SANITATION AND ITS IMPACT ON THE BACTERIOLOGICAL QUALITY OF WATER: A STUDY IN THREE COMMUNITIES IN GHANA

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ABSTRACT

Water constitutes about 70% of the earth's total mass and all life is dependent on water. Inadequate sanitation is a major cause of disease worldwide and improving sanitation is known to have a significant beneficial impact on health both in households and across communities. Water and sanitation are closely related and cannot be isolated. If uncontaminated water is available, reliable and convenient to collect, more water is consumed, both for hygienic purposes and for drinking which can improve health. In this study, the effect of sanitation on the bacteriological quality of water was evaluated. The study also assessed the sanitation facilities available in the three communities, the water facilities used and the bacterial contamination of household water. A cluster survey system was employed in three communities namely Tetegu, Mayera and Ashongman village in the Greater Accra Region of Ghana. Thirty households were clustered within each community. Within each household in each community, domestic water stored was analyzed for bacterial contamination using UriSelect 4 medium. This was used because it allows the isolation and counting of all organisms using a standard bacteriological loop plating method. Standardized questionnaires were administered in each household to ascertain the type of water and sanitation infrastructure. Seventy-seven percent and 87% of respondents relied on public standpipes in the Ashongman and Tetegu communities, respectively. Eighty-three percent of respondents in Mayera relied on the Nsaki river. Eighty percent of respondents used the KVIP at Mayera, 97% of respondents at Tetegu resorted to open defecation, and 57% of respondents also used the pit latrine at Ashongman community. A total of ten bacterial species namely: *Escherichia coli, Pseudomonas aeruginosa, Klebsiella pneumoniae, Enterococcus faecalis, Proteus mirabilis, Streptococcus agalactiae. Enterobacter cloacae, Staphylococcus saprophytic, Candida albicans* and *Staphylococcus aureus* were identified in domestic water stored. This study therefore recommends that policy makers must ensure the provision of basic infrastructure such as toilet facilities to reduce the likely contamination of water sources from poor sanitation facilities.

Key words: Sanitation, Coliform, Households, Water Quality

INTRODUCTION

Water constitutes about 70% of the earth's total mass and all life is dependent on water. The average adult consumes and excretes 10 cups of water daily. Adults should drink six to eight cups of water per day [1]. Water not only plays vital roles in the maintenance of the body's homeostasis but also serves as a very essential component of life, but water can be injurious if its source is not free from contaminations and impurities.

Along with differences in mineral composition, water contains different levels of microorganisms. Bacteriological tests are available to determine if water is bacteriologically safe for human consumption. Contaminated water plays an important role in the transmission of endopathogens, and there are usually strong desires at many levels of society for the provision of readily available, potable water [2].

Sanitation means different things to different people, but it generally refers to the provision of facilities and services for the safe disposal of human urine and faeces [3]. Inadequate sanitation is a major cause of disease worldwide and improving sanitation is known to have a significant beneficial impact on health. Improved sanitation involves access to sanitation facilities which allow for safe disposal of excreta. It is defined with respect to connection to a sewer or septic tank system, pour-flush latrine, simple pit or ventilated improved pit latrine [4]. The excreta disposal system is considered adequate if it is private or shared (but not public), and if excreta are hygienically separated from human contact [5]. Consequently, improved sanitation interventions in developing countries do not necessarily include treatment or re-use of waste water, and sewage either stays in the location or is discharged to the wider environment [6]. In fact, it is estimated that less than 10% of all sewage is treated worldwide before it is discharged into the receiving environment [7].

