inadequate water treatment, contaminated sources and improper storage and handling practices at the household level [8-10]. Identifying these factors and assessing their impact on water quality is essential for designing effective interventions to reduce the risk of cholera transmission and improve public health outcomes.

This study aimed to investigate the bacteriological quality of household drinking water and its association with cholera-risk in the Greater Accra Region of Ghana. The presence and levels of faecal indicator bacteria were assessed in the household drinking water samples collected from different communities in the cholera endemic and non-endemic communities in the Greater Accra Region.

Materials and methods

Description of study area

This study was carried out in the Greater Accra Region (GAR), one of the 16 administrative regions of Ghana. It is in the south-most part of the country and bordered by the Central Region to the west, Volta Region to the east, Eastern Region to the north, and the Gulf of Guinea to the south (Figure 1). It is the smallest land area of the 16 regions, with estimated population to be 5,055,805 [11]. The capital city of Ghana, Accra is also located in the region with a daily influx of people from within and outside the country. The region is the most urbanized and has the highest population density in the country [12]. There are highly

populated slums, squatters and informal settlements in parts of the region due to the rapid urbanization being experienced [13, 14].

The region has 29 districts of which two are metropolitans; namely Accra and Tema and 23 municipalities. Twelve communities such as; Agbogbloshie, James Town, Adabraka, Kaneshie, Maamobi, Nima, Chorkor, Mamprobi, Agege and Dansoman in the Accra Metropolitan Assembly, and Teshie and Nungua in the Ledzokuku Krowor Municipality located in the cholera endemic communities. In addition, Dawhenya North, Kofikope, Awhiam, and Dawa in the Ningo Prampram district; Addokope, Dogobom, Anyaman East, Adjumanikope in the Ada West district; Adedetsekope, Angomya-Ada, Kophemm Kasseh and Asigbekope in the Ada East district all located in the non-cholera endemic communities shown in Fig 1.

ALN-Ablekuma North, ABC-Ablekuma Central, ABW-Ablekuma West, ACC-Accra Metropolis, KKT-Korle Klottey, WGB-Weija Gbawe, OKN-Okaikoi North, AYW-Ayawaso West, LDK-La Dade Kotopon, ASH-Ashaiman

Study design

A community-based cross-sectional design was used for this study. The study area was classified into cholera endemic and non-endemic communities. The cholera endemic communities were cholera 'hotspots' in the Accra Metropolitan Area, Ledzokuku and Krowor Municipal Areas which have consistently been reporting cases of cholera over the past five years, preceding start of this study, with evidence of local transmission. The cholera non-endemic communities were the Ningo Prampram, Ada West and East Districts that have rarely recorded any case of cholera over the same period with no evidence of local transmission in the area. Household drinking water from randomly selected households were sampled for bacteriological water quality assessment. The study was conducted in the wet (April to August 2019) and dry (January to March 2020) seasons.

Sample size determination

The sample size was determined using the Cochran's formula:

$$N = \frac{z^2\, p(1-p)}{e^2}$$

$$N = \frac{(1.96)^2 \times 0.838(1-0.838)}{(0.05)^2}$$

$$N = 208.608$$

By assuming z: 95% confidence interval, e: 5% margin of error and p: proportion of households drinking water contaminated with *V. cholerae* as 83.8% reported in Accra Metropolis [15], to obtain a minimum sample size of 209 for each of the endemic and also the non-endemic communities for the wet season and repeated in the dry season.

