COMPARATIVE STUDY OF COLIFORM CONTAMINATION OF PUBLIC WELLS AND PIPE BORNE WATER SUPPLIES IN BOSSO, MINNA, NIGER STATE

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Abstract

This study was carried out to determine the coliform contamination of public wells and pipe borne water supplies within Bosso town. Twenty (20) water samples comprising of 10 each of wells and pipe borne samples were aseptically collected from Bosso Town and analyzed using membrane filtration technique. The results obtained showed that all the water samples from the well and pipe had coliform counts above 10cfu/100ml. The organisms isolated and identified through various biochemical tests, included species of Escherichia, Pseudomonas, Streptococcus, Staphylococcus, Salmonella, Shigella, Campylobacter, Bacillus, Proteus, Helicobacter, Klebsiella, and Yersinia. E.coli had the highest frequency of occurrence (24.4%) followed by Helicobacter pylori (13.3%), Staphylococcus aureus (10.0%), Salmonella typhi (8.9 %), Shigella flexneri (6.7%), Streptococcus faecalis (5.6%), Streptococcus pyogenes (5.6%), Campylobacter jenuni (4.4%), Pseudomonas aeruginosa (4.4%), Bacillus subtilis (4.4%), Proteus mirabilis(4.4%), Klebsiella pneumonia (3.3%), Proteus vulgaris (3.3%) and Yersinia enterocolitica (1.1%). This study revealed that well water and pipe borne water samples were contaminated, with greater contamination observed with well water. This highlights the need for a continuous assessment of the quality of public water supply and intervention measures to prevent outbreak of water-borne diseases.

Keywords: Pipe borne, Well, water, organisms, water-borne disease

Introduction

Water, as one of the basic components of life is important to man, animals and plants (Ajewole, 2005). It is an essential medium required to sustain life of all living organisms, due to its unique chemical and physical properties (Obi and Okocha, 2007). According to Third World Academy of Science (TWAS), safe drinking water is a basic human requirement and it is essential for sustainable development (Omar, 2008). Also, when water is distributed to the end users, in a condition in which it is produced with required treatments, the microbial load would be reduced to a safe level (Nwachukwu *et al.,* 2000). Unfortunately, prior to the time water gets to its end users, it is usually prone to various microbial contaminations with pathogenic microorganisms, which constitute serious threat to public health (Stender *et al.,* 2001). Many people, especially in the developing world, depend on untreated surface and ground water sources for their daily water needs, and water from these sources are often contaminated (Omar, 2008).

Most water bodies contaminated with faecal coliforms clearly indicate that the water body contains other opportunistic organisms that are medically important to humans, which may cause severe illness and subsequently death. Environmental Protection Agency (EPA) (2009) reported that high pathogens in water bodies may result from inadequately treated sewage discharged from various septic tanks, and use of such water by the general populace leads to

acquisition of pathogens through various routes of transmission such as: Oral, Dermal and as Aerosol (Hailer *et al.,* 1999; APEC, 2010).

The faecal pathogens in most water supplies are diverse groups of organisms such as bacteria (e.g*. E. coli* 0157: H7, *Shigella* spp, *Campylobacter jejuni*, *Salmonella* spp and *Yersinia* spp), protozoa (for example, *Entamoeba histolytica*, *Gardia* spp and *Cryptosporidium* spp) and viruses (e.g. Noroviruses, Enteroviruses, Adenoviruses, Rotaviruses and Hepatitis A and E viruses) (Jorge *et al.,* 2008). Also, some water borne pathogenic diseases that may coincide with faecal contamination include ear infections, dysentery, typhoid fever, cholera, encephalitis, giardiasis, gastroenteritis and hepatitis (Hailer *et al*., 1999).

Generally, the water obtained from most public water supplies, is expected to be a life-supporting medium, but studies have shown such water from various water supplies does not only improve the standard of life but can also serve as a carrier of dangerous pathogens (Oyedum, 2010). However, the role of contaminated water in the transmission of disease and the importance of water in public health cannot be overemphasized, based on the fact that it is difficult for the general public to distinguish between safe water and portable water, thereby increasing their vulnerability to illness that normally arises from the consumption of contaminated water. Therefore, it is imperative that various public water supplies are evaluated continuously to enable the detection and prevention of disease outbreaks. This study is therefore aimed at evaluating the quality of various public water supplies to Bosso and its envions, where the general populace depends on it for their daily activities and survival.