Sanitation is described as having access to facilities for the safe disposal of human waste (faeces and urine), as well as having the ability to maintain hygienic conditions, through services such as garbage collection, industrial/hazardous waste management, and wastewater treatment and disposal (http://who.int/topics/sanitation/en). Many developing countries cannot provide adequate sanitation for their populations, leaving many people at risk for diseases caused by unsafe drinking water and unsanitary living conditions. Throughout the world, there are 2.6 billion people living without basic sanitation, almost 40% of the world's population (http://esa.un.org/iys/health.shtml; www.census.gov/ipc). Inadequate waste disposal facilities can further drive the infection cycle of many agents that can be transmitted through contaminated soil, food, and water, such as soil-transmitted helminths, also called intestinal worms. Without proper sanitation facilities, waste from individuals infected with soil-transmitted helminths can contaminate a community's land and water, increasing the risk of infection for others. Proper waste disposal can slow the infection cycle of many disease-causing agents. Furthermore, sanitation facilities

should include soap, water, and a sink or an area for hand washing, to reduce the risk of disease transmission from contaminated hands.

In the less developed countries of the world, 80% of all ailments are attributed to inadequate supplies of water and sanitation facilities. This includes the effects of drinking contaminated water or water acting as a breeding ground for vectors of diseases [8].

In developing countries, it is not only water contaminated at source or during distribution that is an issue, but water stored within the home which may also become contaminated. For example, VanDerslice and Briscoe found 11 observational studies showing that mean coliform levels (an indicator of contamination) were considerably higher in household water containers than in the original source waters. In an experiment to determine whether faecal contamination of drinking water after collection was associated with household water handling and hygienic practices, Eschol *et al.* , observed that 92% of water samples tested at water supply points were adequately chlorinated, and bacterial contamination was found in two samples with no residual chlorine.

The study objectives were to find out the sanitation facilities available for use in the selected study areas, the water infrastructure used and the presence of bacteria in household source of water.

METHODOLOGY

Study Area
A cluster survey system was employed in three communities in the Greater Accra Region: Ashongman village (Ga East Municipality), Tetegu (Ga South Municipality) and Mayera (Ga West Municipality).

Ashongman village (5° 44' 17'' N 0° 11' 42° W) is a community in the Ga East Municipality and covers a land area of about 166 sq km (Figure 1). It is boarded on the west by the Ga West Municipality, on the east by the Tema Municipality, the South by Accra Metropolitan Area (AMA) and the North by the Akwapim South District in the Eastern Region. The population is concentrated mainly along the urban and the peri-urban areas of the municipality. The urban/peri-urban population constitutes about 73% with the remaining 27% residing in the rural portion towards the Akwapim hills. Ashongman village falls in the Savannah agro-ecological zone. Rainfall pattern is bi-modal with average annual temperature ranging between 25.1°C in August and 28.4°C in February and March.

Mayera (5° 029' -5° 048'N 0° 008' -0° 030'W) is a community in the Ga West Municipality (Figure 1). The Municipality occupies a land area of approximately 710.2 sq km. The community lies wholly in the Coastal Savanna Agro-ecological Zone. The Mayera community has a major river called the Nsaki River which serves

as a major source of water for most households in this community. There are about seventy households with an average of six persons per household.