Sampling technique

A multistage cluster sampling approach was used to determine the household of which to sample the water. The first cluster represented a cholera endemic or non-endemic community. The second stage involved the random selection of 12 communities from both the endemic and also the non-endemic communities. The households were subsequently listed for each community and 9 households randomly selected by a ballot. An additional water sample was collected from the main drinking water source in each of the communities (e.g public tap, pipe, or dam) as a control sample. The 12 selected cholera endemic communities were; Agbogbloshie, James Town, Adabraka, Dansoman, Agege, Mamprobi, Chorkor, Kaneshie, Nima, Maamobi, Teshie, and Nungua. Whereas the 12 non-endemic communities were; Addokope, Dogobom, Adjumanikope, Anyaman, Adedetsekope, Agomya-Ada, Kopehem-Kasseh, Asigbeykope, Awhiam, Dawa, Kofikope, and Dawhenya North. In all 216 households drinking water and 24 from the water source were collected during the wet season and repeated in the dry season from the same households and water sources to determine the temporal variation in water quality.

Water sample collection

Households' drinking water samples were collected for bacteriological quality analysis. Head of households or representative were asked to provide a cup of drinking water as they would give to a child or guest to be collected to ensure that they will provide the best of water quality to sample. Approximately 500 ml of the stored household drinking water was sampled using the container usually used to scoop water from the storage container into a sterile plastic bottle. In case the household drank sachet water, they were collected and a selected edge of the sachet water decontaminated by cleaning with 70% ethanol, then cut aseptically with sterile scissors and the water poured into the sterile plastic bottle. On the other hand, if the household drank bottled water, they were only collected and labelled. The water samples from the source point were directly collected from the pipe, standpipe, or unprotected well. The collection of water from the tap or pipe water was done by cleaning the outside of the tap with 70% ethanol and allowing flow at maximum for about a minute before directly collecting into the sterile plastic bottle [16]. A drop of sodium thiosulphate (0.5 ml of 10% solution) was added to the pipe-borne water to neutralize residual chlorine before transporting it to the laboratory [16]. The water samples collected from the field were transported in insulated boxes at 4^0C to the laboratory within six hours. In case of a delay, the water samples were stored in the refrigerator (2^0C to 8^0C) and processed the next day (within 24 hours).

Ethical statement

Prior to the initiation of this study, ethical approval was given from the Ghana Health Service Ethical Review Committee (GHS-ERC) under the approval number GHS-ERC 006/01/19. Community leaders granted initial permission, followed by written consent from

the household's head or representative, using a structured consent form. The informed consent form was explained to the participants in a dialect they could understand by a research assistant. The participants were provided with information regarding the study's purpose, rationale, selection process, procedures, and interview duration.

Those individuals who willingly agreed to take part in the study expressed their consent by either signing the consent forms or providing a thumbprint. A duplicate of the signed or thumb printed consent form was furnished to each participant. Participation in the study was entirely voluntary, with an assurance that participants could withdraw at any point with no consequences. Confidentiality of the gathered information was guaranteed to all participants.

Laboratory analysis

The water samples were analyzed in accordance with the American Public Health Association (APHA) standard methods for examining drinking and waste water using the membrane filtration method as described by Eaton, Clesceri [17]. In instances that the growth was heavy and uncountable (i.e. greater than 200 colony count), 10 ml, 1 ml, 0.1 ml, or 0.01 ml of the water was used and diluted with buffered peptone water to make up the 100 ml before filtration. The 0.45µm membrane filter was aseptically removed and placed in the respective appropriate media. The inoculated Plate Count Agar (PC) and Violet Red Bile (VRB) agar were incubated at 36^0C±1, while the Eosin Methylene Blue (EMB) agar and Thiosulfate-Citrate-Bile-Sucrose (TCBS) agar were incubated at 44^0C±1. The plates were observed after 24 hours and 48 hours. The plates for PC and VRB were counted and estimated respectively for the total viable count and total coliform. The EMB was estimated for faecal coliforms (thermotolerant coliforms) and TCBS for suspected *Vibrio* species.

