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Microbiological Evaluation of Drinking Water in a Sub-Saharan Urban Community (Yaoundé)

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ABSTRACT

Yaoundé residents collect water from various points to fulfill their freshwater needs. Many microorganisms, including parasites, bacteria, viruses and even alga, are present in water where they form a complex ecosystem. These microorganisms are held responsible for most of the contamination in drinking water and related diseases that threaten health of many individuals. The aim of this study was to evaluate the microbiological quality of drinking water in some Yaoundé neighborhoods. A total of 508 drinking water samples were randomly collected from a variety of water resources in different neighborhoods in Yaoundé. The microbiological analyses were performed for bacterial parameters, namely to trace the presence of organisms and opportunistic pathogens indicative of fecal contamination. During the study, 1.242 isolates of enteric bacteria (Enterobacteriaceae) were identified, of which 0.24% was *Shigella*, 1.30% was *Salmonella*, 5.15% were *Escherichia coli*, 12.40% were *Enterobacter*, 13.44% were *Citrobacter*, 22.06% were *Proteus* and 37.76% were *klebsiella*. And of the 461 aerobic bacteria, 28.20% were *Acinetobacter* and 71.80% were *Pseudomonas*. The results of our study showed that 95% of tested drinking water samples are of low microbiological quality and therefore do not fulfill requirements of World Health Organization standard.

Key words: Microbiological quality, drinking water, bacteria, coliforms, Yaoundé

INTRODUCTION

Water is essential to sustain life and a satisfactory supply must be made available to consumers (WHO, 2004). But in spite of the promises made during these ten last years and owing to the fact that the right to drinkable water is nowadays part of human rights, one-sixth of the world population still does not have access to safe drinking water (United Nations, 2008). In Yaoundé for example, out of the 1, 700 000 inhabitants only 20% have access to drinkable water provided by SNEC, the national drinking water company. Thus, Yaoundé dwellers do suffer a severe drinking water supply crisis, particularly during the dry seasons when the network is intermittent. The growing imbalance between supply and demand has led to chronic shortages and to the use of waters collected from springs, wells and even rivers and rains. Apart from quantitative shortages, the quality of drinking water is becoming a serious public health issue for the past few years. The quality of water for drinking has deteriorated because of inefficient management of the piped water distribution system and because of direct discharge of untreated sewage into the Nyong River, where raw water is collected. The contamination of natural water with fecal material, domestic and industrial waste may result in an increased risk of disease transmission to individuals who use those waters. Diarrheas which are caused by poor sanitation and by contaminated water are part

of those diseases in developing countries (Ashbolt, 2004). According to World Health Organization, (1) there were an estimate of 4 billions cases of diarrhea and 2.2 million deaths annually in these countries and (2) the consumption of unsafe water has been implicated as one of the major causes of this disease (WHO, 2005). In Cameroon for example, they are the most prevalent water borne disease among children below five years of age. In Yaoundé in particular, the prevalence of diarrhoea is increasing. Studies conducted in the city amongst children under five years of age show that the prevalence rate has shifted from 13.01% in 2004 to 14.4% in 2005 (DHS, 2004; Hénock Blaise *et al.*, 2007). The most important pathogenic pathogens transmitted by the water route were *Salmonella typhi*, *E. coli*, Campylobacter, Shigella, Cryptosporidium, Giardia, the organisms causing diarrheas (Mahvi and Karyab, 2007). Thus, human pathogenic microorganisms that are transmitted by water include bacteria, viruses and protozoa. Most of them usually grow in the human intestinal tract and reach out through the feces. Ideally, drinking water should not contain any microorganisms known to be pathogenic or any bacteria indicative of faecal pollution. Since the presence of these microorganisms has been traditionally seen as an indicator of fecal contamination, tests are useful for monitoring the microbial quality of water used for consumption. Recognition that water is source of pathogenic microorganisms dates back to 1800 (Doestch, 1960). Because it was and still is, very expensive and time consuming to test for all the pathogens, it is suggested that a single group of microorganisms that comes from the same source as human pathogens can be used to indicate the presence of pathogens (Wyn-Jones *et al.*, 2000). Therefore, the present work focuses on bacterial agents with the most common indicators such as total coliforms, fecal coliforms and *Escherichia coli*. Thus, the purpose of this study is to use bacterial counts to evaluate the microbial quality of water samples from sources and points of consumption. Also, it seeks to determine the relationship between microorganisms' occurrence and types of water supply.

MATERIALS AND METHODS

Conceptual framework: Contamination by human or animal feces is the most regular and pervasive health risk associated with drinking water (Lee and Schwab, 2005). When such defect is recent and when those responsible for it include carriers of communicable enteric disease, microorganisms that cause these diseases may be present in the water. Then, drinking the water or using it in food preparation may result in outbreak of infections. Recognition that water was a source of pathogenic microorganisms was made in the late 1800's. The pathogenic agents implicated consist of bacteria, viruses and protozoa. The most common microorganisms are total coliform bacteria, fecal coliforms and *Escherichia coli* (*E. coli*).

Coliform bacteria are a group of bacteria including *Enterobacter*, *Klebsiella*, *Aeromonas*. Adopted as an indicator of fecal contamination in water in 1914, they make up around 10% of the intestinal microflora of the human and animal intestine (Chan *et al.*, 2007). They are defined as any bacteria capable of fermenting lactose with the production of acid and gas in 48 h at 35°C under aerobic conditions. Their presence in water is designed to indicate the possible presence of fecal contamination and therefore the presence of pathogens.