Tetegu is also a community of the Ga South municipality (Figure 1). This is a newly created municipality which was part of Ga West municipality. Most of the inhabitants are farmers and fishermen.
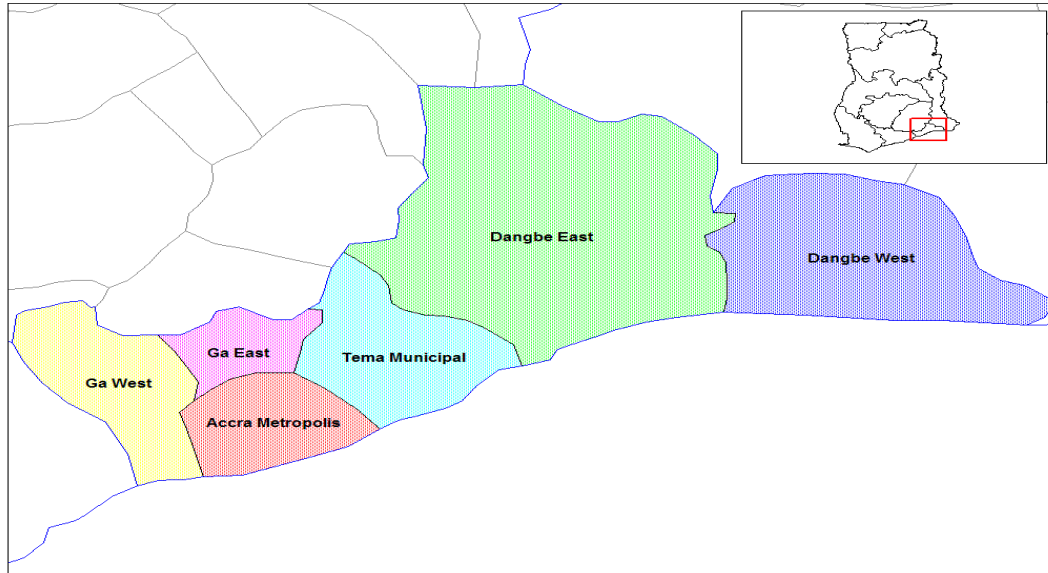
Figure 1: Map showing the study area

Sampling
Each selected community formed a cluster with 30 households, making 90 households from the three clusters. A household referred to individuals who occupy the same living space and normally share food and amenities. The households in each cluster were selected by a systematic sampling technique. The households were arranged serially and selection was based on a random number. Random procedure was then used to select the starting number. The researcher then picked every third household until the thirtieth household was reached.

Data collection and analysis
Standardized questionnaires were administered to the participating households for the collection of demographic information such as age, sex, type of water and toilet facilities used and the number of individuals in each household. Knowledge, attitude and practices concerning diarrhoeal diseases and soil-transmitted helminthic infections were also assessed. Analysis of questionnaires was done using Statistical Package for Social Scientists (SPSS) version 16. The domestic water stored at home in each household in all the three clusters was assessed for faecal contamination as well as other water quality measurements.

Water Quality Analysis

Water was collected from the various households in the three clusters and transported to the Bacteriology Department of the Noguchi Memorial Institute for Medical Research for bacteriological analysis of the water.

Bacteriological Analysis

Testing water for the presence of bacteria

Only qualitative analysis was done. The UriSelect 4 medium (Bio-Rad Laboratories) was used in the analysis of bacteria, because it allows the isolation and counting of all urinary tract organisms using a standard bacteriological loop plating method. It also allows for direct identification via demonstration of enzyme activities of the bacteria most often responsible for urinary tract infections, namely *Escherichia coli*, *Proteus* and enterococci.

The UriSelect 4 is a non-selective agar medium composed of:
- a rich nutrient base containing four peptones, which sustain growth of all urinary tract pathogens,
- two chromogenic substrates for detection of the bacterial enzymes β galactosidase and β glucosidase,
- tryptophan for detection of tryptophanase activity (indole production) and of tryptophan deaminase activity.

Preparation of the Medium

An amount of 56.8 g of the powder was weighed and suspended in one litre of distilled water, then stirred continuously for about 10 minutes until a homogenous suspension was obtained. It was then put in a water bath, and stirred frequently, until optimal dissolution of the agar. The medium was sterilized by autoclaving at 120°C for 15 minutes, and poured into the plates and incubated overnight at 37°C according to the Manufacturer's guide.

Plating of Medium with Water Samples

The water samples were vortexed to produce an even mixture and sterilized inoculating tube was used to pick up the water sample. The water samples were then inoculated onto the medium by the streaking method. It was then incubated at 37°C for 18 to 24 hours.

