Full Length Research Paper

Bacteriological examination of households drinking water in some local Government areas of Kano state, Nigeria

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Abstract

Over large parts of the world, humans have inadequate access to portable water and use sources contaminated with disease vectors, and pathogens. Such water is not portable and drinking or using such water in food preparation leads to wide - spread of acute and chronic illnesses and serve major cause of death in many countries. The aim of this study was to evaluate the bacteriological quality of household drinking water in some part of Kano, Nigeria. Bacterial species were isolated by using membrane filtration method with subsequent cultivation on differential and selective media. Of the 212 samples analyzed, 135(17.92%) were from households, 38(17.92%) from wells, 36(16.98%) from taps and 3(1.40%) from boreholes. Two hundred and thirty two (232) isolates of enterobacteriaceae, 31 of *Staphylococci,* and 25 of fecal *Streptococci,* were obtained and identified. The most important organisms detected in terms of frequency were *E. coli* (15.6%), *Proteus vulgaris* (11.5%), and *Klebsiella pneumoniae* (10.8%). The mean value colony forming units (CFU) were 16.78, 26.05, 95.47 and 43.03cfu/100ml for Kumbotso, Gwale, Dala and Ungogo respectively.

Keywords: Coliforms, contamination, drinking water, pathogens.

INTRODUCTION

Groundwater is the major source of the public water supply in Kano; therefore its protection is important both socially and economically. In most developing cities where ground water is the major source of the public water supply, population growth precedes the development of an infrastructure capable of handling water and wastewater, which tends to lead to widespread contamination of groundwater by domestic and industrial effluents (Maziri-Hiriart *et al.*, 2005). Exposure to waterborne and food borne pathogens can occur via drinking water (associated with fecal contamination) , sea food (due to natural microbial hazards, toxins or wastewater disposal) or fresh produce (irrigated or processed with contaminated water) (Rose *et al.*, 2001).

Pathogenic bacteria like *Shigella* spp., *Leptospira* spp., *Salmonella paratyphi* B, *Vibrio, Staphylococcus aureus, Pseudomonas aeruginosa,* and *Aeromonas* spp. can be isolated from drinking water samples (Ford, 1999; Rajendran *et al.*, 2006; Levesque *et al.*, 1994). A number

of waterborne disease outbreaks of "unknown etiology" in the United States have been suspected to be caused by *Escherichia coli* and *Salmonella* serovar B (Goyal and Gerba, 1980). Epidemics of Cholera have been reported from different parts of India. The outbreak was caused by *Vibrio cholerae* 01 isolated from municipal taps and wells (Sur *et al.*, 2006).