Materials and Methods

Study Area: The study was conducted between May and August 2015 in Bosso Central, Bosso Low-cost, Bosso Estate, Okada Road, El-waziri, Anguwan Tukura, Tudun Fulani, Rafin Yanshi, Federal University of Technology (FUT) Bosso Campus and Maikunkele all in Bosso Local Government Area of Niger State. All the taps and wells sampled were constructed close to buildings with soakaways, pit latrines or refuse dump sites and were frequently used by the inhabitants around the area for drinking and other domestic purposes.

Collection of Samples: Aliquots of two hundred milliliters (200 mls) each of twenty samples (made up of 10 samples of tap and 10 samples of well water) were collected aseptically in sterile sampling bottles and taken to the laboratory immediately for analysis within 3 hours (Adabara *et al.,* 2011).

Analyses of Samples: The samples were analyzed using membrane filter technique. Prior to filtration, each of the two hundred milliliters (200 mls) of water sample aseptically collected was divided to obtain two sets of 100ml of the water sample. The two sets of the hundred milliliters (100mls) were filtered simultaneously using 0.45µm pore sized membrane filter with 47mm diameter. The filter papers for each sample were then aseptically transferred onto two Petri dishes containing absorbent pads soaked previously in membrane lauryl sulphate broth using sterile forceps. These steps were subsequently repeated for each other sample of the water collected. The two Petri dishes for each sample were inverted and incubated at 30^{o}C for 4 hours. After which, one of the Petri dishes was then transferred to an incubator at 37°C for 14 hours, to isolate the total coliform, while the second Petri dish was placed in an incubator for 44°C for 14 hours for the isolation of faecal coliform respectively. The yellow colonies appearing on the plates were counted immediately following the incubation period (Oyedum, 2010).

Identification of Isolates: Isolates from primary cultures incubated at (37°Cand 44°C) were aseptically subcultured on to fresh media (such as, MacConkey agar and Nutrient agar) to obtain pure cultures using the streak plate technique. The pure isolates were identified and characterized and were stored into already prepared slant bottles. This was done using cultural characteristics and appropriate biochemical tests such as Coagulase, Catalase, Urease, Indole, Sugar fermentation, Citrate utilization, Mannitol salt and Starch hydrolysis. The isolates were identified using the schemes of Cheesbrough (2006).

