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Bacteriological quality of drinking water obtained from main sources, reservoirs and consumers' tap in Arba Minch town, Southern Ethiopia

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The most common and wide spread health risk associated with drinking water is microbial contamination. The aim of this study is to assess microbial contamination of drinking water, starting from source to distribution systems. Water samples from the Arba Minch town of Southern Ethiopia were collected randomly from the main source before chlorination, reservoir after chlorination and from different points of distribution lines. Total coliforms, fecal coliforms and heterotrophic plate count (HPC) were determined from collected water samples. Coliforms were analyzed by using the most probable number (MPN) method. About 93.3% of collected water samples were contaminated with total coliforms and 16.7% of distributed tap water was contaminated with fecal coliforms. Most of the analyzed water samples had high number of viable bacteria or HPC (>5 log), and total coliforms. The HPC ranged from 1.9 log of bacteria in the chlorinated water in reservoir tank to 8.44 log in the source water before chlorination. Overall, the quality of drinking water suggests that the distribution lines are the most likely point of microbial contamination. Therefore, regular bacteriological monitoring and maintaining residual chlorine in distribution system is mandatory.

Key words: Coliforms, drinking water, heterotrophic plate count, microbiological point of contamination.

INTRODUCTION

Water contamination is the most common and widespread health risk in developing countries. About 663 million people in the world lacked contaminants-free drinking water sources according to UNICEF and WHO (2015)

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reports. According to the report, Ethiopia is one of the countries that have met the millennium development goal drinking water target (UNICEF and WHO, 2015). In the protection of drinking water, identification of the point of contamination is very important. The health and well-being of a population is directly affected by the coverage of water supply and sanitation.

The impact of poor water quality on the transmission of communicable diseases is well established (Usman et al., 2016; Schlipköter and Flahault, 2010). The main problem associated with ingestion of water is microbial risk due to water contamination by human and animal feces. Some of the microorganisms found in water may cause diseases, thereby questioning its safety. Drinking such contaminated water or using it in food preparation may lead to new cases of infection. Many common and wide spread health risks have been found to be in association with drinking water in developing countries (Suthar et al., 2009). Furthermore, in developing countries, unsafe water, poor sanitation and hygiene problem have been reported to rank third among twenty leading risk factors for health burden (WHO, 2003).

Most of the population of Ethiopia does not have access to safe and reliable sanitation facilities. On top of these, majority of the households do not have sufficient understanding of hygienic practices regarding water and personal hygiene. As a result, over 75% of the health problems in Ethiopia are communicable diseases which resulted from having unsafe and inadequate water supply, and unhygienic waste management, particularly human excreta (WWAP, 2004). About three-quarter of health problems in children in the country is communicable disease arising from poor water supply and sanitation, most of which is associated with microbial contamination of drinking water (Kumie and Ali, 2005). In a study conducted in northern part of Ethiopia, about 46% of mortality in children of less than five year was due to diarrhea mainly related to unsafe drinking water (Asmassu et al., 2004).

The microbial quality of drinking water attracted great attention worldwide because of implied public health effects (Abdelrahman and Eltahir, 2011). The effective way of assessing water safety is by using water quality indicators microbes. The fecal indicator bacterium has been considered as biological indicators of drinking water for a long period of time (Enriquez et al., 2001). Detection of bacterial indictors in drinking water shows the presence of pathogenic organisms that are the source of water borne diseases which could be fatal. The point of contamination can vary depending on the water treatment condition and residual chlorine concentration in distribution lines (Amenu et al., 2013). Thus, water quality problem can be assessed by identifying indicator organism that shows existence of water contamination. Limited studies have been carried out to assess the point of microbial contamination of drinking water in southern part of Ethiopia. Therefore, this study was conducted to assess the microbial contamination of drinking water, starting from point source to distribution systems.

MATERIALS AND METHODS

Study design and setting

A cross sectional study was conducted to assess bacteriological quality of drinking water obtained from main sources, reservoirs and consumers' tap in Arba Minch town, Southern Ethiopia. Arba Minch is the capital town of the Gamo Gofa zone, located 500 km south of Addis Ababa in southern Ethiopia. It is situated in the great African rift valley with an elevation of 1285 m above sea level. The total area of the town is estimated to be about 1095 hectares. Its temperature is about 29°C and the average rain fall is 900 mm. The drinking water source of the Arba Minch town is from forty spring sources. The drinking water in the study area is treated by chlorination.