Identification of the Various Bacterial Species

After incubation for 18 to 24 hours at 37°C, the various bacteria present in the water samples were identified as follows:
- a pink colony formed represented the presence of *Escherichia coli;*
- orange-brown colonies represented *Proteus mirabilis*;
- *Enterococcus faecalis* were identified as turquoise blue colonies;
- blue-purple colonies represented *Klebsiella pneumoniae*;
- white colonies were identified as *Staphylococcus aureus.*

- the rest are *Enterobacter cloacae* (deep blue colonies), *Streptococcus agalactiae* (whitish brown colonies), *Candida albicans* (cream colonies) and *Staphylococcus saprophyticus* (deep brown colonies).

RESULTS

At the Mayera community, the sources of water for domestic use were borehole and a river. Out of 30 households sampled, 25 (83%) used the river as their water source. Fourteen (46%) out of the 25 households used the river because it was closer to them. Eight households (26%) stated that the river was far away while 3 households (10%) stated that the river was very close to them.

Four out of the 30 households (13%) sampled used both the borehole and the river. Two households stated that both the river and the borehole were closer to them whereas one respondent each stated that both facilities were very close and very far from them. Only one out of the 30 households sampled (3%) used only the borehole since it was closer to them (Table 1).

At the Tetegu community, the sources of water were public stand-pipe, river and dug well. Out of the 30 households sampled, 26 (86%) used the public stand-pipe. Twenty-two respondents (73%) who used the public stand-pipe stated that the public stand-pipe was closer to them. Three households (10%) stated that the public stand-pipe was very close to them whereas one household (3%) stated that the facility was very far away. Three households (10%) used the river and one household used the dug well (Table 1).

At the Ashongman community, the water sources were a public stand-pipe, borehole, rain water, dug well and a pond. The public stand-pipe was the most used water source. Twenty-three households out of the 30 sampled (76%) used the public stand-pipe. Nineteen households (63%) stated that the facility was closer to them. It was far away for one household (3%) whereas three households had the public stand-pipe very close to them. Only one respondent (3%) out of the 30 households used the rain water. Three households (10%) had dug wells and one household used the pond which was closer to them (Table 1).

Type of Toilet facilities used in the various communities
Most of the respondents from the Mayera community used Kumasi Ventilated Improved Pit (KVIP) as their main toilet facility. Respondents from 24 out of the 30 households sampled used the KVIP. Respondents from six households in this community used the Pit latrine (Table 2).

With only one respondent from one household out of the 30 households using water closet and the absence of public toilets at the Tetegu community, meant that most of the respondents resorted to open defecation. Respondents from 29 households resorted to open defecation in Tetegu.

Respondents from 17 out of 30 households at the Ashongman village used pit latrines, while respondents from 12 households resorted to open defecation and respondent from one household used a water closet at Ashongman community (Table 2).

**Presence of bacteria in household source of water**
A number of bacteria, most of which were coliforms, were present in both the community source of water and water stored at home (Figure 2). These bacteria included *Escherichia coli, Pseudomonas aeruginosa, Klebsiella pneumoniae, Enterococcus faecalis, Proteus mirabilis* and *Streptococcus agalactiae. Enterobacter cloacae, Staphylococcus saprophytic, Candida albicans* and *Staphylococcus aureus* were also found in the water.

At the Ashongman community, *Pseudomonas aeruginosa*, *Klebsiella pneumoniae* and *Staphylococcus aureus* were the commonest bacteria, being present in the water of 14 households. *Enterococcus faecalis* was found in 12 households. Ten households also recorded *Escherichia coli.* Other bacteria included *Proteus mirabilis* (present in seven households), *Streptococcus agalactiae* (present in three households), *Enterobacter cloacae* (present in two households) and *Staphylococcus saprophytic* (present in one household). In this community, nine households (30%) had two different bacteria present in their water. Seven households (23%) had three different bacteria present in their water. Six households (20%) had their water contaminated with four different coliforms. Seven households (23%) were infected with only one form of coliform. One household (3%) had more than one coliform present in their water.