Fecal coliform bacteria are a sub-set of the total coliform group. Also, they are a group of microorganisms (*Citrobacter*, *Hafnia*, *Klebsiella*, *Serratia*) with the same definition as total coliform bacteria except that they grow at 44.5°C. The reason for testing for fecal coliforms is that they are more restricted in their source to the gastrointestinal tract of warm-blooded animals. Again, their presence in water could indicate fecal contamination.

Escherichia coli are a single species of bacteria that are a subset of total and fecal coliform. They are found in human and animal intestines and are the most reliable indicator of fecal contamination in water (Edberg *et al.*, 2000). Their presence in drinking water represents a health concern because they are usually associated with sewage or animal wastes. While some strains of *Escherichia coli* are pathogenic, others are not. Pathogenic strains of *Escherichia coli* include Enteropathogenic, Enteroinvasive, Enterotoxigenic and Enterohemorrhagic.

Other indicator bacteria used to determine water quality are *fecal streptococcus* often found in the gastrointestinal tract of warm blooded animals although not exclusively and *Enterococcus* bacteria determined to be a valuable bacterial indicator for evaluating the extent of fecal contamination in water.

All of these infectious agents are associated with diseases like dysentery, hepatitis, typhoid fever, severe and sometimes fatal diarrheas, most of them are widely spread throughout the world (Hunter *et al.*, 2002). The vast majority of diarrhoeal disease in the world (88%) is attributable to unsafe water as the World Health Organisation estimates that about 1.1 billion people globally drink unsafe water (WHO, 2003). In 2001, infectious diseases accounted for an estimated 26% of deaths world-wide (Kindhauser, 2003). Furthermore, social and environmental changes continue to result in new or re-emerging waterborne pathogen issues. For example, climate change is estimated to be responsible in the five to ten forthcoming years for approximately 2.4% of world-wide diarrhoea in some developing countries (Reena Singh *et al.*, 2001). Fecal contamination of drinking water is only one of several feco-oral mechanisms by which they can be transmitted from one person to another or, in some cases, from animals to people. Ideally, all samples taken from the distribution system including consumers' premises should be free from pathogenic organisms. In practice, this is not always attainable. To control purity of water, the following microbiological parameters for water collected in the distribution system is therefore recommended: (1) samples should not contain any coliform organisms in 100 mL, (2) no sample should contain *E. coli* in 100 mL, (3) no sample should contain more than 10 coliform organisms per 100 mL and (4) coliform organisms should not be detectable in 100 mL (Rompré *et al.*, 2002). Due to the interactions between exposure to enteric pathogens via poor quality water and also lack of inadequate hygiene, data resolving the waterborne component is not generally available, particularly in developing regions where there is a higher rate of endemic gastrointestinal disease and pathogen concentrations in drinking and waste water (Abu Amr and Yassin, 2008). Hence, this study is an attempt to fill the gap by assessing the microbiological quality of drinking water in a city of one of those developing countries.

Year of study, scope area and sampling sites: The study started in June 2005 with the environmental investigations and updated in July 2008 during the rainy season with the microbiological assessment of water.

The study was conducted in Yaoundé, the capital of Cameroon, situated in Central Africa between latitudes 3° 47' and 3° 56' North and 11° 10' and 11° 45' East (Fig. 1). Yaoundé displays the classical Equatorial Guinea climate (regular and abundant rainfall of more than 1,600 mm per annum and a fairly high average annual temperature of 23°C). Like many sub Saharan African cities, Yaoundé is currently experiencing very rapid urbanization. In the first population census in 1926, Yaoundé had 100, 000 inhabitants. With an estimated annual growth rate of 4.5% since 1980, its population has grown from 812,000 inhabitants in 1987 to 1,500, 000 inhabitants in 2000 and to about 2, 100, 000 inhabitants in 2007 (CIA, 2008). However, this population growth has not