Sub-culturing of colonies

The morphological characteristics of the colonies on the filter membrane were described. Colonies that appeared as; large, smooth, yellow, slightly flattened, and translucent peripheries on the TCBS medium were presumptively identified as *Vibrio species*. These colonies were sub-cultured onto another TCBS plate for purification. The suspected *Vibrio* colonies were further sub-cultured on Tryptone Soy Agar (TSA) (a non-selective media) for biochemical testing and serotyping. Other suspected coliform bacteria growing on the PC agar, VRB, EMB were sub-cultured on MacConkey agar plate for purification. Distinct colonies were sub-culture on TSA for presumptive identification and biochemical testing using the Mini Antigenic Profile Index 20 Enterobacteriaceae (API 20E) ((bioMérieux, France) for confirmation.

Quality control

All the containers used for the collection of water samples from the field were sterilized by autoclaving and checking with an autoclave tape to ensure sterilization.

All the bacteriological media were prepared in accordance with the manufacturer's instructions and dispensed into disposable pre-sterilized plastic Petri dishes. A sterility test was performed on each batch of media prepared by incubating a plate at 35 to 37^0C overnight (18 to 24 hours) and examined for any contamination.

A media performance test was also conducted by culturing in-house or reference bacteria strains obtained from the National Public Health and Reference Laboratory, Ghana to assess the growth characteristics of the media. The reference strains and in-house control strains were used as reference points to validate the results of the biochemical tests.

Blank membrane filtration was carried out after every fifth sample. This was to ensure growths on the filter membrane were not influenced by the laboratory conditions. The filtration techniques were carried out in a laminar flow hood to avoid contamination as much as possible.

Data processing and analysis

Result of the analysis of the water samples were entered into Microsoft Excel. It was exported into STATA software version 14.0 (State Cooperation, USA), cleaned and analyzed. Descriptive statistics such as means and standard deviation for continuous variables and frequencies and percentages for categorical variables were computed. Inferential statistics were applied to estimate the water parameters such as the total coliform, faecal coliform and vibrio counts. Kruskal Wallis rank test, a non-parametric equivalent of the Analysis of Variance (ANOVA) test was performed to determine whether there were any significant differences between the means of the log of bacteria counts among some selected factor variables.

Results

Assessment of the bacteriological quality of drinking water and cholera risk in Greater Accra Region

In the endemic communities, household drinking water stored in vessels was also analyzed in both seasons. Of the 216 water samples; 110 were private pipes, 23 were public pipes, and 83 were sachet water. High levels of total coliform counts (TCC) were observed in ten communities with a mean count of 7.73 log cfu/100ml and 9.86 log cfu/100ml respectively in the dry and wet seasons. The mean counts for faecal coliforms (FCC) were generally high

242 in the private pipe water sources in both seasons except in a few communities such as Agege
243 and Dansoman which did not record any counts. *Vibrio* counts (VC) were absent in the
244 private pipe water sources except in Mamprobi, which recorded 6.91 log cfu/100ml in the
245 wet season. The direct public pipe also had a high mean TCC of 7.82 log cfu/100ml in the
246 dry season and 9.64 log cfu/100ml in the wet season. The mean FCC was also found to be
247 5.24 log cfu/100ml and 10.06 log cfu/100ml respectively in the dry and wet seasons. No VC
248 was observed in the communities (Agbogbloshie and James Town) during both seasons.
249 The highest mean TCC and FCC in both seasons were found in stored public pipe water
250 compared to stored private pipe water and sachet water in the households. *Vibrio* counts
251 were present in all household stored drinking water samples (Table 1).

252

253 **Table 1: Mean log of bacterial counts in the dry and wet seasons across some selected background characteristics in endemic**
254 **communities**