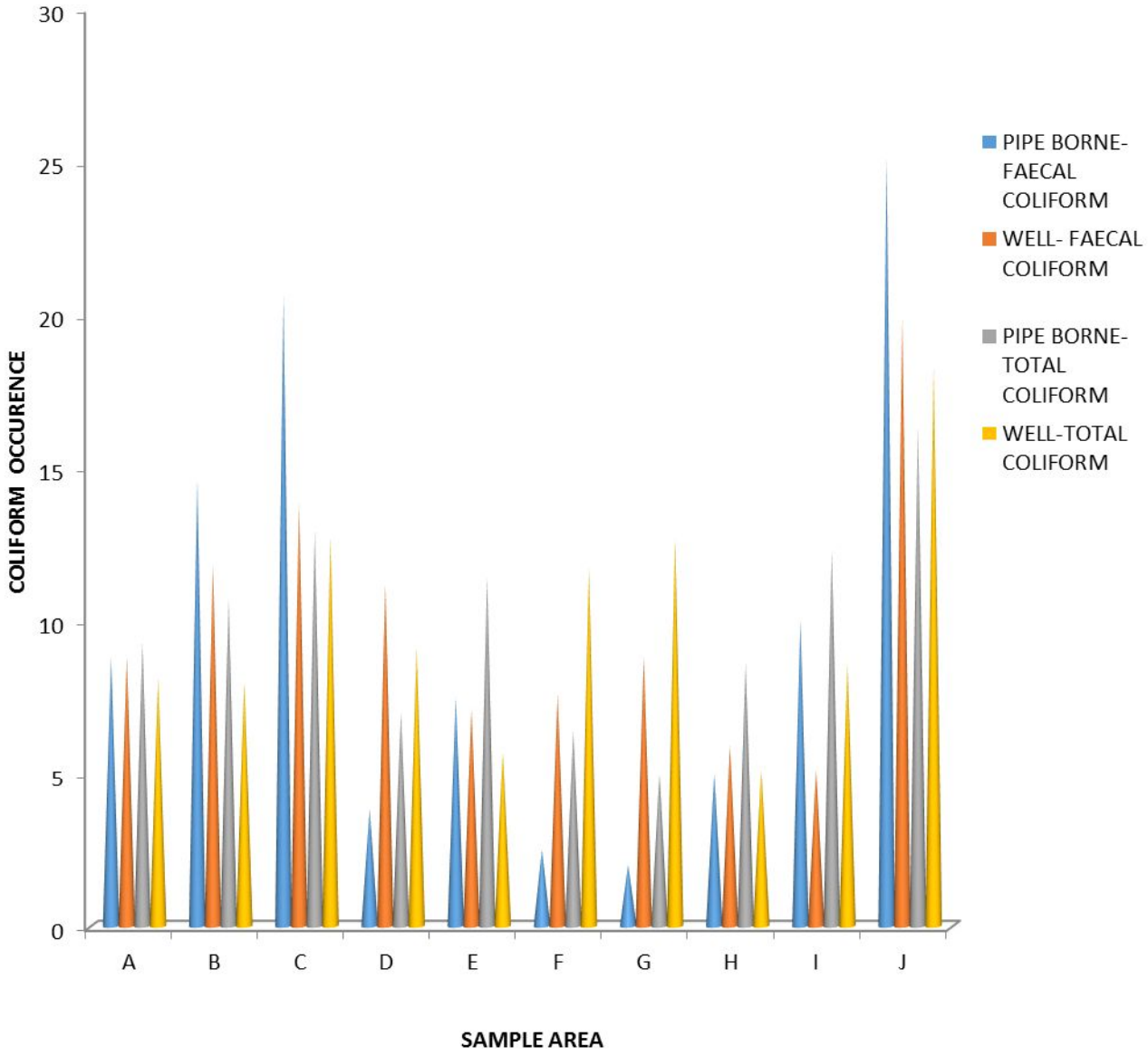
Results

The result obtained showed that faecal coliform count from the wells ranged from 35.0 to 135.0 cfu/100ml while faecal coliform count from the taps ranged from 8.0 to 100.0 cfu/100ml.The result also showed that total coliform count from the wells ranged from 100.0 to 360.0 cfu/100ml while total coliform count from the taps ranged from 70.0 to 228.0 cfu/100ml (Table 1).

Ninety (90) isolates were identified and characterized from the water samples analysed. *E.coli* had the highest frequency of occurrence followed by *Helicobacter pylori, Staphylococcus aureus*, *Salmonella typhi*, *Shigella flexneri, Streptococcus faecalis*, *Streptococcus pyogenes*, *Campylobacter jenuni, Pseudomonas aeruginosa*, *Bacillus subtilis*, *Proteus mirabilis, Klebsiella pneumoniae, Proteus vulgaris*, and *Yersinia enterocolitica* (Table 2).

TABLE 1. Coliform count in samples of well and pipe borne water

Location of sample collected	Faecal coliform counts for well water x10²(cfu/100 ml)	Percentage faecal coliform count for well water (%)	Total coliform count for well water x10² (cfu/100ml)	Percentage total coliform count for well water (%)	Faecal coliform count for Pipe borne water x 10² (cfu/100ml)	Percentage faecal coliform count for pipe borne water (%)	Total coliform count for pipe borne water x10² (cfu/100ml)	Percentage total coliform count for pipe borne water (%)
Rafin Yashi	0.60	8.8	1.60	8.1	0.35	8.8	1.30	9.3
Bosso Low cost	0.80	11.8	1.58	8.0	0.58	14.6	1.50	10.7
EL-Waziri	0.94	13.8	2.50	12.7	0.82	20.6	1.80	12.9
Anguwan Tukura	0.76	11.2	1.80	9.1	0.15	3.8	0.98	7.0
Okada Road	0.48	7.1	1.12	5.7	0.30	7.5	1.60	11.4
Maikunkele	0.52	7.6	2.30	11.7	0.10	2.5	0.90	6.4
F.U.T Minna	0.60	8.8	2.50	12.7	0.08	2.0	0.70	5.0
Tudun Fulani	0.40	5.9	1.00	5.1	0.20	5.0	1.20	8.6
Bosso Estate	0.35	5.1	1.00	8.6	0.40	10.0	1.72	12.3
Bosso Central	1.35	19.9	3.60	18.3	1.00	25.1	2.28	16.3