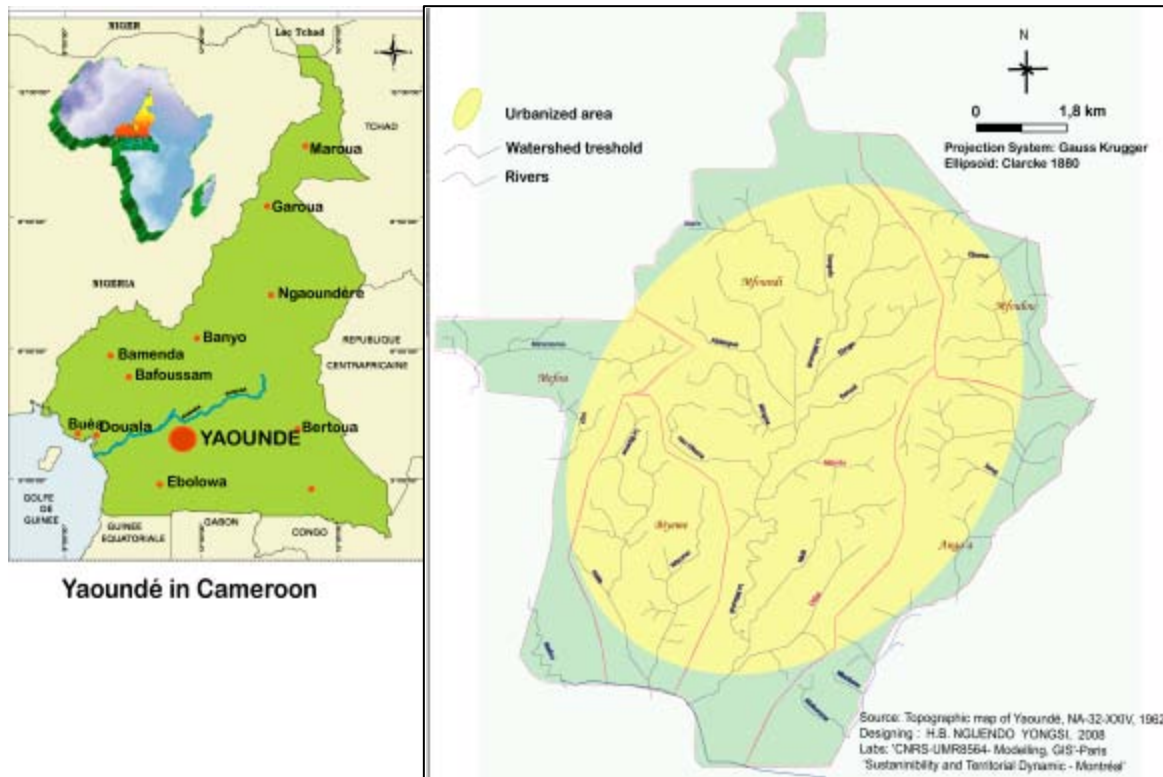


Fig. 1: Location of Yaoundé in Cameroon

been monitored by the city planners and decision makers. Consequently local authorities have failed to provide neighborhoods with adequate utilities, services and infrastructure. Therefore, city dwellers are facing difficulties such as getting access to water supply systems.

Sampling design: Collection of samples was done on five neighborhoods out of the 105 that made up the city (Fig. 2). Selection of these five neighborhoods was based on three criteria: they all belonged to the urbanized area; they have a diversity of water supplies representative of those found in the metropolitan area, enough information was available to allow for adequate statistical design of the study. The sample size varies according to sources of water collection: (1) the sample size of 302 households directly connected to piped water supply network at home (i.e., who possess a tap water) was based on an estimated prevalence of coliforms contamination of 8.9% (Nola *et al.*, 1998) and on a desired level of precision of 4%; in each selected neighborhood, the first house at the end of a randomly chosen street was selected for sampling followed by the systematic random sampling of every second house along the same street and if the resident of the second house did not respond, the next house in sequence after that one was targeted. A semi-structured questionnaire was administered to each participative household. The questionnaire included variables such as family size, devices used to collect and store water, storage duration and water treatment. (2) Community standpipes, wells and springs sampling size was determined according to their total number and to their importance (i.e., whose waters are collected for consumption use) in any neighbourhood.

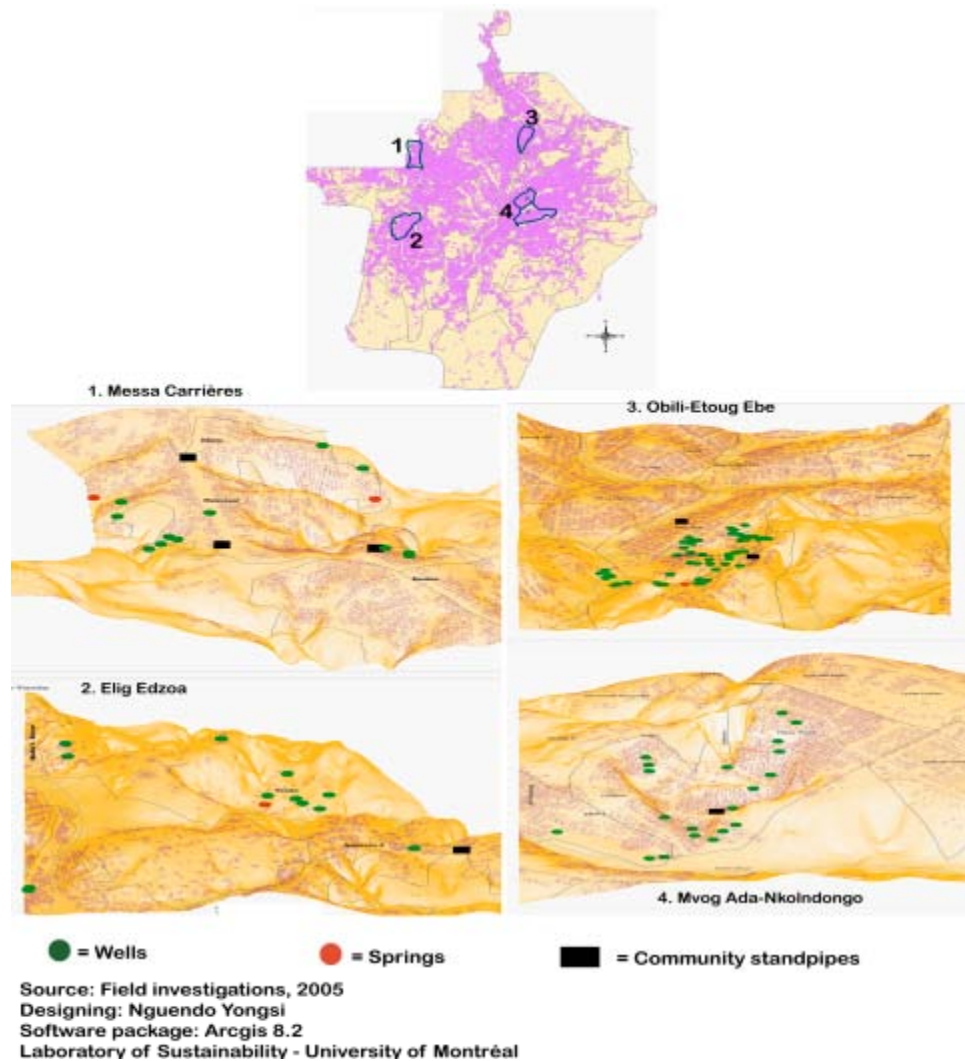


Fig. 2: Geographical location of the sampling sites and 3D image of some areas of the studied neighborhoods