Study variable	Characteristics	TCC (log cfu/ 100 ml)		FCC (log cfu /100 ml)		VC (log cfu /100 ml)	
		Dry	Wet	Dry	Wet	Dry	Wet
Direct water sources	**Community**	**Mean(sd)**	**Mean(sd)**	**Mean(sd)**	**Mean(sd)**	**Mean(sd)**	**Mean(sd)**
Private pipe	Adabraka	8.16	10.04	5.35	9.30	0	0
	Nungua	7.24	12.10	4.50	10.57	0	0
	Agege	8.07	8.85	0	0	0	0
	Chorkor	7.60	8.52	4.60	0	0	0
	Dansoman	7.74	9.39	0	0	0	0
	Kanehsie	8.16	10.93	0	6.91	0	0
	Mamobi	8.04	10.46	4.79	8.29	0	0
	Mamprobi	6.91	9.61	5.13	0	0	6.91
	Nima	7.60	8.52	4.79	8.52	0	0
	Teshie	7.74	10.20	4.50	10.13	0	0
	Total	**7.73(0.41)**	**9.86(0.36)**	**4.81(0.32)**	**8.95(1.34)**	**0**	**6.91**
Public pipe	Agbogbloshie	8.04	10.60	5.13	10.34	0	0
	James town	7.60	10.78	4.79	9.80	0	0
	Total	**7.82(0.31)**	**9.64(1.29)**	**5.24(0.65)**	**10.06(0.38)**	**0**	**0**
Water stored in vessels	Private pipe	8.26(0.38)	10.76(1.13)	5.53(0.45)	10.04(1.09)	2.40 (0.69)	9.91(1.15)
	Public pipe	8.49(0.37)	11.75(0.38)	5.80(0.44)	11.16(0.76)	1.77(0.88)	9.76(1.52)
	Sachet	8.45(0.39)	10.51(1.08)	5.60(0.41)	10.18(0.99)	2.29(0.71)	10.49(0.57)

When the differences between the mean rank score of the log of TCC (χ^2 =0.182, p=0.669), FCC (χ^2=2.591, p=0.107) and VC (χ^2=0.200, p=0.655) were assessed among the direct water sources in the endemic communities, there were no statistical differences as shown in Table 2. However, when the differences between the bacterial mean counts were assessed for the stored household drinking water, the mean rank score of the log of TCC (χ^2=7.704, p=0.021), FCC (χ^2 =2.591, p<0.001) and VC (χ^2=12.101, p=0.002) differed significantly (Table 2). The bacterial counts were generally higher in the wet season than the dry season during the period for both the water collected directly from the source and that stored in vessels in the households.

Table 2: Assessing the differences in log bacterial count among household drinking water stored in vessels and from direct water sources in endemic communities

	n	Rank Sum	χ^2 with ties	P-Value
Total coliform count				
Direct source			0.182	0.669
Private Pipe	4	55.50		
Public Pipe	20	244.50		
Water stored in vessels			7.704	0.021
Private Pipe Stored	110	12068.50		
Public Pipe Stored	23	3198.50		
Sachet water	83	8169		
Faecal coliform count				
Direct source			2.591	0.107
Private Pipe	4	70.50		
Public Pipe	20	229.50		
Water stored in vessels			17.156	**<0.001**
Private Pipe Stored	110	12170		
Public Pipe Stored	23	3532.50		
Sachet water	83	7733.50		
Vibrio count				
Direct source			0.200	0.655
Private Pipe	4	48		
Public Pipe	20	252		
Water stored in vessels			12.101	**0.002**
Private Pipe Stored	110	12094		
Public Pipe Stored	23	3289		
Sachet water	83	8053		

In the non-endemic communities also, 24-direct water sources were sampled from private pipe (4), public pipe (16), and unprotected wells (4) in both seasons (Table 3). The direct private piped water sources were found in Dawhenya and Kofikope and recorded a mean TCC of 8.57 log cfu/100ml in the dry season and 10.12 log cfu/100ml in the wet season. The mean FCC was 4.50 log cfu/100ml and 8.61 log cfu/ml in the dry and wet seasons respectively, with no recorded VC. The public pipe samples recorded a mean FCC of 8.44

