Bacteriological safety of water analysis

Comparison of bacteriological safety of water at collection points and drinking water at household level in Kizungu slum Mbarara municipality

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Abstract

Background:

Efforts have been made to provide safe water to the public through construction of safe water sources in communities together with widespread sensitization on the practice of boiling of drinking water. Despite those efforts, there is still frequent consumption of contaminated water that has caused a persistently high prevalence of water related illnesses. We hypothesized that the safety of water from safe water sources can be maintained up to consumption at household level. This study compared the bacteriological safety of water at collection points and drinking water at household level in Kizungu slum Mbarara municipality

Materials and methods: We conducted a cross-sectional study. We collected samples from water sources used by respondents and from their domestic drinking water. Samples were analyzed in the Microbiology laboratory . Petrifilms were used to enumerate coliform bacteria in water.

Results: A total of 60 drinking water samples were analyzed. Although most households (88. 3%) reported to have boiled drinking water, 21. 7% of drinking water samples were positive for E. coli. A total of 24 water sources

were analyzed, 22 of which were taps whilst 2 were open wells. Of the 22 tap samples, 22% were positive for total coliforms. Both well samples were positive for E. coli with numbers over 1100cfu/100ml.

Conclusion: Health benefits of providing access to improved water sources to communities can be threatened by significant re-contamination at household level. Strategies to address the sources of recontamination of clean water at household level need to be strengthened. Continued education pertaining good household sanitary practices urgently requires re- addressing.

Key words: Bacteria, contamination, water sources, drinking water, Mbarara

Background

Water is the most essential component of human health, food security, economic growth and environmental sustainability. Although water is essential for life, it can and does transmit pathogens that are a major of 2. 2 million diarrheal disease deaths occurring annually [1]. Diarrheal disease remains one of the leading killers of children around the world, responsible for the deaths of nearly 1. 6 million children annually, yet is no longer considered a global health priority [2]. In developing countries, as much of 80% of illnesses are linked to poor water and sanitation conditions [2]. The government of Uganda together with several Non-Government Organizations (NGOs) has made efforts to provide safe water to the public through construction of safe water sources together with widespread sensitization on the practice of boiling of drinking water. 2012 statistics shows a 64% access to safe water in rural settings and a 68% access to safe water in urban settings [4]. Despite all the above efforts, there is still frequent consumption

of contaminated water that has caused a persistently high prevalence of water related illnesses [3]. Improving the quality of drinking-water is a powerful environmental determinant of health. It continues to be the foundation for the prevention and control of waterborne diseases [4]. We hypothesized that the safety of water from safe water sources can be maintained up to consumption at household level. We conducted a cross sectional study to compare the bacteriological contamination of water at collection points and drinking water at household level.

Methods

We conducted a cross-sectional study that involved both quantitative and qualitative methods of data collection. Upon approval from the university Institutional Review Board, consenting adult household members aged 18 years or abovein Kizungu, Kakoba division, Mbarara municipality, were enrolled in the study between June and July 2013. Questionnaires were administered through face-to-face interviews and data collected on handling practices of drinking water. They included; boiling drinking water, source of water and storage. Domestic water sources and drinking water were subsequently sampled and microbiologically analyzed.

Sampling was systematic. The study area was divided into five cells; Market cell, Central cell, Upper cell, Agip cell and Kabateraine cell. The sample size was then divided amongst the five cells to obtain the number of household to participate in each cell. These were selected as follows; two main streets in a cell were randomly picked and from these, 15 plots were picked. One household out of the 15 plots was selected to participate. The 15 households

were selected as follows: starting from the extreme end of the selected street and walking across one street towards another in more or less a straight line, one plot on the straight line was selected until the sample of 15 was reached. From each of these plots, the first household that had an eligible respondent was enrolled in the study.

From each selected household’s drinking water was sampled 100ml. Each participating household was asked for their source of water and a water sample was taken from this source so long as it had not already been taken. Water samples were aseptically collected using sterile containers. The samples were transported within 2 hours of collection in a cool box containing ice packs to a microbiology laboratory. Sample collection was in accordance to the standard procedures as documented by Monica, 2006 [5].

Petrifilms were used for the analysis. From 100ml of each sample was pipetted 1ml. Lifting up the cover sheet on the plate, the pipetted volume was gently release onto the center of the pink circle of the petrifilm. Slowly, the top cover was rolled back down onto the sample, which spread it. The inoculated petrifilms were incubated at $37\ ^{0}$ C for 24 hours to allow any bacteria that might have been present in the inoculum to grow and form visible colonies. The colonies associated with gas bubbles on each petrifilm were counted and the obtained figure multiplied by 100 to obtain a coliform count per 100ml.