Collection, transportation and storage: In each targeted household, 500 mL of water was sampled in the form usually consumed by inhabitants. Drinking water the households stored in bottles or other containers was poured into 500 mL sterilized free bottles. For pipe borne water, standpipes were allowed to run for at least 1 min and sanitized before water was aseptically collected in sterile wide mouth glass bottles. Waters from wells and springs were collected in pre-sterilized devices and then poured in sterile autoclave polypropylene bottles. All collected samples were labelled with different codes for analysis purposes. The same alphabet in the code represented water from the same source and the numbering that follows differentiates the geographical location (neighborhood) and the physical aspects of the source (Table 1). Samples were sealed and transported to the laboratory ice-cooled (4°C) and were processed as soon as practicable on the day of collection.

Table 1: Coding and sources of sampling study

Code	Sample	Neighborhood
A-Households water		
A1	Water stored, treated before consumption	Mvog Ada
A2	Water not stored, treated before consumption	Messa Carrières
A3	Water stored/stored and untreated	Mvog Ada
A302		Nkolndongo
B-Community standpipes		
B1	Old and well maintained	Mvog Ada
B2	New and well maintained	Messa Carrières
B3	Old/New and poorly maintained	Mvog Ada
B27		Nkolndongo
C-Wells		
C1	Located on the plateau, improved/not improved	Mvog Ada
C2	Located on the slope, improved/not improved	Messa Carrières
C3	Located in the valley, improved/not improved	Mvog Ada
C154		Nkolndongo
D-Springs		
D1	Located on the plateau, improved/not improved	Mvog Ada
D2	Located in the valley, improved/not improved	Messa Carrières
D25		Nkolndongo

Microbial examination of water samples: The microbiological analyses performed on the samples were total viable count. The total plate count was conducted by pour plate technique on Plate Count Agar (PCA) and counting the colonies developed after the incubation at 37°C for 24 h (APHA, 1998). The total coliforms were enumerated by the Membrane Filtration (MF) technique as described by APHA (1998). Detection of *Salmonella* and *Shigella* species were done by the enrichment of water samples on Selenite F broth, followed by isolation of the typical organism on selective medium, Xylose Lysine Deoxycholate Agar (XLD) (Zvikomborero, 2005). All colonies with different characteristics on M-Endo agar, Xylose Lysine Deoxycholate Agar (XLD) agar and Thiosulphate Citrate Bile salt sucrose Agar (TCBS) were sub cultured onto Nutrient agar (NA) for purification. The detection of *Pseudomonas* was done by placing filtered cellulose nitrate membrane filters onto basic *Pseudomonas* Agar. The media was incubated at 42°C for 40-44 h. Later the agar was checked under ultra violet light to detect pigment thought to be *Pseudomonas aeruginosa* or *Pseudomonas* sp. To detect *E. coli*, all colonies of coliforms which showed characteristic occurrence on endo agar and mFC agar were subcultured on Eosin Methylene Blue (EMB) agar, incubated over-night at 37°C and subjected to biochemical tests to identify *E. coli* (Reynolds *et al.*, 2008). Other enteric bacteria isolated on respective selective or differential media were identified on the basis of their colonial, morphological and Biochemical properties following Bergey's Manual of Determinative Bacteriology (Hensyl and Holt, 1994).

Analysis of data: In view of the high counts of total coliforms and according to Djeuda Tchapgna *et al.* (2001), samples were classified as good/fair (0-20 total coliforms per 100 mL), poor (21-100 total coliforms per 100 mL) and very poor (over 100 total coliforms per 100 mL). For fecal coliforms, the categories used were good/fair (0-5 fecal coliforms per 100 mL), poor (6-20 fecal coliforms per 100 mL) and very poor (over 20 fecal coliforms per 100 mL). Statistical approaches such as frequency distribution and student t-test were used to analyse the data.

Epi Info version 6.04 and SPSS package version 11.1 was used for data recording and analysis and p-values less than 0.05 were considered statistically significant.

RESULTS

A total of 508 drinking water samples were collected from different Yaoundé neighborhoods, of which 302 were from households connected to a piped water supply at home, 154 from wells, 27 from community standpipes and 25 from springs. Ground water contributed 35.24%, while 64.76% were collected from SNEC (the National drinking water provider). The quantity and nature of pathogens in the water samples will determine the risk of consumer after consuming the water. Bacterial analyses are indicative of the bacteria found within the points of collection.

Quantitative bacteriological analysis

Total plate count: Total plate count for total bacterial count performed for all water samples showed only 25 samples, i.e., 4.92% were within the WHO guideline value ($<10 \text{ cfu mL}^{-1}$). In source wise distribution of samples (Table 2), 96.7% of households, 44.5% of community standpipes, 100% of wells and springs samples were exceeded the guideline value.

Coliforms count: Source wise distribution of coliforms count has shown that the 11.11% of community standpipes and 100% of wells, springs as well as households crossed the WHO guideline value i.e., 0 cfu/100 mL (Fig. 3).

Qualitative bacteriological analysis: From the microbiological analyses performed on the 508 samples, 1,242 isolates of enteric bacteria (Enterobacteriaceae) and 461 isolates of strict aerobic bacteria were obtained and identified (Table 3). Of the 1,242 isolates of enteric bacteria, 0.24% was *Shigella*, 1.30% was *Salmonella*, 5.15% were *Escherichia coli*, 12.40% were *Enterobacter*, 13.44% were *Citrobacter*, 22.06% were *Proteus* and 37.76% were *klebsiella*. And of the 461 aerobic bacteria, 28.20% were *Acinetobacter* and 71.80% were *Pseudomonas*.