There were an estimated 4 billion cases of diarrhea and 2.2 million deaths annually in developing countries and consumption of unsafe water has been implicated as one of the major causes of this disease (WHO, 2005). The most important pathogens transmitted by the water route were *Salmonella typhi, E. coli, Campylobacter, Shigella, Cryptosporidium and Giardia* (Mahvi and Karyab, 2007). Thus, human pathogenic microorganisms that are transmitted by water include; bacteria, viruses and protozoa and most of these organisms usually grow in the human intestinal tract and reach out through feces. Ideally, drinking water should not contain any
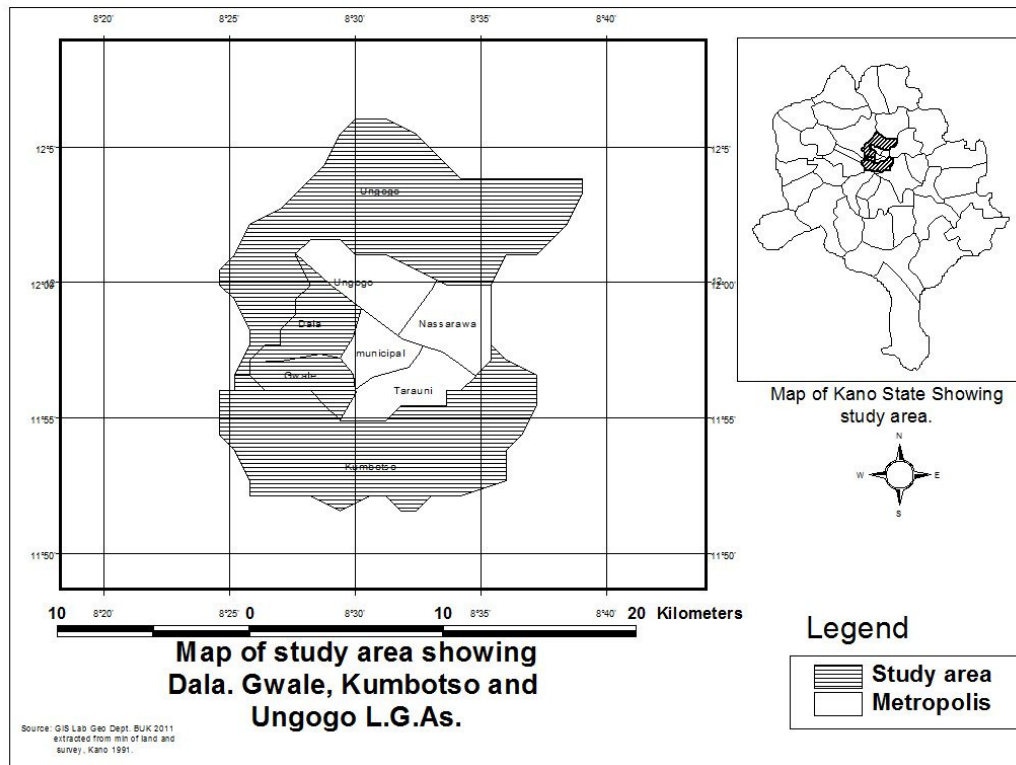
Figure 1. Map of Kano metropolis showing study areas.

microorganism known to be pathogenic or any bacteria indicative of fecal pollution, since the presence of these microorganisms has been traditionally seen as an indicator of fecal contamination, tests are useful for monitoring the microbiological quality of water used for consumption. Recognition that water is source of pathogenic microorganisms dates back to 1800 A. D. (Doestch, 1960). Because it is very expensive and time consuming to test for all pathogens, it is suggested that a single group of microorganisms that come from the same source as human pathogens can be used to indicate the presence of pathogens (Wyn, *et al.,* 2000).

MATERIALS AND METHODS

Study area

The study was conducted in four local government areas of Kano State viz: Ungogo, Dala, Kunbotso, and Gwale within Kano metropolis (Figure 1).

Sample size

A total of 212 water samples were collected from four different local government areas of Kano state.

Sample collection

Standard method described by American Public Health Association (APHA, 1999) was used for the collection of samples. During collection of samples, in each targeted house, 300ml of water was poured aseptically in to 300ml sterilized bottles. For tap water and borehole, the samples were collected by allowing the water to run to waste for 2 or 3 minutes and then the water was aseptically collected in sterile bottles. Water from wells was collected by means of a sterilized bottle fitted with a weight at the base. All samples collected were then labeled with sample number, date of collection, and sample source for analysis purposes, and then sealed. After sampling a structured questionnaire was administered to each participating household. The questionnaire included variables such as family size, devices used to collect and store water, storage duration and water treatment. Samples collected were then transported to the laboratory in an iced cooler for storage as soon as possible.

Sample filtration

Membrane filter assembly was set up by inserting the glass funnel bottom in to the opening of arm jar flask. At the side of the flask, there is narrow opening; this was

then connected to the vacuum pump machine through rubber tubing. During filtration, membrane filter was placed in to the funnel using sterile forcep. Sample was shaken vigorously at least 25 times up and down to mix the sample and then 100ml of sample was poured in to the funnel and the vacuum pump was then turned on to drain the sample through the sterile 47mm, and 0.45μm membrane filters (Whatman, Maidstone, Japan). After filtering the sample, the funnel walls were rinsed three times with 20-30ml of sterile peptone water, then the vacuum pump was turned off and the funnel top was lifted up to remove the membrane filter using sterile forcep and the filter was placed on MacConkey agar, followed by incubation at 35^{0}C for 24hours (APHA, 1999).