At the Tetegu community, the commonest bacteria were *Staphylococcus aureus*, which was found in 19 households. *Enterococcus faecalis* was present in 14 households. *Escherichia coli*, *Pseudomonas aeruginosa* and *Klebsiella pneumoniae* were present in nine, seven and eleven households, respectively. *Proteus mirabilis* was present in the water of one household. In this same community, 14 households (47%) had only one type of coliform present in their water. Seven households (23%) had two different coliforms present in their water. Eight households (27%) had three different coliforms present in their water.

At the Mayera community, *Enterococcus faecalis* was found in the water of 15 households. This was followed closely by *Klebsiella pneumoniae* which was present in 13 households. *Escherichia coli*, *Pseudomonas aeruginosa* and *Proteus mirabilis* were present in seven, eight and four households, respectively. *Candida albicans* was also present in three households in this community. Thirteen households (43%) had only one type of coliform or the other present in their water. There were two different bacteria found in 13 households (43%). Two households (7%) had three different coliforms present. One household (3%) had more than four coliforms present in their water. However one household did not have any coliform present.
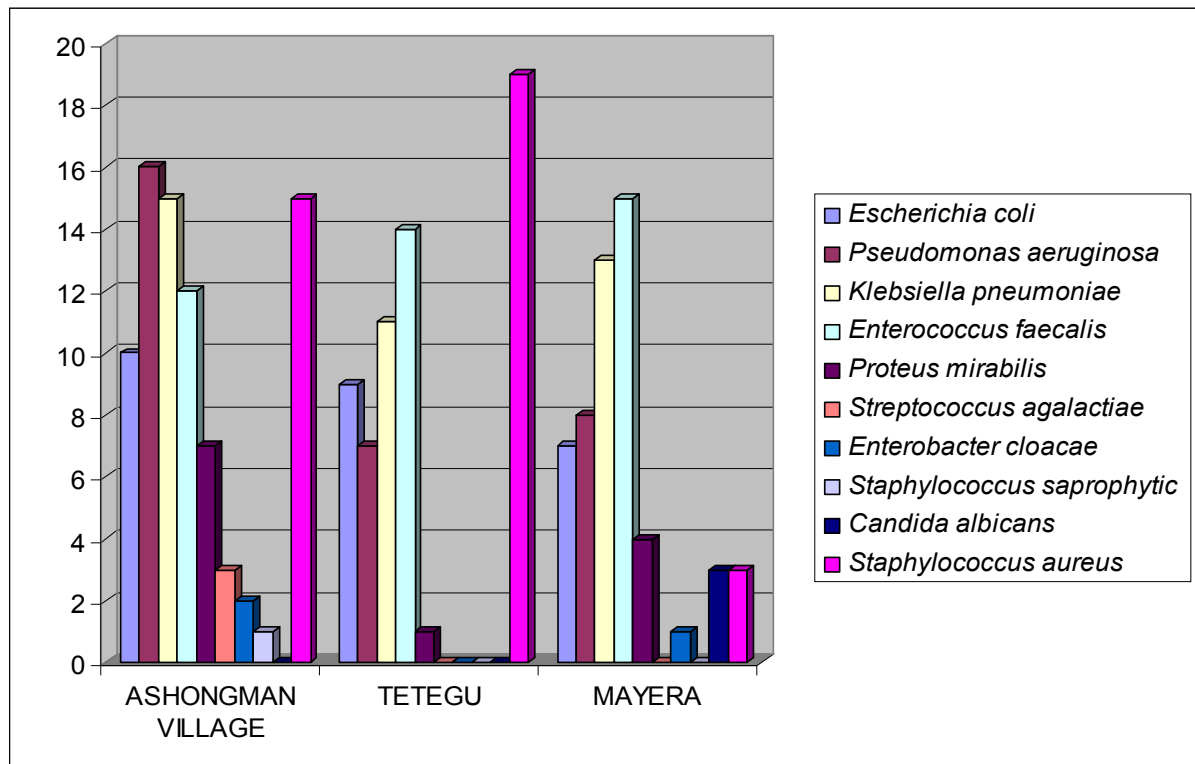
Figure 2: Different bacterial species found in the water of households of the three communities

DISCUSSION

The transmission of disease through drinking of faecally-contaminated water particularly in developing and under-developing countries has long been recognized and documented [9, 10].