Both enteric and aerobic bacteria belong to twelve different genres. The most important in terms of frequency were: (1) *Pseudomonas* with species such as *Pseudomonas aeruginosa* (03.9%) *Pseudomonas* sp. (22.2%), *Pseudomonas baumannii* (25.6%); *Enterobacter* that included *Enterobacter cloacae* (37.8%), *Enterobacter aerogenes* (0.2%) and *Enterobacter asburiae* (0.2%), *Klebsiella* with *Klebsiella levinea* (11.1%), *Klebsiella pneumoniae* (79.1%), *Klebsiella oxytoca* (0.2%), *Proteus* with isolates such as *Proteus mirabilis* (22.6%), *Proteus vulgaris* (31.3%), *E. coli* (12.6%) and *Salmonella* sp. (3.1%).

Table 2: Source wise quality of total bacterial count of water samples

Samples sources	Percentage of samples compared with the WHO guideline value		
	Total No. of samples	Guideline value ($<10 \text{ cfu mL}^{-1}$)	Excess to guideline value ($>10 \text{ cfu mL}^{-1}$)
Households	302	96.7	302
Community standpipes	55.5	44.5	27
Wells	0.0	100.0	154
Springs	0.0	100.0	25

Table 3: Distribution of bacterial isolates according to the source of drinking water

Bacterial isolates	Drinking water source							
	Springs		Wells		Community standpipes		Households	
	Frequency	Percentage	Frequency	Percentage	Frequency	Percentage	Frequency	Percentage
<i>Enteric bacteria (Enterobacteriaceae)</i>								
<i>Citrobacter freundii</i>	6	24.0	93	60.4	...	...	68	22,52
<i>Escherichia coli</i>	7	28.0	29	18.8	...	...	28	09.3
<i>Klebsiella levinea</i>	7	28.0	17	11.1	...	...	32	10,6
<i>Shigella</i>	1	04.0	1	00.6	...	...	1	00,7
<i>Enterobacter cloacae</i>	7	28.0	36	23.4	4	14.8	145	48.0
<i>Klebsiella pneumoniae</i>	24	96.0	137	88.9	2	07.4	239	79.1
<i>Klebsiella oxytoca</i>	...	...	...	...	1	03.7	...	...
<i>Serratia</i>	2	08.0	4	02.6	...	...	8	02.6
<i>Morganella morganii</i>	3	12.0	12	07.8	...	...	24	07.9
<i>Proteus mirabilis</i>	5	20.0	37	24.0	...	...	73	24.1
<i>Proteus vulgaris</i>	3	12.0	53	34.4	...	...	103	34.1
<i>Providencia</i>	...	...	4	02.6	...	...	8	02.6
<i>Salmonella</i> sp.	1	04.0	5	03.2	...	...	10	03.3
<i>Enterobacter aerogenes</i>	...	...	...	...	...	...	1	00.3
<i>Enterobacter asburiae</i>	...	...	...	...	...	...	1	00.3
<i>Strict aerobic bacteria</i>								
<i>Acinetobacter baumannii</i>	3	12.0	15	09.7	...	...	112	37.1
<i>Pseudomonas aeruginosa</i>	12	48.0	57	37.0	2	07.4	147	48.7
<i>Pseudomonas</i> sp.	7	28.0	75	48.7	1	03.7	30	09.9

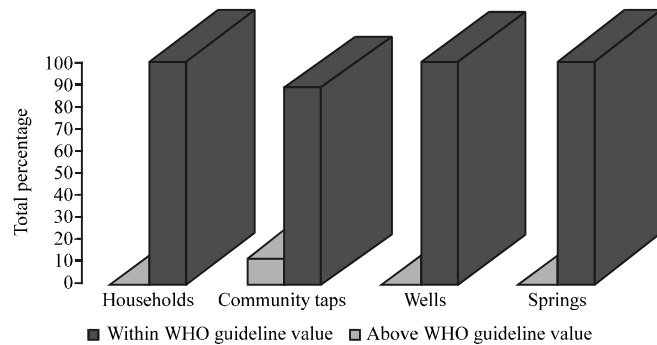


Fig. 3: Source wise quality of coliform count

Presence of coliform or fecal coliform bacteria does not determine whether a sample will make someone ill. Therefore, it is important to determine levels of contamination. Considering total coliform counts, 23.6% of water samples tested were classified in the fair category, 05.6% were poor and 70.8% were very poor. Allowing for fecal coliform counts, 35.9% of water samples tested were classified in the fair category, 19.1% were poor and 45.1% were very poor. The breakdowns for the four sources are illustrated in Fig. 4a-d. There were significant differences in total coliform counts, fecal coliform counts, fecal streptococcus and strict aerobic bacteria counts among the four sources ($p < 0.001$). Community standpipes had the highest percentage of water samples in the fair category while springs and wells had the lowest one.