Sample collection and sampling point

Samples were collected from fifteen different locations grouped into three types of water sources. Twelve tap water samples were collected from different sites of distribution system (customer taps), one from reservoir just after chlorination, two water samples from spring water as initial source before chlorination. The method of sample collection was according to WHO (2008) guidelines for sample collection for drinking water quality assessment. Samples were collected aseptically from each sampling site in sterile bottles with capacity of 250 mL and transported to the laboratory in ice box and the samples were analyzed within two hours of collection. For the chlorinated water samples, about 2.5 mL of 10 mg/mL sodium thiosulphate was added into each sampling bottle to stop the chlorination process during transportation. Microbiological analysis of water sample was done as soon as possible after collection to avoid unpredictable changes in the microbial population (WHO, 2008).

Microbial analysis

Water samples were analyzed for heterotrophic plate count (HPC), total coliforms and fecal coliforms. The HPC which aims to count all microorganisms that is capable of growing on nutrient agar was performed by using serial diluted water sample from 10^{-1} to 10^{-6} dilution level. Then, 1 mL of each diluted water sample was inoculated on nutrient agar using pour plate method and incubated at 37°C for 24 h. The bacterial count was done and expressed as colony forming units (CFU) per mL (APHA, 1992).

Coliforms were enumerated by the most probable number (MPN) techniques using sets of three tubes inoculated with 10 mL of MacConkey broth (Oxoid®) with 1 mL of serial diluted at 1, 0.1 and 0.01 mL. The water analyses were carried out in two stages. The first test is presumptive test and it is performed by inoculating the three level diluted samples in tubes which contain the MacConkey broth and incubated at 37°C for 48h. After the period of incubation, the inoculums were examined for gas formation by inspecting displacement of liquid media by air in Durham's tubes. The first reading was taken after 24 h to record positive tubes, and negative tubes were incubated for another 24 h. Then, the formation of gas in the incubated culture media was considered as positive presumptive test.

A positive presumptive sample was further confirmed by confirmatory tests. In confirmatory test, 1 mL of inoculums in positive presumptive tubes were transferred to the three different

Table 1. Risk indicator microorganisms in different samples of pre and post chlorinated drinking water.

Source of water sample	HPC CFU/mL (log/ml)	Total coli form MPN/100 mL (95% CI)	Fecal coli form MPN/100 mL
Sample from Ss_1	2.8×10^7 (7.45 log)	>2,400	-
Sample from Ss_2	2.8×10^8 (8.45 log)	1,100 (150, 4800)	-
Sample from Rs	8.0×10^1 (1.9 log)	-	-
Sample from Ds_1	2.6×10^7 (7.4 log)	460 (71, 2,400)	3
Sample from Ds_2	1.9×10^8 (8.29 log)	240 (36, 1,300)	-
Sample from Ds_3	1.2×10^8 (8.1 log)	150 (30, 440)	-
Sample from Ds_4	1.0×10^8 (8 log)	460 (71, 2,400)	15
Sample from Ds_5	1.2×10^5 (5.1 log)	240 (36, 1,300)	-
Sample from Ds_6	8.0×10^6 (6.9 log)	20 (7, 89)	-
Sample from Ds_7	7.0×10^5 (5.8 log)	9 (1, 36)	-
Sample from Ds_8	1.6×10^4 (4.2 log)	7 (1, 23)	-
Sample from Ds_9	6.0×10^4 (4.77 log)	14 (3, 37)	-
Sample from Ds_{10}	1.2×10^7 (7.1 log)	93 (15, 380)	-
Sample from Ds_{11}	2.7×10^8 (8.4 log)	460 (71, 2,400)	-
Sample from Ds_{12}	2.1×10^8 (8.3 log)	240 (36, 1,300)	-

Ss = Source of water sample; Rs = reservoir water sample 1; Ds = water sample taken after distribution. CFU: colony forming units; MPN: most probable number; CI: confidence interval.

dilution tubes of MacConkey broth and inoculated at 44.5°C for 48 h. Then gas produced samples inoculums in the respective tubes were recorded. Finally, the value obtained was interpreted using MPN table and expressed as MPN of coliform per 100 mL of the water sample.