Microbial enumeration

Bacterial colonies on the membrane on MacConkey (Applichem Biochemica. Germany) agar were counted based on lactose fermentation (APHA, 1999).

Isolation and identification of bacteria

After incubation at 35°C for 24hours, colonies were counted based on lactose fermentation. The colonies that appear pink in color were sub cultured by using straight wire loop on to lactose broth as a presumptive test. Colonies that produce gas in the Durham tubes were sub cultured on to Brilliant green lactose bile broth (BGLB) to confirm the presence of coliforms because it suppresses the growth of anaerobic lactose farmenters like *Clostridium perfringens* which may give rise to false positive on MacConkey (APHA, 1999). Colonies that produce gas on BGLB were subjected to biochemical tests to identify the species. Motility-indole-ornithine medium was used to detect motility, indole and ornithine production (Macfaddin, 1980). *Salmonella- Shigella* agar which is a selective and differential medium was used for the differentiation of *Salmonella* and *Shigella*. Other biochemical tests such as triple sugar iron agar, Voges – proskauer, and methyl red were used to differentiate coliforms.

RESULTS

A total of 212 water samples were collected from 4 different Local Government areas of Kano metropolis, out of which 3 were from boreholes, 135 from households, 36 from taps and 38 from wells as in Table 1. Distribution of coliform counts has shown that the 2 (66.7%) of boreholes, 127 (94.1%) of households, 12 (33.3%) of taps and 34 (89.5%) of wells were contaminated (Table 1).

From the microbiological analyses performed on the

212 samples, 232 isolates of enterobacteriaceae, 31 of *Staphylococci,* and 25 of fecal *Streptococci,* were obtained and identified (Table 2). Of the 232 isolates of enteric bacteria, 7.6% was *Citrobacter fruendii,* 9.0% *Enterobacter aerogenes,* 15.6% *E. coli,* 3.1% *Salmonella typhi,* 5.6% *Shigella sonnei,* 3.8% *Yersinia* spp, 11.5% *Proteus vulgaris,* 8.3% *Providencia,* 10.8% *Klebsiella pneumoniae,* 5.2% *Serratia* spp (Table 2).

The average colony forming units were 8.33±5.77, 44.96±53.04, 6.50±6.72 and 59.16±58.05cfu/100ml for Borehole, household, tap and well respectively. And the average colony forming units were 16.78±25.81, 26.05±37.44, 95.47±66.30 and 43.03±41.71cfu/100ml for Kumbotso, Gwale, Dala and Ungogo respectively (Table 3).

DISCUSSION

In this study, twelve bacteria isolates were identified on the bases of morphological and biochemical tests and according to Bergy's Manual of Determinative Bacteriology. The majority of bacterial species identified were members of the family Enterobacteriaceae, and some *Streptococci* and *Staphylococci*. The most important organisms detected in terms of frequency were *E. coli* (15.6%), *Proteus vulgaris* (11.5%), and *Klebsiella pneumoniae* (10.8%). It is important to note that coliform bacteria are widely found in nature and do not necessarily indicate fecal pollution (Binnie *et al.*, 2002; Griffith *et al.*, 2003). *Salmonella* and *Shigella* were identified using selective and differential medium SS agar. Enteric pathogens cannot normally multiply in water hence water is not its mode of transmission to humans (WHO, 1996). However, the infective dose in people whose local or general natural defense mechanisms are impaired would be significantly low. The people likely to be at risk would be the very old or the young as well as patients undergoing immunosuppressive therapy. Other immunocompromised individuals suffering from AIDS would also be at risk. Also, water polluted by bacteria when permitted to contaminate food would lead to the multiplication of the pathogens to very large doses (Zvidzai *et al.*, 2007).