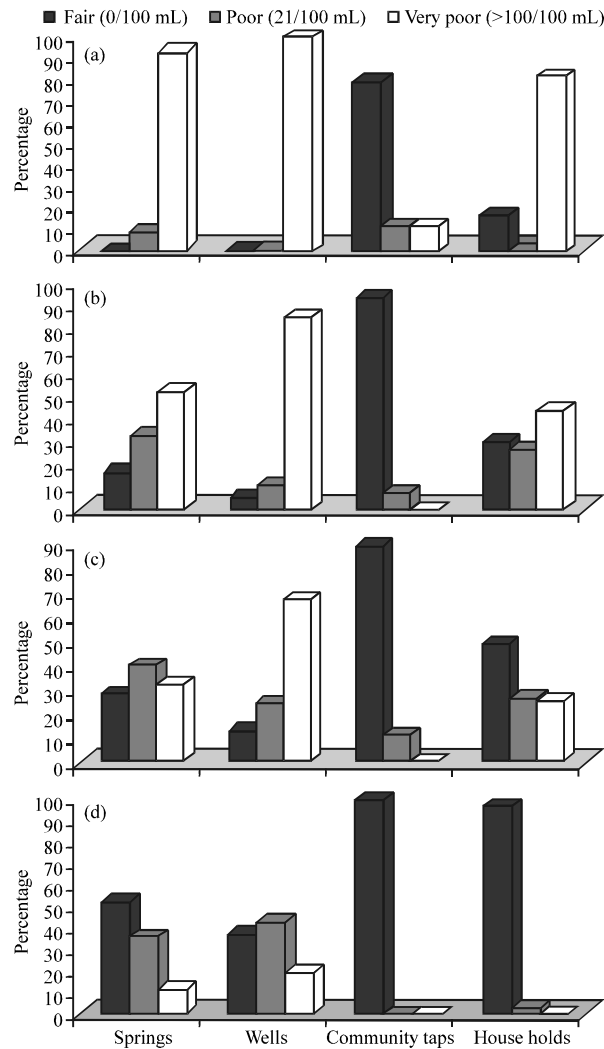


Fig. 4: levels of drinking water quality in Yaoundé, in terms of four bacteriologic variables counts. (a) Total coliforms, (b) fecal coliforms, (c) fecal streptococcus and (d) strict aerobic bacteria

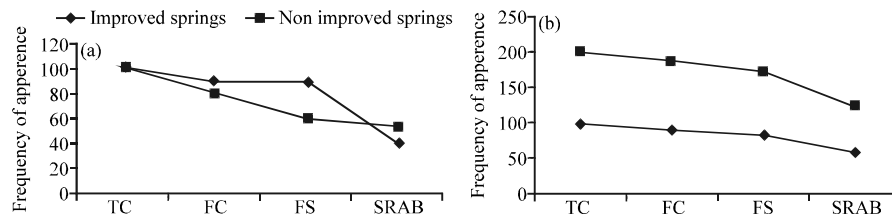


Fig. 5: Compared profiles of bacteria occurrence in (a) springs and (b) wells (TC: Total coliform, FC: Fecal coliform, FS: Fecal streptococcus, SRAB: Sulfito-reducers aerobic bacteria)

The compared profiles of bacteria occurrence in the springs are tangled up. We did not observe a clear hierarchy between the improved and no improved springs. With a frequency of fecal coliform and fecal Streptococcus higher in the ten improved springs than in the fifteen non improved springs and with an inverse tendency with sulfito-bacteria, one finally obtains a

Table 4: Distribution of drinking water in Yaoundé, according to microbiological quality

Condition	Water resource									
	Total		Wells		Springs		Households		Community standpipes	
	No.	%	No.	%	No.	%	No.	%	No.	%
Safe	0	00.0	0.0	0	10	03.3	15	55.6	25	04.9
Contaminated	154	100.0	25.0	100	292	96.7	12	44.4	483	95.1
Total	154	100.0	25.0	100	302	100.0	27	100.0	508	100

confusing profile (Fig. 5a). Considering wells, the frequency of occurrence of bacteria is lower in improved and protected wells than in non improved wells (Fig. 5b).

Finally, the distribution of drinking water resources according to microbiological quality is presented in Table 4. The result clearly showed that the quality of the water consumed is critical in controlling infectious diseases and other health problems.

DISCUSSION

Fresh water is a vital resource for humans. We need water for drinking purposes as well as for services such as transportation and recreation (Welch *et al.*, 2000). Hence, assessment of water for microbial pollution is an important public health undertaking. Identification of bacteria that constitute the drinking water ecosystem is essential for understanding their individual contributions to drinking water. Heterotrophic plate counts and Coliform counts have been used as a basis for regulating the microbial quality of drinking-water. In this study, both regulatory parameters were above the WHO guideline values. We identified twelve bacterial isolates on the bases of morphological and biochemical and serological tests and according to Bergy's Manual of Determinative Bacteriology. Actually, Groundwater as well as surface water contains generally microorganisms of several species, which cannot be always differentiated properly in autochthonous flora and contaminants with health significance (Bohm, 2000). In previous studies, other investigations isolated such genres from water (Wright *et al.*, 2004; Signoretto *et al.*, 2005).

This study highlights the presence of coliforms, fecal coliforms and *Escherichia coli*. Most coliforms are present in large numbers among intestinal flora of humans and other warm-blooded animals and are thus found in fecal wastes (Chug, 2008). Thus, they are used as an index of the potential presence of entero-pathogens in water environments (Jakopanec *et al.*, 2008). All samples showed positive results for the presence of *Streptococcus* and *P. aeruginosa*. This indicates that the water was not free from faecal contamination as *Streptococcus* is one of the indicators for faecal contamination in drinking water (Suthar *et al.*, 2008). Though *Pseudomonas* does not harm a healthy individual but only cause problem in individual with weak immune system (Da Silva *et al.*, 2008), it is more reliable and safe if the drinking water does not show their presence. According to guideline values for bacteriological parameters, the total and fecal coliform bacteria should at least be absent, if not less than 10/100 mL water intended for drinking.