log cfu/ml in the dry season and 9.64 log cfu/ml in the wet season. The mean FCC was 5.24 log cfu/100ml in the dry season and 9.39 log cfu/100ml in the wet season, although six of the communities (Dawa, Dogobom, Adedetsekope, Asigbeykope, Awhiam, Adjumanikope) did not record any feacal coliforms. Anyaman East community, on the other hand, recorded the highest TCC and FCC in both seasons. Except for Awhiam community that had a VC of 6.91 log cfu/100ml, all other communities did not record any counts. The unprotected wells also recorded a mean TCC of 8.61 log cfu/100ml in the dry season and 10.20 log cfu/100ml in the wet season. The mean FCC was 5.53 log cfu/100ml in the dry season and 9.45 log cfu/100ml in the wet season with a mean VC of 10.31 log cfu/100ml.

296 **Table 3: Mean log of bacterial counts in the dry and wet seasons across some selected background characteristics in non-endemic**
297 **communities**

Study variable	Characteristics	TCC (log cfu/ 100 ml)		FCC (log cfu /100 ml)		VC (log cfu /100 ml)	
		Dry	Wet	Dry	Wet	Dry	Wet
Direct water sources	**Community**	**Mean(sd)**	**Mean(sd)**	**Mean(sd)**	**Mean(sd)**	**Mean(sd)**	**Mean(sd)**
Private pipe	Dawhenya	8.48	10.09	0	8.70	0	0
	Kofikope	8.66	10.16	4.50	8.52	0	0
	Total	**8.57(0.13)**	**10.12(0.06)**	**4.50**	**8.61(0.13)**	**0**	**0**
Public pipe	Addokope	8.63	9.21	4.79	0	0	0
	Dawa	8.29	0	0	0	0	0
	Dogobom	8.34	8.00	0	0	0	0
	Adedetsekope	8.27	0	0	0	0	0
	Anyaman East	8.81	10.60	5.70	9.39	0	0
	Asigbeykope	8.57	0	0	0	0	0
	Awhiam	8.48	10.76	0	0	0	6.91
	Adjumanikope	8.16	0	0	0	0	0
	Total	**8.44(0.22)**	**9.64(1.29)**	**5.24(0.65)**	**9.39**	**0**	**6.91**
Unprotected Dug well	Angomya-Ada	8.41	11.00	5.67	9.80	0	10.31
	Kopeheum Kasseh	8.81	9.39	5.39	9.10	0	0
	Total	**8.61(0.28)**	**10.20(1.14)**	**5.53(0.19)**	**9.45(0.49)**	**0**	**10.31**
Water stored in vessels	Private pipe	8.92(0.26)	11.10(0.68)	6.16(0.36)	10.27(0.71)	1.84(0.62)	9.92(1.24)
	Public pipe	8.77(0.26)	10.45(1.13)	6.03(0.34)	9.59(1.08)	2.23(0.92)	9.73(1.08)
	Sachet	8.88	12.21	5.74	10.93	0	0
	Unprotected dug well	8.81(0.31)	11.16(0.61)	6.10(0.40)	10.39(0.77)	2.48(0.59)	11.19(0.78)
	Dam	9.05(0.23)	11.83(0.13)	6.44(0.23)	10.60(0.18)	2.91(0.77)	9.24(0.34)

The differences in the mean rank score between the log of FCC among the direct water sources were assessed and found to be statistically significant (χ^2 = 10.212, p=0.006). Whereas the mean rank score of the log of TCC and VC among the direct water sources did not differ (χ^2=5.171, p=0.075: χ^2=2.029, p=0.363) as shown in Table 4. Two hundred and sixteen (216) households stored drinking water in the non-endemic communities made up of 34 private piped water, 136 public pipe water, 36 unprotected dug well, 8 dam water and 2 sachet waters stored in the household. Except VC, which was not found in sachet water, TCC, FCC, and VC were generally present in all household water stored in vessels for the period. The bacterial counts in the stored water samples were higher than those collected from the direct water sources. The TCC and FCC were generally observed to be higher during the wet season than the dry season. The differences between the bacterial mean counts were assessed for the household drinking water stored and a statistically significant difference was found in the mean rank score of the log of TCC and FCC (χ^2=14.165, p=0.007: χ^2=33.901, p<0.001), whiles the mean rank scores for log of VC (χ^2=6.051, p=0.195) was not significant (Table 4).