Results clearly indicated that most of the water sources were highly contaminated. It might be either due 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 or poor hygienic conditions. However some studies have associated the occurrence of coliform bacteria in drinking water system with rainfall events (Stukel *et al.,* 1990). According to these

Table 1: Microbial quality of drinking water with respect to sources

Sources	Safe (%)	Contaminated (%)	Total (100%)
Boreholes	1 (33.3)	2 (66.7)	3
Households	8 (5.9)	127 (94.1)	135
Taps	24 (66.7)	12 (33.3)	36
Well	4 (10.5)	34 (89.5)	38

Table 2. Species of bacteria identified in drinking water

Bacteria Isolates	Frequency	Percentage (%)
Citrobacter fruendii	22	7.6
Enterobacter earogens	26	9.0
E. coli	45	15.6
Salmonella typhi	9	3.1
Shigella sonnei	16	5.6
Yersinia spp	11	3.8
Proteus vulgaris	33	11.5
Providencia spp	24	8.3
Klebsiella pneumonia	31	10.8
Serratia spp	15	5.2
Staphylococci	31	10.8
Streptococci	25	8.7
Total	288	100

Table 3. Mean, standard deviation of moulds cfu/100ml with respect to sources and sites.

Source	Coliforms Cfu/100ml $X \pm mx$	Site	Coliforms Cfu/100ml $X \pm mx$
Borehole	8.33 ± 5.77	Kumbotso	16.78 ± 25.81
Household	44.96 ± 53.04	Gwale	26.05 ± 37.44
Tap	6.50 ± 6.72	Dala	95.47 ± 66.30
Well	59.16 ± 58.05	Ungogo	43.03 ± 41.71

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 in to the system through leaks and cross connections and that it can wash dissolved nutrients in to the watershed and increase organic carbon levels.

The present study indicated that about 83% water resources qualities were not fit for drinking purposes. This could be largely attributed to inadequate hygiene and sanitation of these communities. These findings were considerably higher than that of Sahelian region of Burkina Faso (30.2%) as reported by Guillemin *et al.,* (1991), but less than that of Sub - Saharan urban community (Yaounde) (95%) as reported by Nguendo – yongsi (2011).

Comparing water from taps and households, the quality of households water was worst, significantly contaminated with coliforms in 94.1% samples of drinking water (P<0.01). This could be associated with inadequate hygiene of collection and storage devices. Straus *et al.* in 2001, in Canada also observed that 20% of households sampled had indicator bacteria above the current Canadian and United States standards for safe drinking water. On comparison, water samples taken from taps were less contaminated than samples taken from wells (p<0.001), in which coliforms were isolated from 33.3% water samples, two times less than water samples taken from wells; This could be attributed to the fact that most of these wells were exposed to contamination, in that most of them were not so deep, not covered and some were very close to

toilets. So there is every chance for the water to become contaminated. Contamination of drinking water by coliforms or *E. coli* can occur from many different sources. But more often *E. coli* occurrence in water is associated with failures during water treatment or disinfection operations (WHO, 2006). This was in accordance with the work of Levesque *et al.* (1994) who also found that 22% of tap water was contaminated by at least one coliform or indicator bacterium or at least one pathogenic bacterium.

On comparison, there was no significant difference in the occurrence of coliforms between water collected from Kumbotso and Gwale and also between that of Gwale and Ungogo (p>0.05). However, there was a significant difference between water from Kumbotso and that of Ungogo in that water from Ungogo was more contaminated (p<0.05). Water collected from Dala was found to be significantly more contaminated than that collected from other sites (p<0.001). This could be attributed to the fact that Dala is an area of high population density. In fact, Dala neighborhoods are often overcrowded 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 in to open system made up of ground. This indicates that individuals from these areas might be prone to water-borne diseases (Nguendo-yongsi et al, 2008).

CONCLUSION AND RECOMMENDATIONS

The results of this work demonstrated that microbial contamination of drinking water remains a common place in some communities of Kano State, Nigeria. Recommendations are made for government actions that would increase the efficiency of efforts to ensure water quality, protect health of vulnerable populations and strengthen waterborne disease surveillance (Gostin *et al.*, 2000). Improve dissemination of information on private water testing, personal hygiene and sanitation.

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