Results clearly indicated that most of the natural water sources are highly contaminated. It might be due either to the failure of the disinfections of the raw water at the treatment plant or to the infiltration of contaminated water (sewage) through cross connection, leakage points and back siphonage. However, some studies have associated the occurrence of coliform bacteria in drinking water system with rainfall events (Stukel *et al.*, 1990). According to these authors, rainfall is a

complex variable and may have many different impacts on drinking water quality, as rainfall can be a mechanism that introduces coliform bacteria into the system through leaks and cross-connections and that it can wash dissolved nutrients into the watershed and increase organic carbon levels. Our data indicated that about 95% water resources qualities were not fit for drinking purposes. These findings are considerably higher than that of Sahelian region of Burkina Faso (30.2%) as reported by Guillemin *et al.* (1991). As the location of water resources can potentially be viewed as a modulating factor for microbiological quality, we assessed relationship between the physical aspects i.e., the environmental conditions and the quality of the water. We did not find a significant difference between the quality of drinking water and improved and non improved springs ($p = 0.20$). This can be explained by the fact that all these springs are located in areas with high density of population and lack of sanitation as untreated waste water and excreta are dumped in the natural milieu (Nguendo Yongsu *et al.*, 2008). In fact, Yaoundé neighborhoods are often overcrowded (particularly spontaneous and informal ones) so that the amount of human fecal wastes may overload the design capacity of sanitary disposal systems. These unhealthier systems (latrines) may also have exceeded their expected life span. Furthermore, dwellers probably excrete greater numbers of pathogens into the open system made up of rivers and ground. This indicates that individuals from these areas might be prone to water-borne diseases and suitable disinfection must be done. Diarrhea has been reported to be four times more frequent among dwellers of these areas than the rest of the urban population (Yongsu, 2009). However, there was a relationship between bacteria occurrence and types of wells ($p < 0.001$): protected and deep wells located on the slopes harbour fewer bacteria than unprotected wells located in the marshy valleys. It seems that geological situations, the use of sanitized and deep wells protected the quality of water resources in these neighborhoods.

The detection of pathogenic enteric bacteria in different sources of drinking water also reveals the alarming situation for households' water. The surprisingly high prevalence of total and fecal coliforms in households' drinking water is a matter of serious concern. It is disturbing that of the 302 households sampled, 292 of them (96.7%) were consuming water considered unfit for human consumption. According to our field investigation (semi-structured questionnaire), this may be a reflection of several factors: (1) post-treatment contamination along the water distribution line; (2) because of shortages and intermittent provision by the drinking water company, almost all of the water supplied to households was kept in storage devices usually uncovered (buckets (45.5%), clay pots (33.2%) and barrels (15.4%), 17 households did not store water at all) and it is known that unsanitary storage containers contribute to substantial reductions in water quality (Genthe and Strausss, 1997) and (3) a third factor may be lack or inadequate post-storage water treatment before consumption. Out of the 83 households that indicated their water treatment practices, 19 (22.9%) did not routinely treat their water; and of the 64 households that treated their water, 36 filtered (56.2%), 21 boiled (32.8%) and 7 (10.0%) bleached their drinking water.

CONCLUSION

The present study investigated water quality at sources and points of consumption of urban communities. Most people of such areas use water directly from available sources, without any treatment and therefore are exposed to a variety of water related diseases since drinking water is contaminated with pathogenic bacteria. On the basis of these findings, it seems logical to suggest that current regulations be revised to include water quality testing both before and during the period of settlement, not only in our sampling sites, but in all the neighborhoods in which dwellers

are served by groundwater sources. Indeed the control of drinking water quality in distribution networks remains a major challenge in sub Saharan urban areas, however comprehensive planning should be made for continuous monitoring of water resources, especially the contaminated ones. Further study is needed to determine the factors responsible for the presence of coliforms in drinking water so that effective intervention can be initiated. As far as possible, water sources must be protected from contamination by human and animal waste.

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REFERENCES

- APHA., 1998. Standards Methods for the Examination of Water and Wastewater. 20th Edn., American Public Health Association, Washington DC.
- Abu Amr, S.S. and M.M. Yassin, 2008. Microbial contamination of the drinking water distribution system and its impact on human health in Khan Yunis Governorate, Gaza Strip: Seven years of monitoring (2000-2006). *Public Health*, 122: 1275-1283.
- Ashbolt, H.J.N., 2004. Microbial contamination of drinking water and disease out comes in developing regions. *Toxicology*, 198: 229-238.
- Bohm, R., 2000. Microbial contamination in human and animal drinking water. *Dtsch Tierarztl. Wochenschr.*, 107: 305-310.
- CIA., 2008. The word factbook. <https://www.cia.gov/library/publications/the-world-factbook/geos/ek.html>.
- Chan, C.L., M.K. Zalifah and A.S. Norrakiah, 2007. Microbiological and physiochemical quality of drinking water. *Malaysian J. Anal. Sci.*, 11: 414-420.
- Chug, T.D., 2008. Emerging and re-emerging bacterial diseases in India. *J Biosci.*, 33: 549-555.
- DHS-Cameroon Demographic and Health Survey, 2004. Mother and Child Mortality. Macro International, Calverton, MD.
- Da Silva, M.E.Z., I.C. Filho, E.H. Endo, C.V. Nakamura, T. Ueda-Nakamura and B.P. Filho, 2008. Characterisation of potential virulence markers in *Pseudomonas aeruginosa* isolated from drinking water. *Antonie Van Leeuwenhoek*, 93: 323-334.
- Djeuda Tchapgna, H.B., E. Tanawa and E. Ngnikam, 2001. L'eau au Cameroun. Presses Universitaires de Yaoundé, Tome I, pp: 345.
- Doestch, R.N., 1960. A History of the People and Events that Led to the Science of Microbiology. Rutgers University Press, New Jersey, USA.
- Edberg, S.C., E.W. Rice, R.J. Karlin and M.J. Allen, 2000. *E. coli*: The best biological drinking water indicator for public health protection. *J. Applied Microbiol.*, 88: 106-116.
- Genthe, B. and N. Strausss, 1997. The effect of type of water supply on water quality in a developing country in South Africa. *Water Sci. Technol.*, 35: 35-40.
- Guillemin, F., P. Henry, N. Uwechue and N. Manjour, 1991. Fecal contamination of rural water supply in the Sahelian area. *Water Res.*, 25: 923-927.
- Hensyl, W.R. and J.G., Holt, 1994. *Bergey's Manual of Determinative Bacteriology*. 9th Edn., Lippincott Williams and Wilkins, Baltimore, ISBN-10: 0683006037, pp: 787.
- Hunter, P.R., M. Waite and E. Ronchi, 2002. Drinking Water and Infectious Disease: Establishing the Links. CRC Press, Boca Raton, pp: 131-141.