Table 4: Assessing the differences in log bacterial count among household drinking water stored in vessels and from direct water sources in non-endemic communities

	n	Rank Sum	χ^2 with ties	P-Value
Total coliform count				
Direct source			5.171	0.075
Private pipe	4	67.50		
Public pipe	16	163		
Unprotected dug well	4	69.50		
Water stored in vessels			14.165	**0.007**
Unprotected dug well	36	4423.0		
Dam water	8	1189.5		
Private pipe	34	4357.5		
Public pipe	136	13168.0		
Sachet	2	298.0		
Faecal coliform count				
Direct source			10.212	**0.006**
Private pipe	4	63.50		
Public pipe	16	155.50		
Unprotected dug well	4	81		
Water stored in vessels			33.901	**<0.001**
Unprotected dug well	36	4972.0		
Dam	8	1257.5		
Private pipe	34	4743.0		
Public pipe	136	12205.5		
Sachet	2	258.0		
Vibrio count				
Direct source			2.029	0.363
Private pipe	4	46		
Public pipe	16	195.50		
Unprotected dug well	4	58.50		
Water stored in vessels			6.051	0.195
Unprotected dug well	36	4206.5		
Dam	8	1152.0		
Private pipe	34	3525.5		
Public pipe	135	14226.0		
Sachet	2	110.0		

Out of 120 household drinking water samples that were collected, in the endemic communities for each of the seasons, 76 (63.3%) and 82 (68.3%) positive growths were found respectively in the wet and dry seasons. In some of the water samples, multiple growths of the bacteria were found. Among the positive isolates, the predominant organism occurring in both seasons was *Klebsiella pneumoniae* 24 (31.6%) followed by *Escherichia*

coli 13 (17.1%). There were no confirmed *Vibrio cholerae* strains in the household drinking water samples in the endemic communities (Table 5).

Table 5: Microorganisms isolated from the household drinking water samples collected in the endemic communities

	Wet Season	
Organisms	**Frequency**	**Percent**
Acinetobacter baumanni/calcoaceticus	1	1.3
Citrobacter freundii	6	7.9
Enterococcus faecalis	1	1.3
Enterobacter sp	9	11.8
Enterococcus sp	3	4.0
Escherichia coli	13	17.1
Klebsiella pneumoniae	24	31.6
Proteus mirabilis	8	10.5
Proteus vulgaris	1	1.3
Pseudomonas aeruginosa	9	11.8
Serratia ficaria	1	1.3
Total	**76**	**100.0**
	Dry Season	
Acinetobacter baumanni/calcoaceticus	3	3.7
Citrobacter freundii	7	8.5
Enterobacter sp	11	13.4
Enterococcus sp	10	12.2
Escherichia coli	16	19.5
Klebsiella pneumoniae	23	28.1
Proteus mirabilis	7	8.5
Pseudomonas aeruginosa	5	6.1
Total	**82**	**100.0**

A hundred and twenty (120) drinking water samples were sampled from the non-endemic communities in each of the seasons (wet and dry). 104 (86.7%) isolates were identified during the wet season (Table 6). Of the 11 different bacteria identified in the wet season, *Escherichia coli* 18 (17.3%) was the most common isolate followed by *Klebsiella pneumoniae* 17 (16.4%). In the dry season, 88 (73.3%) had positive growth with *Klebsiella pneumoniae* (22.7%) as the most frequently occurring followed by *Escherichia coli* (18.2%). There were also multiple growths in some of the water samples. No *Vibrio cholerae* strains were isolated in the household drinking water samples.