Analysis of data was descriptive involving determination of frequencies, and presentation in form of statistical tables. Statistical Package for Social

Scientists (SPSS) was used to analyze the data. Results were interpreted using WHO Guidelines for Drinking water quality assessment [6, 4].

Results

A total of 60 household were included in the study. From each of these households, an adult was interviewed. Of the 60 respondents, 6 were males whereas 54 were females. The mean number of members in each household was 4.

Source of Domestic Water

A total of 24 sources were sampled. Of these, 22 were from taps whereas 2 were from shallow wells (defined as a hand-dug well). One of the wells was located just close to a kraal with cattle excreta flowing into the well. In most circumstances, residents of a plot shared one water source. In a few cases, several plots shared a water point.

Water analysis

Sources

Analyses of water sources revealed that, of the 22 tap samples, 5 (22%) were positive for total coliforms with minimum and maximum number of coliforms being, 100cfu/100ml and 700cfu/100ml respectively. Both well samples were positive for E. coli with numbers over 1100cfu/100ml (Table 1).

Table 1: Bacteriological analysis of water sources in Kizungu slum Mbarara Municipality

May-June, 2014 (n= 22)

	Water Sources	
Type of Organisms	Tap No (%)	Well No (%)
Total coliforms	5 (22)	2 (100)
E. Coli	0 (0)	2 (100)
Had no any kind of bacteria	17 (78)	0 (0)

Drinking water

A total of 60 samples were analyzed. Of these, 21. 7% were positive for E. coli with minimum and maximum number of coliforms being, 100cfu/100ml and 3400cfu/100ml respectively (Table 2).

Treatment and storage of drinking water

Of the 60 households interviewed, majority (88. 3%) boiled drinking water. Majority, 86. 7% used charcoal as a fuel for boiling. 76. 7% stored drinking water in jerry cans. Regarding storage conditions, majority (85%) stored water at room temperature. Of the 60 participants, 20% reported to have had an episode of diarrhea in the past 3 months.

Table 2: Bacteriological analysis of drinking water in households of Kizungu slum Mbarara Municipality

May-June, 2014 (n= 22)

Type of Organisms	No (%)
Total coliforms	44 (73)
E. Coli	13 (21. 7)
Had no any kind of bacteria	3 (5)

Discussion

In this study, we found that the quality of water from sources significantly depreciates at household level, with only a few water sources fecally

contaminated compared to close to a quarter of drinking water sampled from 60 households that were feacally contaminated. These results are consistent with other large studies [7, 8, 9, 10], whose findings also indicated that contamination increased along the water chain starting from the source to stored drinking water. Tragically, our results show that interventions aiming to improve the safety of drinking water to household level such as boiling have had lee impact in the urban poor. Target 7. C of the Millennium Development Goal 7 aimed at halving the proportion of people without access to improved sources of water. Although this has been achieved [11] [11], our findings have reavealed threats to the health benefits of that achievement since even with access to these safe sources, re-contamination an occur at household level. The fact that drinking water in developing countries requires subsequent storage after boiling still poses a risk on the microbiological quality of drinking water due to unsanitary handling in households.

We also observed that close to a quarter of water taps sampled were contaminated with other indicator bacteria. This emphasizes the fact that even piped water can be potentially contaminated during distribution [12] [13][12]. Total coliforms are present in both fecal and non-fecal environments hence are not useful as an index of fecal pathogens. However, there presence can be used to assess the cleanliness and integrity of distribution systems, potential presence of biofilms and as indicators of contamination through ingress of foreign material, including soil or plants. Detection of total coliform in the distribution system, but absent in water

leaving the treatment plant is indicative of a likelihood of bacterial regrowth or post-treatment contamination [13, 6].

Our data showed that all the 2 open wells sampled were heavily contaminated. One of the wells was located close to a kraal. Rains often wash off disposed excreta into open wells which may also have also contributed to the heavy contamination of these open wells with fecal matter. This is in agreement with results of survey of bacteriological quality of drinking water in North Gondar [14]

Our study however did not infer the cause of the contamination at household level neither did it isolate contaminants. Nevertheless, the analytical method we used isolated *Escherichia coli* , an indicator organism of choice for faecal pollution [6]

In conclusion, our results show that health benefits of providing access to improved water sources to communities can be threatened by significant re-contamination at household level. Strategies to address the sources of recontamination of clean water at household level need to be strengthened. Continued education pertaining good household sanitary practices urgently requires re- addressing.

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