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BACTERIOLOGICAL QUALI TY OF HAND DUG WELLS IN MOSHIE ZONGO, KUMASI, GHANA

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Abstract

Water is life and good drinking water is good life. However, not all the populace of Ghana has access to treated piped water. The alternative sources of drinking water to piped water especially in deprived communities are hand dug wells, boreholes, dugouts and dams. However, the quality of these drinking water sources is questionable. Consequently, this study investigated wells in Moshie Zongo, Kumasi for indicator and pathogenic bacteria. Bacteria identifications were carried out according to standard techniques (Anon, 1992; American Public Health Association, 1995; Acumedia Manufacturers, 2011). The groups of bacteria identified in the sampled wells were total coliform, faecal coliform, E. coli and shigella spp. Total coliform counts ranged between 2.5x106 cfu/100 ml and 16.3x106 cfu/100 ml while faecal coliform counts ranged between 0.7x106cfu/100 ml and 13.2x106 cfu/100 ml. Also, E. coli and shigella spp. counts ranged from 0.87x104cfu/100 ml to 16.66x104 cfu/100 ml and from 0.4x105cfu/100 ml to 3.22x105cfu/100ml respectively. The presence of pathogenic bacteria in sampled wells is against the recommended standard by WHO for drinking water, therefore water from these wells were considered unsafe for drinking.

Keywords: Bacteriological, Wells, Total, faecal Coliforms, E. coli, shigella spp.

Introduction

Water has always been an important life-sustaining resource to humans. It facilitates metabolism and serves as a solvent for many bodily solutes (Akuffo *et al*., 2013). However, its availability in readily usable forms is limited (World Health Organization, 1997). Where piped water supply to households is inadequate, well water and other related sources of underground water are relied on. A well is a hole drilled into the ground to a certain depth in order to obtain water (Chunlong, 2007).

Wells, whether shallow or deep can be contaminated with pathogens. Impurities from the surface can easily reach wells with short outer casings/walls. Contamination of water supplies by pathogens needs to be avoided. A contaminated well can be a medium for the spread of various waterborne diseases (Wolf, Steinch & Wurm, 2015). About 2,500 people die each day in the world as a result of diarrheal diseases which result from the consumption of faecal contaminated water (WHO, 2002). Also, Larry (2006) reported that ground water contamination leads to the death of several people most of whom are children under 5 years.

In recent years, growing reports of pollutants in groundwater have drawn attention to its quality (Nkwachukwu *et al.,* 2013). The need to test for quality of groundwater is particularly important in areas that the inhabitants heavily rely on it. Such is the case of Moshie Zongo where irregular supply of water has created the need for reliance on well water. However, the nature and management of wells in Moshie Zongo, is appalling. A number of wells have been noted to be uncovered and some are surrounded with filth. These create sources of microbial contaminations. Microorganisms play a major role in water quality (Adetunde & Glover, 2010). Depending on the type and numbers, a given water source can be declared unsafe for human

consumption. It is therefore important to screen wells in Moshie Zongo, Kumasi for the presence of bacteria of public health concerns.