The positive confirmatory test was further checked to complete the tests. In this case, the suspected organisms were inoculated on nutrient agar slant and tube of lactose broth. After 24 h at 37°C, the lactose broth was checked for the production of gas, and a Gram stain was performed from organisms grown on the nutrient agar (APHA, 1992). After the analysis which indicates the quality status of drinking water, the results were compared with the Ethiopia and WHO guideline values (WHO, 2004).

Quality control

Bacteriological quality of drinking water was processed according to standard operating procedures and laboratory safety rule was followed. Sample collecting bottles was sterilized before sample collection. To check sterility of prepared media, 5% of prepared batch of media were incubated overnight and checked for microbial growth in the media. Both positive and negative controls were inoculated together with test water sample.

Data analysis

Descriptive statistical methods were used to summarize data and the result of bacteriological analyses was compared with national and WHO guidelines for drinking water during interpretation.

RESULTS

The HPC of collected water samples ranged from 8×10^1 to 2.80×10^8 CFU/mL water. The lowest HPC 8×10^1 CFU/mL was observed in the sample which was collected from the reservoir immediately after chlorination before entering distribution line, while the high number of HPC was detected from the spring water source before chlorination. Total coliforms and fecal coliforms determined for all the water samples are presented in Table 1.

Microbial analysis of source spring water sample taken from different points before chlorination showed heterotrophic plate count of 2.85×10^7 and 2.8×10^8 CFU/mL in both samples. The highest values (>2,400 MPN/100 mL) were detected for total coli forms in the spring water before chlorination and no fecal coliforms were detected after chlorination.

In order to assess the effectiveness of treatment, microbial properties of the drinking water was also assessed after chlorination before entering distribution lines. The number of cultivable microorganisms after chlorination was determined by heterotrophic plate count and about 2.9 log/mL organisms were detected. Unlike other water samples, the MPNs showed no total coliform and fecal coliform bacteria (Table 2). Microbial analysis was also performed on distributed tap water (chlorinated) taken from 12 different parts of the town (Figure 1). The heterotrophic plate count of tap water ranged from 1.6×10^4 to 2.8×10^8 CFU/mL with a mean of 7.8×10^7 CFU/mL. The total coliform counts ranged from 7.4 to 460 MPN/100 mL, while the fecal coliform counts were detected in two water samples which accounts 3 and 15 MPN/100 mL (Table 1).

All the spring source water and distributed tap water were positive for total coliforms. About 16.7% of distributed tap water samples also had fecal coliforms by most probable number analysis method. The reservoir water sample was free of both total coliforms and fecal coliforms (Table 2).

Table 2. Occurrence of indicator bacteria at source, from reservoir and tap water.

Type of water sample	Type of indicator microorganisms		Total number of collected samples
	Total coli form	Fecal coli form	
Source (spring water)	2	-	2
Reservoir after chlorination	-	-	1
Distributed tap water	12	2	12
Total	14	2	15

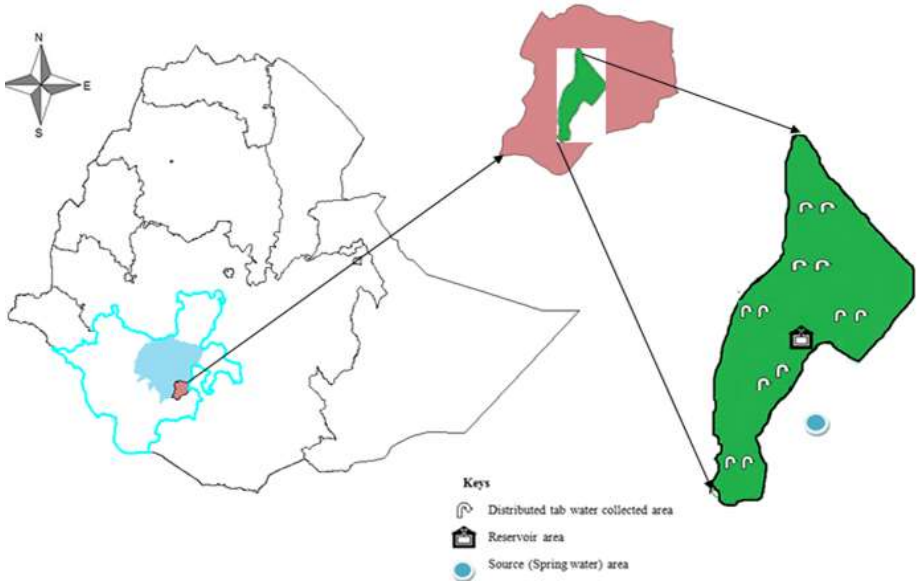

Figure 1. Map of the study sites, Arba Minch, Ethiopia.