Regular closure of the public stand-pipe used in the communities has necessitated the storage of water at home. It was realized that most households who stored their water in plastic containers without covers and those who used barrels had the highest number of coliforms present in their water, thus putting them at a higher risk of waterborne diseases.

In many parts of the developing world, drinking water is collected from unsafe surface sources outside the home and then is held in outside storage vessels. There has always been a problem with water storage at home. This is because there is the risk of microbiological contamination [11]. This was consistent with other studies in which a systematic meta-analysis of 22 studies measured bacteria counts for some water stored at home [12]. The conclusion was that half of the studies identified significant contamination after water collection. The issue with plastic containers without covers

and barrels is that contaminated hands could be a source, thus introducing bacteria into the water.

Another source for concern was that most of the households in all the three clusters did not treat their water before drinking. This is worrying because a test for the presence of bacteria in the communities' source of water revealed one bacterium or the other in the water. This supports point-of-use water treatment interventions which could reduce diarrhoea. A study observed that point-of-use treatment of water decreased diarrhoea morbidity by 39% [3]. Boiling and chlorination are two means of treating water before use.

Isolation and enumeration of specific pathogens in water are often not feasible or very precise; thus the commonest measure of faecal contamination is derived from the use of indicator bacteria. There have been studies using such indicator species that have demonstrated the faecal contamination of drinking water sources in both developed and the developing world [13]. Drinking water may be contaminated at source or during storage. For disinfected water supplies, there should be no coliforms (especially faecal coliforms) present in drinking water as required by WHO's Water Quality Guidelines [14].

A total of 10 bacterial species: *Escherichia coli, Pseudomonas aeruginosa, Klebsiella pneumoniae, Enterococcus faecalis, Proteus mirabilis, Streptococcus agalactiae, Enterobacter cloacae, Staphylococcus saprophytic, Candida albicans* and *Staphylococcus aureus* were identified in drinking water samples stored at home. This is consistent with other studies done in Western Nigeria where *Escherichia coli, Pseudomonas aeruginosa, Klebsiella pneumonia, Staphylococcus aureus, Proteus vulgaris* and *Aeromonas sp.* were identified in sachet-packaged drinking water [15].

The presence of these bacteria (both total and faecal coliforms) does not point to the occurrence of water borne diseases. Coliforms are not by themselves harmful. Total coliforms proliferate naturally in the environment- in the soil or on vegetation. However, their presence in water suggests that other pathogenic organisms such as *Vibrio cholerae*, *Salmonella typhi* and *Shigella* may be present in the drinking water supply [14]. Bacteria were found in both the community's source of water and the water stored at home. At the Ashongman village, the main source of water for drinking was the public stand-pipe. *Enterococcus faecalis* and *Pseudomonas aeruginosa* were found in the public stand-pipe. *Pseudomonas aeruginosa* thrives at warm temperatures and can be found naturally in the ground and in drinking water sources such as aquifers. However, *Pseudomonas aeruginosa* is often not completely eliminated with proper disinfection and pH control. Its presence is therefore an early indication of breakdown of the disinfection process due to its increased resistance [15]. This may explain why *Pseudomonas aeruginosa* was recorded in high numbers in this study. Most households in this community also had these bacteria in their water.

Additionally, 10 households recorded *Escherichia coli* in their stored water. This was not originally found in the public stand-pipe. *Escherichia coli* and *Klebsiella pneumoniae* are not often found in chlorinated main water supplies but are often found in unchlorinated private water supplies and stored water.