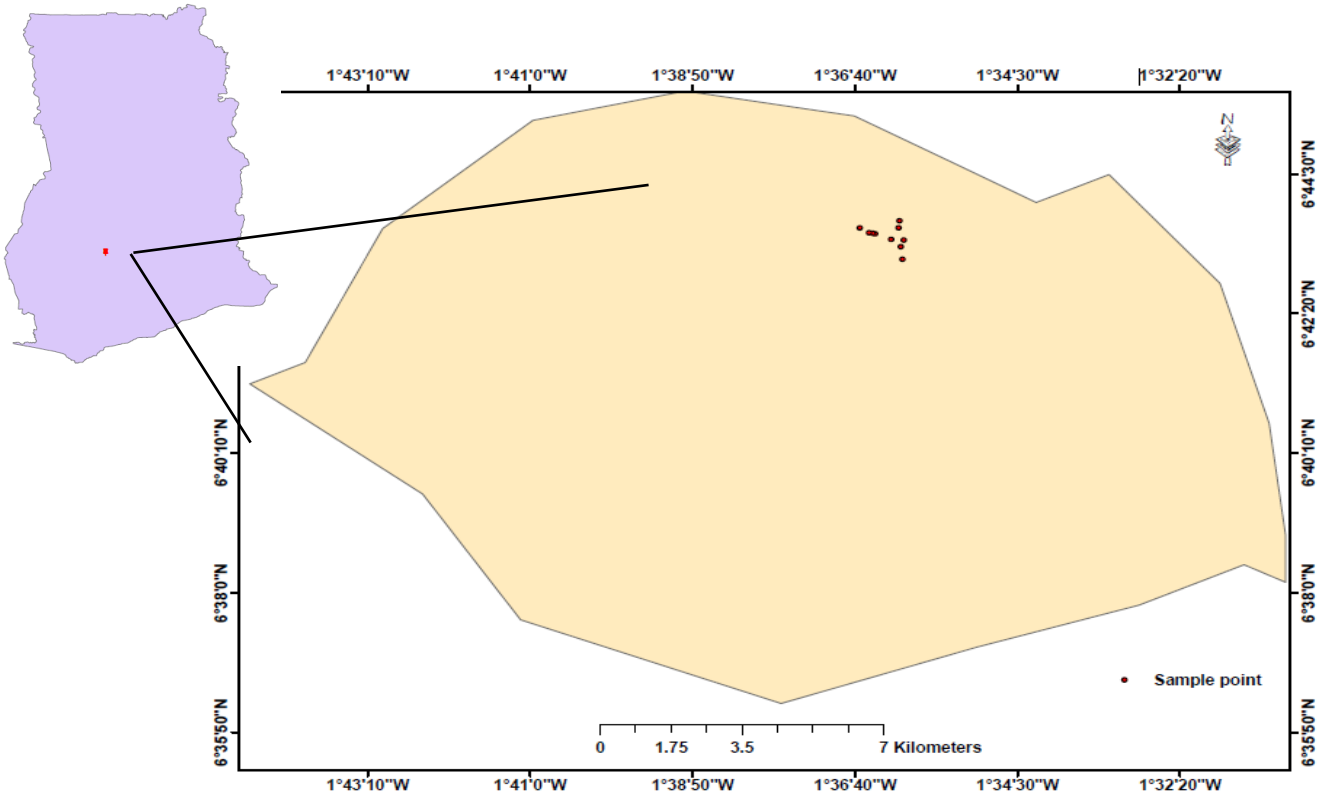
Materials and Methods

Study Community

The study was carried out in Moshie Zongo, Kumasi, Ghana. It is one of the urban communities, located in a densely-populated inner city neighbourhood with few social and infrastructural amenities (Alison, 2002). The Moshie Zongo community has parts of it in valleys and the entire community is bordered by three rivers (Boawini, Abrewa Nsuo and Turuba) (Alison, 2002). During rainy seasons the community is often cut off from the rest of the city due to flooding. The majority of the population are employed in the informal sector, with the women folk mostly into petty trading (Alison, 2002). The few in the formal sector of work are engaged as unskilled labourers, drivers or security men. The community is poorly served with sanitation facilities (Alison, 2002). Its piped water supply is irregular and prone to contamination, since some main pipelines in the community pass through a heavily contaminated stream. In common with other poor urban areas of Ghana, families of sizes between 10 and 23 people live in 'compound' houses and share sanitation facilities if any.

Sample collection

Ten (10) functional wells were sampled in this study. Sampling points (wells) were chosen based on convenience after the study area had been put into five zones according to the distribution of wells. Samples were collected in March, 2018 when water production from the selected wells were high and reliable. Also, this period was chosen because of the high likelihood of contamination of wells by runoff from rains. Water samples were collected according to the recommendations of American Public Health Association (1998) guidelines. Figure 1 below shows the locations of the various sampling point.



Source: author's own map. (March, 2018)

Figure 1. Sampling points

Description of wells.