KEY: A=RAFIN-YASHI; B=BOSSO LOWCOST; C=EL-WAZIRI; D=ANGUWAN TUKURA; E= OKADA ROAD; F=MAIKUNKELE; G= FEDERAL UNIVERSITY OF TECHNOLOGY; H=TUNDUN FULANI; I=BOSSO ESTATE; J=BOSSO

Table 2 shows a total of 90 isolates in the descending order of their frequency of occurrence as *E.coli, Helicobacter pylori, Staphylococcus aureus*, *Salmonella typhi*, *Shigella flexneri, Streptococcus faecalis*, *Streptococcus pyogenes*, *Campylobacter jenuni, Pseudomonas aeruginosa*, *Bacillus subtilis*, *Proteus mirabilis*, *Klebsiella pneumoniae, Proteus vulgaris*, and *Yersinia enterocolitica.*

Table 2. Frequency of occurrence of bacterial isolates

Organisms	Frequency	Percentage (%)
E.coli	22	24.4
Helicobacter pylori	12	13.3
Staphylococcus aureus	9	10.0
Salmonella typhi	8	8.9
Shigella flexneri	6	6.7
Streptococcus faecalis	5	5.6
Streptococcus pyogenes	5	5.6
Campylobacter jenuni	4	4.4
Pseudomonas aeruginosa	4	4.4
Bacillus substilis	4	4.4
Proteus mirabilis	4	4.4
Klebsiella pneumoniae	3	3.3
Proteus vulgaris	3	3.3
Yersinia enterocolitica	1	1.1
Total	90	100

Discussion

The results shown in Table 1 revealed that the public water analysed within the study areas were contaminated. All the well water samples had coliform counts above the World Health Organization (WHO) recommended standard, of not more than 10 coliform organisms / 100ml of water (WHO, 2003). This result could be attributed to the fact that, well water which is one of underground sources of water is commonly used, due to the fact that wells are easily constructed and affordable and based on this, little or no attention is given to the adequate construction of wells. For this reason, most of these wells sampled in the study area lacked adequate concrete lining and were inadequately elevated, thereby collecting the runoff of surface water that contained coliforms. This result agrees with the findings of Bala (2006), Oyedum (2010) who reported that most of the wells sampled were not lined with concrete and were lowly elevated. However, the entire pipe borne water sampled had coliform counts above 10 coliform organisms /100ml of water. The pipe borne water contamination observed in this study maybe due to the fact that most water distributors pay less attention in flushing the head pumps and pipes of these pipe borne- water adequately to prevent the accumulation of microorganisms. Also, in most cases the head pumps and the pipes are not protected from formites regularly. Based on these, they are thus said to serve as habitats for various coliforms which give rise to the development of biofilms and this constantly contaminates the water that flows out, for the populace to use. This result is similar with the result of Okoko and Idise, (2014) who reported that the presence of biofilms in the various tap water could be attributed to defective joints on the pipes, rusted pipes crossing over the sewage or low/ high pressure in sewage pipes.