Based on World Health Organization (1997) guidelines for drinking-water level of risk category for total coliform and fecal coliform, 16.7% of tap water sample fell within the low risk category, about 25% of tap water sample was classified as medium risk, and 58.3% of tap water was classified under high risk. The same as for total coliform level of risk for fecal coliform was determined. For fecal coliform indicator, about 83.4% of tap water samples had no risk, 8.3% was classified under low risk and similarly, 8.3% fell within the medium risk category (Figure 2).

DISCUSSION

Heterotrophic plate count of non-chlorinated source water (spring water) was higher (>7 log) when compared with chlorinated reservoir water. This indicates that the action of chlorine in reducing high bacteria load of source water was very important. Although, the bacteria load of reservoir water was low, there were about 8×10^1 CFU/mL microorganisms. This may be due to the use of insufficient concentration of chlorine or due to the resistance organisms to effective concentration of chlorine disinfectant. According to a study conducted by Chouhan (2015), the number of HPC bacteria in drinking water ranged from <0.02 to 1×10^4 CFU/mL. Reductions of HPC levels from the raw source water to the finished water after treatment ranged from <1 log to 2 log for upland catchment water, and 1 log to 4 log for river derived water (WHO, 2003). Bacteriological quality changes may cause aesthetic problems involving taste and odor development, slime growths and colored water.

The microbial load of drinking water after leaving the treatment reservoir was high (> 4.2 log) as compared to its load before leaving the treatment reservoir (1.9 log). This result shows recontamination of drinking water in the distribution lines and the microbial load was higher than the amount of organism recommended by WHO (2004) standard. The growth of microorganisms after leaving the treatment site at the distribution network can be explained from different points of view. One possible reason for this high load of HPC in the distribution line is the insufficient residual chlorine level which is unable to inhibit the growth of microorganism. The other possible reason could be the distribution line damage and cross contamination with microorganisms. Similar findings were

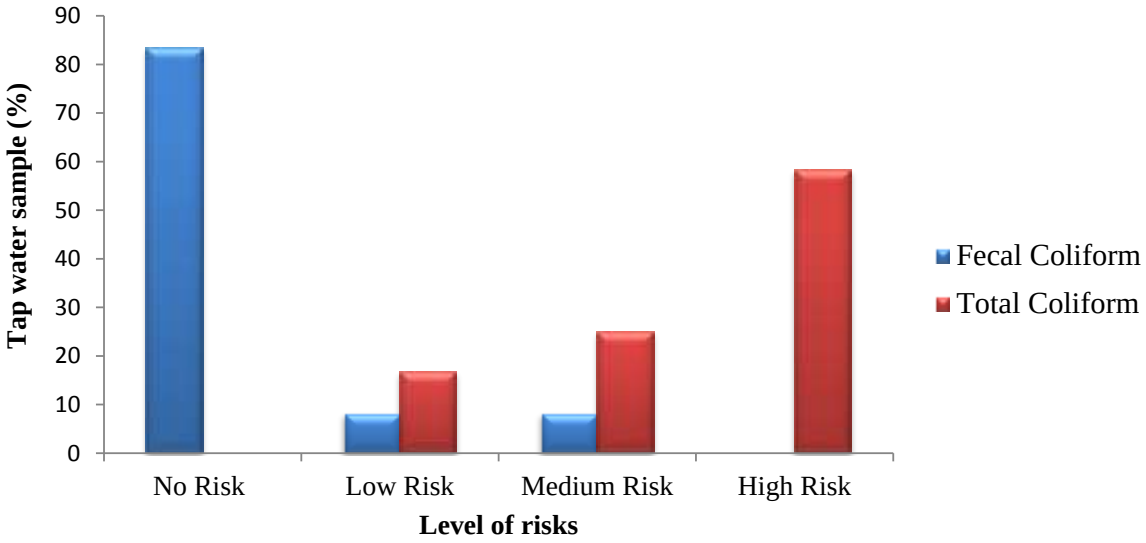

Figure 2. Level of the risk indicator organisms in chlorinated water collected from distribution lines.

exhibited in Ismailia canal water with HPC ranging from 1.0×10^6 to 4.13×10^8 CFU/mL (Abdo et al., 2010). In contrast, low HPC was observed in a study conducted on Gezira State drinking water (Elbakri, 2015). This might be due to lack of frequent repair of broken pipe line and less residual chlorine in the current study.