Wells in the study area were described considering their depth, presence of a cover and distance from the nearest pollution source. According to Arjen van der Wal (2010), the minimum depth of a hand-dug well should be 35-meters but in the study area, only wells C and F (Table 1) had depths (36m and 38m respectively) which met this standard. Thus for the purposes of comparisons in this study, wells had to be re-classified taking a depth of 3 m and beyond as deep wells and less than 3 m as shallow wells (Table 1).

Table 1: Description of Wells

Well Label	Estimated Depth	Presence of cover/lid	Nearest Pollution source	Distance from pollution source
A	4m	Yes	drainage system	5m
B	2m	no	goat pen	4m
C	36m	Yes	septic tank	11m
D	5m	Yes	gutter	13m
E	4m	Yes	drainage system	3m
F	38m	no	drainage system	4m
G	6m	Yes	toilet facility	13m
H	2m	no	gutter	8m
I	4m	Yes	toilet facility	11m
J	7m	Yes	gutter	3m

Source: field work. (March, 2018)

Microbial Analysis

Total and faecal coliforms

Serial dilutions of 10^{-1} to 10^{-6} were prepared from water samples from wells. Aliquots (0.1 ml) from the highest dilutions were dispensed in 5 ml MacConkey Broth with inverted Durham tubes and incubated at 44^{o} C for faecal coliforms and 35^{o}C for total coliforms for 24 hours. After 24 hours, tube showing colour change from purple to yellow and the gas collected in the Durham tubes were considered positive for both faecal and total coliforms. The most probable number method was used to estimate the number of both total and faecal coliforms by adhering to standards of the method (Anon, 1992). Microbial numbers were reported in cfu/100 ml (Feng, Weagent & Grant, 2002).

Analysis for Possible Pathogenic bacteria

Escherichia coli

Water samples (10^{-1} to 10^{-4}) were inoculated aseptically on MacConkey sorbitol agar and incubated at 37 ^{o}C for 24 hours. Developed pink colonies were identified as *Escherichia coli* (American Public Health Association, 1995).

Shigella and Salmonella spp.

1 ml each of 10^{-1} to 10^{-5} serial dilutions of samples were picked aseptically and inoculated on solidified *Salmonella Shigella* agar at 30-35 ^{o}C for 24-48 hours. The growth of colourless colonies without black centres indicated the presence of *Shigella spp* (Acumedia Manufacturers, 2011), while the growth of colourless colonies with black centres gave an indication of the presence of salmonella spp.

Results

Identified bacteria in water samples

All water samples collected were contaminated with bacteria. The following groups of bacteria were identified in water samples; total coliforms, faecal coliforms, *Escherichia coli* and Shigella spp. Table 3 below presents the minimum, maximum and mean values in cfu/100 ml of isolated bacteria. The minimum bacteria count for the target bacteria ranged between 0.87 x 10^4 cfu/100 ml and 2.5 x 10^6 cfu/100 ml whereas the maximum counts for the target bacteria ranged between 16.66 x 10^4 cfu/100 ml and 16.3 x 10^6 cfu/100 ml.

Table 2: Bacteria estimates in water samples

Samples/wells	Total Coliform (cfu/100ml)x10^6	Faecal Coliform (cfu/100 ml)x10^6	*E. Coli* (cfu/100 ml)x10^4	Shigella spp. (cfu/100ml)x10^5
A	6.5	1.6	0.87	3.22
B	2.5	1.2	0.94	3.22
C	6.0	3.2	1.94	3.22
D	13.2	1.9	12.02	2.30
E	6.7	0.7	16.66	1.60
F	3.1	1.5	15.83	2.30
G	3.2	0.8	14.08	1.60
H	16.3	5.8	1.92	0.65
I	13.2	13.2	3.12	0.40
J	12.8	12.8	1.51	2.30
Mean	8.4	4.3	6.89	1.92
Min	2.5	0.7	0.87	0.4
Max	16.3	13.2	16.66	3.22
STDEV	4.76	4.59	6.46	0.95