Furthermore, the heavy coliform contamination of these well water sampled could be attributed to the fact that most of these wells were observed to lack proper covers/lids. Unfortunately, due to the fact that these wells sampled were inappropriately protected, most of these wells were exposed to animal droppings, dead animals, nasal droplets, rain splash, seepage splash, sewage, formites and wind heavily contaminated with coliforms. This result

is similar with the result of Adabara *et al.* (2011). In addition, most of the wells sampled lacked sterile and permanent water fetchers to draw water from these wells, due to this practice, these wells are faced with heavy microbial contamination. This result is similar to that of Bala (2006), who reported that well due to inadequate coverings could be polluted by dirt on different tins or buckets that are lowered into the wells. On the other hand, the high microbial contamination observed in the various taps is an indication that the pipes due to improper handling during their production and their lack of adequate maintenance, prior to their usage in the supply of water, serve as habitat to various contaminants in the environment and base on this, they are said to enhance the contamination level of the water that passes through them. According to the report of WHO (2003), the level of contaminations in various water supplies, is regarded as a risk factor, which enhances the outbreak of diseases like cholera or typhoid. In addition, the contamination of these tap water is also based on the fact that, the source of the water that is channeled through the pipes, are heavily contaminated with coliforms and in most cases such pipe borne water lack adequate chlorination (chlorine residual of 1mg/l or greater for at least 30mimutes) (Ibrahim *et al.,* 2013) to eradicate these coliforms before the water is supplied.

The area with the highest percentage of faecal coliform contamination is Bosso central (Figure 1). This result could be attributed to the fact that various unhygienic life styles such as localize and mechanize farming with human faeces, construction of soakaways, septic tanks and pit latrines and irregular defecation are highly practiced around the locations of the wells and taps in this area. The farming and construction activities lead to violation of the pipelines and this in turn could lead to the penetration of various microorganisms including coliforms into the various pipelines within this area. This result agrees with the findings of Bala (2006); Mashi (2013) who reported that damage on the pipelines in the environment where they are laid permit the contamination of the tap water by sewage that easily seeps into the broken pipes. Consequently, such contaminated water in turn, lead to the cause and spread of waterborne infections, such as typhoid fever, amoebic dysentery, bacillary dysentery, cholera, poliomyelitis and hepatitis as reported by Geldreich (2005), Okoko and Idise (2014).

Organisms isolated from the water samples in this study were species of *Escherichia, Helicobacter, Staphylococcus, Salmonella, Shigella, Streptococcus, Campylobacter, Pseudomonas, Bacillus, Proteus, Yersinia* e.t.c. This findings agree with result of Benka-Coker and Olimani (1995); Edema *et al.* (2006) and Ukpong (2008) whose works revealed that these organisms are basically regarded as water resident organisms. *E.coli* had the highest frequency of occurrence (24.4%) followed in descending order by *Helicobacter pylori* (13.3%), *Staphylococcus aureus* (10.0%), *Salmonella typhi* (8.9 %), *Shigella flexneri*(6.7%), *Streptococcus faecalis* (5.6%), *Streptococcus pyogenes* (5.6%), *Campylobacter jenuni* (4.4%), *Pseudomonas aeruginosa* (4.4%), *Bacillus subtilis* (4.4%), *Proteus mirabilis*(4.4%), *Klebsiella pneumonia* (3.3%), *Proteus vulgaris* (3.3%), and *Yersinia enterocolitica* (1.1%). *E. coli* with the highest frequency in this study indicates that the water from these various sources were faecally contaminated recently because *E.coli* is an indicator of recent faecal contamination. The result obtained from this study also agrees with the findings of Bala (2006), who isolated various organisms from the water samples from various areas in Jimeta, Yola, Adamawa State with *E.coli* having the highest frequency of occurrence.

Conclusion

In conclusion, the indication of contamination in both well and tap water is basically due to inadequate attention given to the various water sources and their constructions, to enable them serve as portable water supplies, which is essential to a human life. It is therefore

recommended that environmental health workers should help in carrying out efficient surveillance on the various water sources on regular basis to help detect lapses on the pipelines or boreholes and immediately give suggestions on how to solve the problem to avoid outbreak of waterborne disease. In addition, the Pipeline and Wells should be adequately constructed and fortified to avoid damage. Effective and sufficient chlorination treatment should be carried out on various water bodies before they are channeled to various pipelines for usage.

References

Adabara, N. U., Mawak, J. D., Momohjimoh, A., Bala, J. D., Abdulrahaman, A. A., Oyedum, U. M., & Jagaba, A. (2011). A relative bacteriological assessment of public borehole and well water in Bosso town, North-Central Nigeria. *International Journal of Biomedical and Advance Research,* 2(10), 416 - 420.