Table 6: Microorganisms isolated from the household drinking water samples collected in the non-endemic communities

	Wet Season	
Organisms	**Frequency**	**Percent**
Acinetobacter baumanni/calcoaceticus	2	1.9
Citrobacter freundii	7	6.7
Enterobacter sp	13	12.5
Enterococcus sp	11	10.6
Escherichia coli	18	17.3
Klebsiella pneumoniae	17	16.4
Proteus mirabilis	15	14.4
Proteus vulgaris	2	1.9
Pseudomonas aeruginosa	16	15.4
Staphylococcus aureus	2	1.9
Yersinia pestis	1	1.0
Total	**104**	**100.0**
	Dry Season	
Aeromonas hydrophilia	2	2.3
Acinetobacter baumanni/calcoaceticus	1	1.1
Citrobacter freundii	7	8.0
Enterobacter sp	14	15.9
Enterococcus sp	10	11.4
Escherichia coli	16	18.2
Klebsiella pneumoniae	20	22.7
Proteus mirabilis	7	8.0
Pseudomonas aeruginosa	11	12.5
Total	**88**	**100.0**

Discussions

The bacteriological quality of water can be affected by the natural presence of microorganisms or from contamination by human activities, which could pose a risk to cholera and other diarrhoeal diseases [18]. In this study, we assessed the bacteriological quality in direct water sources and household drinking water storage.

In the cholera endemic communities, the water source collected for drinking was from a private pipe or public pipe. In the non-endemic communities on the other hand the water sources were from private, public and unprotected wells. This study demonstrated that the direct pipe, public pipe, unprotected well water sources collected from most of the

communities during the dry and wet season were contaminated with total and/or faecal coliform counts above the WHO and Ghana standards of zero (0) cfu/100 ml for drinking water both in the endemic and non-endemic communities, making them unwholesome for consumption [19, 20]. These findings are consistent with other studies that recorded high total and faecal coliform counts in directly collected piped and well water [21, 22]. The high bacterial counts in the piped water sources may be attributed to the practice of laying pipelines in gutters and the lack of maintenance of the pipelines. Inadequate chlorination may also account for these high bacterial counts as reported by Karikari and Ampofo [23] in an earlier study that revealed unsuitable chlorine levels and the presence of faecal coliform in the Accra water network. The difference in bacteria counts between the direct pipe and public taps in the endemic communities did not show any statistical significance, indicating that their contamination levels were similar.

The same was the bacteria counts in the non-endemic communities except faecal coliform counts that showed significant differences in private, public and unprotected well water. The private and public piped water are supplied by Ghana Water Company and may just reflect their service delivery that needs improvement to reduce the risk of cholera and diarrheal disease transmission. The unprotected wells may have run-off water contamination of the wells especially during the rainy season that might account for the high counts from the direct well water. This notwithstanding, the direct main public tap water in Dawa, Aedetsekope, Asigbeykope, and Adjumanikope did not record any coliform counts and was considered wholesome by the standards in the wet season. These communities have a community public standpipe located at a central point in the community and either connected to a borehole or directly to a high-level elevated tank, thus have few pipeline connections, unlike in the endemic communities where the public standpipes were connected to the general pipeline distribution and subject to more contamination.

With regards to seasonality, higher total and faecal coliform counts were generally observed in the wet season than in the dry season in both the endemic and non-endemic communities. This finding is in agreement with other studies that similarly found higher total and faecal coliform counts in the wet season than the dry season [24, 25]. This may occur because of the poor environmental conditions around some of these water sources in the communities.