Source: **Theoretical and Applied Biology laboratory, KNUST *(March, 2018).***

Sampling points A, B and C located in zone 1 and 2 recorded the highest *shigella spp*. counts (3.22 x 10^5 cfu/100 ml) followed by D, F and J in zone 2, 3 and 5 respectively (2.30 x 10^5 cfu/100 ml). The least *shigella spp*. counts were recorded in sample I in zone 5 with a value of 0.40 x 10^5 cfu/100 ml). On the other hand, the least *E. coli* counts were recorded in zone 1 (0.87 x 10^4 cfu/100 ml) at point A followed by zone 5 (3.12 x 10^4 cfu/100 ml) in sample J and the highest in sample E (16.66 x 10^4 cfu/100 ml) at zone 3. Zone 5 recorded the highest faecal coliform count from sample I (13.2x10^6 cfu/100 ml) followed by zone 4, at point H (5.8x10^6 cfu/100ml), zone 2 (3.2x10^6 cfu/100 ml) in sample C, zone 1 (1.6 x 10^6 cfu/100 ml) in sample A and the least recorded from E (0.7 x10^6 cfu/100 ml) at zone 3. In the case of total coliform, zone 4 (16.3 x 10^6 cfu/100 ml) in sample H had the highest count, followed by both zone 2 (13.2 x106 ^{cfu}/100 ml) and zone 5 (13.2 x 10^6 cfu/100 ml) at point D and I respectively. The least values recorded in both B and F at zone 1 (2.5 x 10^6 cfu/100 ml) and zone 3 (3.1 x $10^{6\ cfu}$/100 ml).

Microbial Contamination Levels between Deep and Shallow Wells

The highest microbial count recoded in deep wells was 13.3 x 10^6 cfu/100ml representing total coliform load. This was followed by faecal coliform (13.2 x 10^6 cfu/100ml), *Shigella spp*. (3.66 x 10^5 cfu/100ml) and *E. coli* (16.66 x 10^4 cfu/100ml) (Table 4). Amongst shallow wells, the highest bacteria count (16.3 x 10^6 cfu/100ml) was recorded for total coliform followed by faecal coliform (12.8 x 10^6 cfu/100ml), *Shigella spp*. (3.66 x 10^5 cfu/100ml) and *E. coli* (1.92 x 10^4 cfu/100ml) (Table 3).

Table 3: Bacteria counts across deep and shallow wells.

Deep well samples	Total coliform (cfu/100 ml)x10^6	Faecal Cliform (cfu/100 ml)x10^6	*E.Coli* (cfu1/00 ml)x10^4	Shigella spp. (cfu/100 ml)x10^5	Shallow well samples	Total coliform (cfu/100 ml)x10^6	Faecal Cliform (cfu/100 ml)x10^6	*E.Coli* (cfu1/00 ml)x10^4	Shigella spp. (cfu/100 ml)x10^5
A	6.5	1.6	0.85	3.22	**B**	2.5	1.2	0.94	3.22
C	6.0	3.2	1.94	3.22	**H**	16.3	5.8	1.92	0.65
D	12.2	1.9	12.02	2.30	**J**	12.8	12.8	1.51	2.30
E	6.7	0.7	16.66	1.60	**-**	-	-	-	-
F	3.1	1.5	15.83	2.30	**-**	-	-	-	-
G	3.2	0.8	14.08	1.60	**-**	-	-	-	-
I	13.2	13.2	3.12	0.40	**-**	-	-	-	-
Mean	7.43	3.27	9.23	2.09	**Mean**	10.53	6.6	1.46	2.06
Min	3.1	0.7	0.87	0.40	**Min**	2.5	1.2	0.94	0.65
Max	13.3	13.2	16.66	3.66	**Max**	16.3	12.8	1.92	3.22
P-v	0.945	0.384	0.027	0.922	**P-v**	0.945	0.384	0.027	0.922
STDV	0.070	0.071	0.048	0.099	**STDV**	0.103	0.129	0.276	0.23

Source: **Theoretical and Applied Biology laboratory, KNUST *(March, 2018).***

Bacteria contamination levels between covered and uncovered wells.