Ajewole, G. (2005). *Water an overview food forum magazine. Nigerian Institute of Food Science analysis.* Retrieved June 10,2010 from http://www.gjournals.org.

APEC (2010). *Water education: How does coliform bacteria affect water quality.* Retrieved June 10,2010 from http://www.freedrinkingwater.com.

Bala, J. D. (2006). Occurrence of fecal coliform in water sources in Jimeta-Yola. *Journal of Environmental Science,* 10 (2), 64 - 66.

Benka-Coker, M. O. & Olimani, E. L. (1995). Investigation of spatial variations in bacteria distribution in surface water of Ikpoba River. *Nigeria Journal of Microbiology*, 10, 27-32.

Edema, M. O., Omenu, A. M. & Fapeta, O. M. (2006). Microbiology and physiological analysis of different sources of drinking water in Abeokuta. *Nigeria Journal of Microbiology*, 13(1), 57 - 61.

Environmental Protection Agency (2009). *Illness related to sewage in water.* Accessed February 20,2009.From http://en.wikipedia.org/wiki/water-pollution.

Geldreich, E. (2005). The Bacteriology of water. In L, Collier, A, Balows, M, Sussman, T. Wilsons, (Eds.), Microbiology and microbial infections 9th edition. London: Hodder Arnold. Pp. 351-363.

Hailer, R. W., Witte, J. S., Gold, M., Cressey, R., McGee, C., Millikan, R. C., Glasser, A., Harawa, N., Ervin, C., Harmon, P., Harper, J., Demand, J., Alamillo, J., Barrette, K., Nides, M. & Wang, G. (1999). The health effects of swimming in ocean water contaminated by storm drain runoff. *Epidermiology*, 10, 355 - 363.

Ibrahim, T. A., Akenroye, O. & Opawale, B. O. (2013). A survey of physicochemical and bacteriological quality of pipe-borne water used for drinking in Rufus Giwa Polytechnic, Owo Ondo State, Nigeria. *Greener Journal of Science, Engineering and Technology Research,* 3(6), 181 - 185.

Jorge, W., Santo, D. & Nicholas, J. A. (2008). *Faecal pollution of water Encylopedia of Earth.* Retrieved March 20,2010.From http://www.ask.com.

Mashi, B. H. (2013). *Comparative bacteriological analysis of drinking water samples in Katsina state.* Retrieved March 20,2010.From www.transcampus.org/journals.

Nwachukwu, N., Caldron, R. L., & Gram, H. F. (2000). Outbreaks in drinking water systems, 1991-1998. *Journal of Environmental Health,* 65,16 - 25.

Obi, C. N. & Okocha, C. O. (2007). Microbiological and physicochemical analyses of selected borehole waters. *Journals of Engineering and Applied Science*, 257, 920-929.

Okoko, F. J. & Idise, O. E. (2014). Assessment of chemical and bacteriological quality of pipe-borne water from various locations in Delta State University, Abraka, Nigeria. *African Journal of Microbiology Research,* 8(21), 2137 - 2143.

Omar, K. B. (2008). *A review article on water.* Retrieved January 25, 2010. From http://ujdigispace.ujac.za:8080/dspace/Stream/10210/859/2/chapter%201%%20Introduction%20and%20Literature%20review.pdf

Oyedum, M. U. (2010). *Occurrence of faecal coliform contamination of well and borehole water.* A project thesis presented to the Department of Microbiology, Federal University of Technology Minna, Niger State, Pp.6.

Stender, A., Broomer, A. J., Olinera, K. & Healthier, P. O. (2001). Detection, identification and enumeration of *Escherichia* in municipal water. *Applied and Environmental Microbiology,* 45, 142 - 147.

Ukpong, J. T. (2008). Water Quality parameter of domestic water source in Uyo local Government Area, Nigeria. *International Journal of Environmental Issues,* 4, 1 - 2.

World Health Organization (WHO) (2003). *Guildlines for drinking water quality.* Pp 81- 87, World Health Organisation, Geneva, Switzerland.