In this study, the water stored for drinking by the households was also assessed for the level of contamination. This source water was collected and stored mostly in plastic containers and a few in earthenware/pot. The study results revealed that irrespective of the water source (a private pipe, public pipe, sachet water or well) the contamination levels for total and faecal coliforms were higher than that directly collected from the water source. In the endemic communities, our study found a significant difference between the bacterial contamination levels and the water sources stored in the household. This was similarly observed in the non-endemic communities, except the *Vibrio* count which did not show any significant differences with the water sources stored. This study is consistent with the findings of Meierhofer, Wietlisbach [26] in Kenya which found higher contamination levels in the storage containers. The reports of Boateng, Tia-Adjei [27] and Agensi, Tibyangye [28] in Tamale, Ghana and Kisoro, Uganda respectively, are similarly in line with this study findings. The cleanliness of the storage vessels, methods of drawing water from the storage container and the length of the storage were implicated for the high bacterial counts [9, 10]. This study findings also revealed that sachet water recorded similarly high levels of contamination with total and faecal coliforms as the private pipe and public tap water. Earlier studies in Ghana and Nigeria have variously indicated sachet water to be contaminated with faecal coliform and other pathogenic bacteria and not wholesome [29-31]. Semey, Dotse-Gborgbortsi [32] explained in their study that the contamination might be due to the unhygienic handling by factory workers during production. It may also occur

if the source water used in the packaging is already contaminated without any further treatment. Dzodzomenyo, Fink [33] have further indicated that some of the sachet water companies are not formally registered by the Food and Drug Authority and might be violating the guidelines of the standard for quality water production. It is therefore not surprising that Aslan, Rochani [29] study which examined the sachet bag observed some bags not to have a batch number, date of manufacture and no information on treatment. This is worrisome as the shift to drinking sachet water might not necessarily be protective against cholera.

Further analysis was conducted to confirm the suspected *Vibrio* isolates that were mostly detected in the household drinking water storage in both seasons. The most frequently isolated organisms in both seasons were *Escherichia coli* and *Klebsiella pneumoniae*. The presence of these organisms indicates the possibility of the presence of potentially harmful bacteria and a high risk of its transmission The suspected *Vibrio* counts observed were confirmed to be negative for *Vibrio cholerae,* instead were identified as *Pseudomonas aeruginosa, Proteus sp.* and *Aeromonas hydrophilia.* Our findings did not detect the presence of *V. cholerae* and contrasts that of Yirenya-Tawiah, Darkwa [15] that found *Vibrio cholerae* O1 strains in household drinking water storage in some communities in Accra just before the major cholera outbreak in 2014. The absence of *V. cholerae* in the current study could explain the reason for the absence of a cholera outbreak during the study period. The findings further strengthen the importance of regular environmental surveillance to predict cholera outbreaks.

Strength and limitation

The findings of this study indeed have significant implications for understanding household drinking water quality and its relationship with cholera transmission in the Greater Accra

Region. By examining the current state of water quality, the study provides valuable insights that can inform policymakers, public health authorities and other stakeholders in their efforts to combat cholera and improve overall water and sanitation practices in the region. However, the type of storage vessels used was not accounted for and could be a significant limitation. Different types of storage vessels may have varying levels of susceptibility to contamination, and this could impact the overall quality of the water. To address these limitations, future research or follow-up studies could consider incorporating the assessment of storage vessel types and their impact on water quality.

Conclusion and recommendations

The household drinking and direct water sources were contaminated with total and faecal coliform counts that exceeded the Ghana and WHO recommendation in both the endemic and non-endemic communities. The bacterial counts followed a seasonal pattern peaking during the wet season than the dry season, possibly resulting from contamination of water sources from run-off flood waters. *Escherichia coli* and *Klebsiella pneumoniae* were the most common coliforms recovered with no *V. cholerae strains* isolated from both the direct or stored household drinking water. The presence of these coliform bacteria gives an indication of faecal contamination and a high risk of waterborne diseases.

It is important therefore, to educate households members to treat their drinking water at the point-of-used to avoid drinking contaminated water and reduce the risk of transmission of cholera and other diarrhoeal pathogens. It is also important for the Ghana Standard Authority to regularly monitor the bacteriological quality of the sachet water manufacturing companies to ensure their operations conform to the quality standards.

Data availability

The raw data supporting the study could be made available by authors without any reservation.

Conflict of interest

The authors declare that they have no conflict of interest.

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