The highest bacterial count recorded from samples from uncovered wells was 16.3 x 10^6 cfu/100ml for total coliform followed by faecal coliform (12.8 x 10^6 cfu/100ml), *Shigella spp.* (3.66 x 10^4 cfu/100ml) and the least was *E. coli* with a value of 1.92 x 10^4 cfu/100 ml (Table 5). With reference to covered wells, the highest concentration (13.3 x 10^6 cfu/100ml) of bacteria was again recorded for total coliform count followed by faecal coliform (13.2 x 10^6 cfu/100ml), *Shigella spp*. (3.66 x 10^5 cfu/100ml) and *E. coli* (16.66 x 10^4 cfu/100ml) (Table 5).

Table 4: Bacteria counts across covered and uncovered wells

Cover well samples	Total coliform (cfu/100ml)x10^6	Faecal Cliform (cfu/100 ml)x10^6	*E.Coli* (cfu1/00 ml)x10^4	Shigella spp. (cfu/100 ml)x10^5	uncover well samples	Total coliform (cfu/100ml)x10^6	Faecal Cliform (cfu/100 ml)x10^6	*E.Coli* (cfu1/00 ml)x10^4	Shigella spp. (cfu/100 ml)x10^5
A	6.5	1.6	0.85	3.22	**B**	2.5	1.2	0.94	3.22
C	6.0	3.2	1.94	3.22	**F**	3.1	1.5	15.83	2.30
D	12.2	1.9	12.02	2.30	**H**	16.3	5.8	1.92	0.65
E	6.7	0.7	16.66	1.60	-	-	-	-	-
G	3.2	0.8	14.08	1.60	-	-	-	-	-
I	13.2	13.2	3.12	0.40		-	-	-	-
J	12.8	12.8	1.51	2.30		-	-	-	-
Mean	7.43	3.27	9.23	2.09		10.53	6.6	1.46	2.06
Min	3.1	0.7	0.87	0.40		2.5	1.2	0.94	0.65
Max	13.3	13.2	16.66	3.66		16.3	12.8	1.92	3.22
P-v	0.945	0.384	0.027	0.922		0.945	0.384	0.027	0.922
STDV	0.070	0.071	0.048	0.099		0.103	0.129	0.276	0.23

Source: **Theoretical and Applied Biology laboratory, KNUST *(March, 2018).***

Microbial contamination levels and proximity to pollution source

Sampling point H recorded the highest total colifo*rm* count (16.3 x 10^6 cfu/100 ml) and the least (2.5 x 10^6 cfu/100 ml) at B with distances of 8 m and 4 m from pollution sources respectively (Table 6). The least (0.7 x 10^6 cfu/100 ml) faecal coliform count was recorded from well E, at a point of 3 m from pollution source and the highest (13.2 x 10^6 cfu/100 ml) in sample I, which was was 11 m away from a pollution source (Table 6). Implying distance from the pollution source was not the determining factor in microbial contamination but the pollution source itself. The nearest pollution source to well E was a septic system while that to I was a toilet facility. *E. coli* counts were highest (16.66x10^4 cfu/100 ml) at point E and least (0.87x10^4 cfu/100 ml) at A, with distances of 3 m and 5 m away from pollution sources. Sampling points A, B and C recorded the highest *shigella spp*. concentration of 3.22 x 10^5 cfu/100 ml at distances of 5 m, 4 m and 11 m to pollution source respectively. The least was 0.40 x 10^5cfu/100 ml in sample I, also 11 m away from its pollution source (Table 6).