- Hénock Blaise, N.Y. and D.B.K. Dovie, 2007. Diarrheal diseases in the history of public health. *Arch. Med. Res.*, 38: 159-163.
- Jakopanec, I., K. Borgen, L. Vold, H. Lund, T. Forseth, R. Hannula and K. Nygård, 2008. A large waterborne outbreak of campylobacteriosis in Norway: The need to focus on distribution system safety. *BMC Infect. Dis.*, 8: 128-128.
- Kindhauser, M.K., 2003. Communicable Diseases 2002. Global Defence Against the Infectious Disease Threat. WHO., Geneva, pp: 241.
- Lee, E.L. and K.J. Schwab, 2005. Deficiencies in drinking water distribution systems in developing countries. *J. Water Health*, 3: 109-127.
- Mahvi, A.H. and H. Karyab, 2007. Risk assessment for microbial pollution in drinking water in small community and relation to Diarrhea disease. *Am. Eurasian J. Agric. Environ. Sci.*, 2: 404-406.
- Nguendo Yongsi, H.B., G. Salem and J.P. Thouez, 2008. Risques sanitaires liés aux modes d'assainissement des excréta en milieu urbain tropical. *Nat. Sci. Soc.*, 16: 3-12.
- Nola, M., T. Njine, A. Monkiedje, V.S. Foko, E. Djuikom and R. Tailliez, 1998. Qualité bactériologique des eaux des sources et des puits de Yaoundé (Cameroun). *Cahiers Santé*, 8: 330-336.
- Reena Singh, B.K., S. Hales, N. de Wet, R. Raj, M. Hearnden and P. Weinstein, 2001. The influence of climate variation and change on diarrheal disease in the Pacific Islands. *Environ. Health Perspect*, 109: 155-159.
- Reynolds, K.A., K.D. Mena and C.P. Gerba, 2008. Risk of waterborne illness via drinking water in the United States. *Rev. Environ. Contam. Toxicol.*, 192: 117-158.
- Rompré, A., P. Servais, J. Baudart, M. de Roubin and P. Laurent, 2002. Detection and enumeration of coliforms in drinking water: Current methods and emerging approaches. *J. Microbiol. Methods*, 49: 31-54.
- Signoretto, C., G. Burlacchini, C. Pruzzo and P. Canepari, 2005. Persistence of enterococcus faecalis in aquatic environments via surface interactions with copepods. *Applied Environ. Microbiol.*, 71: 2756-2761.
- Stukel, A., E.R. Greenberg, B.J. Dain, F.C. Reed and N.J. Jacobs, 1990. A longitudinal study of rainfall and coliform contamination in small community drinking water supplies. *Environ. Sci. Technol.*, 24: 571-575.
- Suthar, S., V. Chhimpa and S. Singh, 2008. Bacterial contamination in drinking water: A case study in rural areas of Northern Rajasthan, India. *Environ. Monit. Assess.*, 129: 101-118.
- United Nations, 2008. The millennium development goals report. <http://mdgs.un.org/unsd/mdg/Resources>.
- WHO., 2003. Environmental Health Organization Guidelines for Drinking-Water Quality. World Health Organization, Geneva, Switzerland.
- WHO., 2004. Guidelines for Drinking-Water Quality. 3rd Edn., Incorporating First and Second Addenda. Vol. 1, World Health Organization, Geneva,.
- WHO., 2005. Guidelines for the control of shigellosis, including epidemics due to *Shigella dysenteriae* type 1. http://www.who.int/child_adolescent_health/documents/.
- Welch, P., J. David, W. Clarke, A. Trinidad and D. Penner *et al.*, 2000. Microbial quality of water in rural communities of Trinidad. *Revista Panamericana Salud Pública*, 8: 172-180.

- Wright, J., S. Gundry and R. Conroy, 2004. Household drinking water in developing countries: A systematic review of microbiological contamination between source and point-of-use. *Trop. Med. Int. Health*, 9: 106-117.
- Wyn-Jones, A.P., R. Pallin, C. Deboussis, J. Shore and J. Sellwood, 2000. The detection of small round-structured viruses in water and environmental materials. *J. Virol. Methods*, 87: 99-117.
- Yongsi, H.B.N., 2009. Human settlement, land management and health in Sub-Saharan cities. *Int. J. Soc. Sci.*, 4: 10-17.
- Zvikomborero, H., 2005. An assessment of the water quality of drinking water in rural districts in Zimbabwe. The case of Gokwe South, Nkayi, Lupane and Mwenezi districts. *Phys. Chem. Earth*, 30: 859-866.p