At the Tetegu community, most people also relied on the public stand-pipe for their domestic activities. Regular closure of the public stand-pipe has necessitated the storage of water at home for up to 48 hours. The public stand-pipe was also found to contain *Staphylococcus aureus.* However, seven other bacteria were found in the water stored at home. This may suggest that the drinking water quality in the community has been compromised due to poor sanitation and unawareness about the impact of poor personal hygienic practices. As many as 29 households (97%) did not have proper sanitation facilities and resorted to open defecation. This has led to a high faecal-oral load in the environment.

The coliforms may find their way into drinking water by heavy rainfall which could seep into the surface water. They may also occur through surface run-off and domestic and agricultural effluents. Also, the practice of good hygiene is a concern in this community. As many as 12 households (40%) did not wash their hands with soap after defecation. These households recorded higher amounts of bacteria in their water.

CONCLUSION

Access to basic sanitation and safe drinking water remains a challenge in Tetegu, Mayera and Ashongman communities in Ghana. Seventy-seven percent and 87% of respondents relied on public standpipes in the Ashongman and Tetegu communities, respectively. Eighty-three percent of respondents in Mayera relied on the Nsaki river. Eighty percent of respondents used the KVIP at Mayera, 97% of respondents at Tetegu resorted to open defecation, and 57% of respondents also used the pit latrine at Ashongman community.

All the households had one form of coliform or the other present in their source of water. The presence of faecal coliform may not be directly harmful, however it indicates an increased possibility of harmful pathogens in the water.

ACKNOWLEDGMENT

Table 1: **Type of water facility used by the various communities and the respective distances**

Community	Water Facility used			Very close	Close	Far away	Total
Mayera	Water Facility used	Bore Hole	Count	0	1	0	1
			% of Total	0.0%	3.3%	0.0%	3.3%
		River	Count	3	14	8	25
			% of Total	10.0%	46.7%	26.7%	83.3%
		River & Borehole	Count	1	2	1	4
			% of Total	3.3%	6.7%	3.3%	13.3%
	Total		Count	4	17	9	30
			% of Total	13.3%	56.7%	30.0%	100.0%
Tetegu	Water Facility used	Public Pipe	Count	3	22	1	26
			% of Total	10.0%	73.3%	3.3%	86.7%
		River	Count	0	3	0	3
			% of Total	0.0%	10.0%	0.0%	10.0%
		Dug well	Count	0	1	0	1
			% of Total	0.0%	3.3%	0.0%	3.3%
	Total		Count	3	26	1	30
			% of Total	10.0%	86.7%	3.3%	100.0%
Ashongman Village	Water Facility used	Public Pipe	Count	3	19	1	23
			% of Total	10.0%	63.3%	3.3%	76.7%
		Bore Hole	Count	0	2	0	2
			% of Total	0.0%	6.7%	0.0%	6.7%
		Rain water	Count	1	0	0	1
			% of Total	3.3%	0.0%	0.0%	3.3%
		Dug well	Count	0	3	0	3
			% of Total	0.0%	10.0%	0.0%	10.0%
		Pond	Count	0	1	0	1
			% of Total	0.0%	3.3%	0.0%	3.3%
	Total		Count	4	25	1	30
			% of Total	13.3%	83.3%	3.3%	100.0%

Table 2: Type of Toilet facilities used in the various communities

			Toilet facility used				Total
			Pit Latrine	KVIP	Water closet	Open defecation	
Community	Mayera	Count	6	24	0	0	30
		% of Total	6.7%	26.7%	0.0%	0.0%	33.3%
	Tetegu	Count	0	0	1	29	30
		% of Total	0.0%	0.0%	1.1%	32.2%	33.3%
	Ashongman Village	Count	17	0	1	12	30
		% of Total	18.9%	0.0%	1.1%	13.3%	33.3%
Total		Count	23	24	2	41	90
		% of Total	25.6%	26.7%	2.2%	45.6%	100.0%

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