Table 5: Contaminated wells and its proximity to pollution sources

Samples/wells	Microbial contamination levels.				Proximity to pollution source	Pollution source
	Total coliform (cfu/100 ml)x 10^6	Faecal coliform (cfu/100 ml)x 10^6	*E. coli* (cfu/100 ml)x 10^4	Shigella spp. ml)x 10^5		
A	6.5	1.6	0.87	3.22	5 meters	Drainage
B	2.5	1.2	0.94	3.22	4 meters	Goat pen
C	6.0	3.2	1.94	3.22	11 meters	Septic tank
D	13.2	1.9	12.02	2.30	13 meters	Gutter
E	6.7	0.7	16.66	1.60	3 meters	Drainage
F	3.1	1.5	15.83	2.30	4 meters	Drainage
G	3.2	0.8	14.08	1.60	13 meters	Toilet
H	16.3	5.8	1.92	0.65	8 meters	Gutter
I	13.2	13.2	3.12	0.40	11 meters	Toilet
J	12.8	12.8	1.51	2.30	3 meters	Gutter

Source: Laboratory of Theoretical and Applied Biology laboratory, KNUST *(March, 2018).*

Discussions

Standard drinking water requires that no coliform bacteria be present in the water. Also, WHO (2011) specified a zero count for coliform bacteria per 100 ml sample of drinking water. Moreover, according to US Environmental Protection Agency Standards (1976), water samples in which coliforms are detected should be considered unacceptable for drinking as they are regarded as the principal indicators of water pollution (Nkwachukwu, *et. al.,* 2013). Consequently, wells sampled in this study could be deemed to be unsafe for drinking.

The groups of bacteria isolated from the well water samples implied that these wells were possibly suffering from faecal or sewage contamination, thus presenting conditions for the cause and spread of diseases. However, this study is not the first to report the presence of bacteria in well water in Ghana.

Abinah (2013) reported the presence of total and feacal coliform*s* in six hand-dug wells at Wamfie in the Dormaa East district of Brong Ahafo region, Ghana. Obiri-Danso *et al.* (2008) also reported of faecal coliform in wells closer to refuse dumps in various suburbs of the Kumasi Metropolis. Outside Ghana, Nkwachukwu *et al*. (2013) reported a 100% total coliform, 66.7% faecal coliform, 13.04% *E. coli*, 4.35% *shigella spp.* and 13.04% *salmonella spp*. in some water samples in Nigeria. The problem of microbial contamination of wells is a developing countries issue which needs sustainable solutions.

Several factors could account for the high bacteria counts in hand dug wells sampled in this study. Noticeable among them are the absence of covers on some wells and others too, the use of faulty covers. In situations where covers to wells do not fit very

well, gaps are left thus presenting routes for contaminations. Contaminations could also result from receptacles and ropes used in drawing water. At some wells (B, C and J) attached ropes and receptacles were left on the floor inviting animal contact and possible contamination from soil. Abinah (2013) reported similar observation in his work on six hand-dug wells at Wamfie in the Dormaa East district of Brong Ahafo region, Ghana. Another likely source of contamination is seepage of contaminants from pollution sources. Contamination of groundwater by pathogenic organisms is common in situations where wells are poorly constructed and failing septic tanks are nearby (Vendrell & Atiles, 2003; Osei, 2014). Geologically when wells are not suitably located, surface run-off, flow of leachate and other contaminants move to the water table to pollute it (Feng, *et al.*, 2002). The high counts of total coliform at point H was not surprising considering its close proximity to a septic tank. The associated consequence of such a situation is that, pathogens that may cause very serious intestinal illnesses may be present in the pollution source. These pathogens are generally considered a discomfort to health and could cause death to some susceptible groups such as children, the elderly and the infirm (Addo *et al.,* 2009; Olowe *et al.*, 2005).

Some other possible causes of contamination to wells in this study were poor construction and lack of maintenance. A number of wells (B, H, E and J) were not lined or grouted with concrete to their basements. Also, obvious cracks were found on wells E, J and E creating channels for filth to get into these wells. The observation that uncovered wells recorded higher contamination levels than covered wells was associated to the possibility that, the absence of protective lids created conditions for easy pollution by wind, humans and animals.

Conclusion

Wells studied in this research contained high microbial indicator counts in excess of WHO recommended guidelines for drinking water. Sampled hand dug wells also contained *Shigella spp*. and *E. coli* which are possible pathogens, consequently water from these wells could be defined as unsafe for drinking if any form of treatment is not considered before use.

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