Highest number of total coliforms was recorded at the spring source water before treatment (>2,400 MPN/ml). Results of total and fecal coliforms revealed that the drinking water was unsafe according to national and WHO drinking water standards which states less than 10 coliform/mL of drinking water (UNEP, 1996). This high number of the coliforms may be due to soil and plant coliforms other than fecal origin. One of the possible reasons for these findings is contamination of water after leaving the reservoir through the damaged water pipe line. The other possible reason can be use of ineffective concentration of chlorine in the treatment reservoir. Furthermore, it can be due to low residual chlorine in the distribution system, contamination due to transient pressure drops leading to infiltration of ground water into water pipes, contamination due to incorrect cross connection with sewer lines, interconnection with toilet, pipe corrosion, pipe breakage and entrance of contaminants into the distribution system (Ailamaki et al., 2003).

Similar findings were obtained in a study done in Sri Lanka (Dissanayake, 2004), Bona District, Sidama Zone, Southern, Ethiopia (Berhanu and Hailu, 2015) and Bahir Dar city (Tabor et al., 2011). In this study, about 93.3% of analyzed water samples were positive to total coliform indicator bacteria and 16.7% of the samples were positive to fecal coliforms. Similar findings were observed in study conducted in Dire Dawa (Amenu et al., 2013). Unlike this study, all samples collected were positive to total coliforms. This difference may be due to differences in the sanitary facilities of the studied area (Amenu et al., 2013). In contrast to this study, a study conducted in Adama town, Oromia regional state of Ethiopia showed acceptable amount of coliforms according to WHO and national standards (Eliku and Sulaiman, 2015). The observed difference may be due to sufficient residual chlorine in the distribution line and appropriate water protection in Adama town.

Any coliform presence in drinking water is unacceptable even though their level of risk indication depend on the type of coliforms and number of coliforms present in a water sample. In drinking water, the presence of fecal coliforms should not be ignored as the basic assumption that pathogens would not be presented in drinking water, but this study shows the presence of fecal coli form. Since they are indicators of possible presence of waterborne pathogens, one can expect waterborne diseases in the study area. Due to the presence of indicator microorganism such as coliforms in drinking water, one can infer that there could also be water associated enteric or other pathogens such as *Salmonella* species, *Shigella* species, *Vibrio cholera*, etc. in the water. Properly constructed spring water may be free of fecal coliform bacteria. The presence of coliforms in spring water indicates leakage of surface water into the spring. It could also be due to poor construction or cracks in the spring casing.

The quality of drinking water is highly associated with the sanitary facility of the water catchment area. Therefore, the poor quality of drinking water observed may be as a result of poor sanitary condition of the area (WHO and UNICEF, 2014). On the other hand, in urban areas of Ethiopia, the availability of improved latrine, shared latrine, unimproved latrine and open defecation

accounts for about 27, 42, 23, and 8%, respectively (WHO and UNICEF, 2014). In 2015, 2.4 billion people in the world still had no access to improved sanitation facilities. The global population living in rural areas had seven out of ten people without improved sanitation facilities and nine out of ten people still practice open defecation (UNICEF and WHO, 2015).

Conclusion

The amount of total coliforms and fecal coliforms detected in Arba Minch town drinking water were not in harmony with the standard set out by WHO for drinking water. The maximum level of HPC from all analyzed water sample at both spring water source and in distribution systems indicates that it is unsafe for drinking. The presence of high number of coliforms in the drinking water showed it is unsafe for consumption. Therefore, this should be considered by regulatory bodies as many diseases can be spread through fecal transmission. Regular monitoring of the distribution system for level of chlorine residue is mandatory. By considering these home water treatment mechanisms like granular-medium filters, home based physical and chemical disinfection is recommended.

CONFLICT OF INTERESTS

The authors have not declared any conflict of interests.

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