Microbial Composition and Abundance in Drinking Water Sources Within Narok Town and its Surrounding, Kenya.

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Abstract

Narok, a fast growing town in Kenya's Rift Valley faces major challenges of water provision due to its arid and semi arid location and there is need to ascertain the quality of water used by the residents. Multiple Tube Fermentation method was used to undertake water quality assessment. Total coliforms ranged between 2.3 x 10^1 MPN/100ml and 1.1 x 10^3 MPN/100ml during the dry season and 4.6 x 10^2 MPN/100ml and 1.1 x 10^3 MPN/100ml during the wet season. Faecal coliforms ranged between 0.9 x 10^1 MPN/100ml and 3.9 x 10^1 MPN/ 100ml during the dry season and 2.3 x 10^1 MPN/100ml to 2.4 x 10^2 MPN/100ml during the wet season. Pathogenic bacteria were isolated; E. coli, Shigella spp, Enterobacter spp, Proteus spp and Salmonella spp. The water sources contained bacteria levels higher than recommended levels. Proper waste management, separation of water pans meant for human and animal consumption and use of hygienically placed and maintained water tanks should be implemented to improve drinking water quality at the point of use and protect water sources from contamination. Other climate smart environmentally sustainable sources of drinking water such as rainwater harvesting and shallow wells should be explored.

Key words: **Narok, SDG 6, drinking water, microbial analysis, water pans.**

Introduction

Water is an enabler to development. One of the greatest challenges faced by rapidly developing urban centres in Africa is provision of sustainable sources of potable water (Stephanie *et al.*, 2017). This problem is compounded in highly water stressed environments such as arid and semi arid areas. Narok is a rapidly growing town located in the water stressed Rift Valley region in Kenya. The onset of the COVID-19 pandemic is going to increase water required by populations thereby further straining available water sources (USAID, 2021).

Microbial quality of water can be determined by presence and quantity of microorganisms. These microorganisms in drinking water are a major concern to consumers, water suppliers, regulators and public health authorities (Nicholas, 2015). One of the most widespread and serious classes of water quality contaminants, especially in areas where access to clean, safe water is limited, is pathogenic organisms such as bacteria, protozoa and viruses. These organisms pose one of the leading global human health hazards. Globally, 500,000 children were reported to have died from diarrheal disease, a majority of which are caused by unsafe water, inadequate hygiene and poor sanitation (GBD, 2015). In Kenya, the disease burden attributed to waterborne infections like typhoid and dysentery is estimated at 19500 including 17,100 children under the age of 5 (WSP, 2012) representing approximately 70- 80% of health issues in Kenya. The greatest risk of microbial contamination comes from consuming water contaminated with pathogens from human or animal faeces (Alexander *et al.*, 2015). In addition to microorganisms introduced into waters through human or animal faecal contamination, a number of pathogenic microorganisms are free- living in certain areas or are, once introduced, capable of colonising a new environment (WHO, 2003). The potential of drinking water to transport microbial pathogens to great numbers of people, causing subsequent illness is well documented in countries at all levels of development (Nicholas, 2015). In addition, bacterial community structure has been found to differ significantly with seasons (Maja *et al.*, 2021). Post treatment contamination of storage reservoirs and contamination of mains from repairs have been identified as causes of distribution-system contamination linked to illness (Craun and Calderon, 2001, Hunter *et al.*, 2005).

The best means of safeguarding against the presence of waterborne pathogens in drinking water is the application of the multi- barrier approach that includes assessment of the entire drinking water system, from the watershed or aquifer and intake through the treatment and distribution chain to the consumer to assess the potential effects on drinking water quality and public health. The primary purpose of drinking water quality guidelines is the protection of public health (WHO, 2006). Diseases related to contamination of drinking water constitute a major burden on human health. Interventions to improve the quality of drinking water provide significant benefits to health. Faecally derived pathogens are the principal concerns in setting health-based targets for microbial safety (Lisa *et al.*, 2019). The objective of zero *E. coli* per 100ml of water is the goal of all water supplies (WHO, 2006). Environment

Protection Agency (EPA, 2006) states that the Heterotrophic Plate Count should be no more than 500 bacterial colonies per milliliter. The total coliform positive should be no more than 5.0% of the samples (EPA, 2006). Presence of faecal coliform and *E.coli* indicates that the water may be contaminated with human or animal wastes. Disease-causing microbes in these wastes can cause diarrhea, cramps, nausea, headaches or other symptoms. These pathogens may pose a special risk for infants, young children and people with severely compromised immune systems. Every year, more people die from the consequences of unsafe water than from all forms of violence, including war and the greatest impacts are on children under the age of five (WHO, 2002). Unsafe or inadequate water, sanitation and hygiene cause approximately 3.1% of all deaths- over 1.7 million deaths annually and 3.7% of Disability Associated Lost Years worldwide (WHO, 2002).

For decades, water scarcity has been a major issue in Kenya, caused mainly by years of recurrent droughts, poor management of water supply, contamination of the available water and a sharp increase in water demand resulting from relatively high population growth (Samantha, 2011). In Kenya, 87% of the urban population enjoys access to at least basic water service compared to 50% of rural inhabitants (UNICEF, 2017). Bacterial, protozoal, viral diarrhea and typhoid fever are the most commonly reported waterborne diseases (UNICEF, 2013). Increasing access to improved drinking water; SDG 6, is critical to make meaningful gains towards meeting the SDGs and even other sustainable development milestones such as Vision 2030 and the Big 4 Agenda (UN, 2018). Bacterial and protozoal diarrhea, hepatitis A and typhoid fever are the most common diseases spread through contact with food or water contaminated by faecal matter or sewage. The microbiological quality of drinking water is a concern to consumers, water suppliers, regulators and public health authorities alike (WHO, 2006). The potential of drinking water to transport microbial pathogens to great numbers of people, causing subsequent illness is well documented in countries at all levels of development (Nicholas, 2015).

The objective of this study was to determine the quality of water in Narok town and its environs with respect to microbial composition and abundance. This is a first step towards providing data that can inform evidence towards management of water resources within the arid landscape and development of policies and strategies aimed at addressing SDG 6.

Materials and Methods

Study Site

21km of the Narok- Bomet highway (B3) running between Narok town ($1^0$5'15.1548" South and $35^0$52'37.4304"East and Katakala centre (1.1001^0 South and 35.7701^0 East) was used as a transect line with 20 km distance on either side to strategically select three water sources which included rivers, water tanks and water pans at points where water for domestic consumption was sourced by the community.

Study Design and Sample Collection

Sampling was undertaken during dry and rainy seasons.

Sample size was determined as per the formula by Israel (2009).

$$n = \frac{N}{1 + N\,(e)^2}$$

Where: N = Population size (households)

n= Number of samples

e = Level of precision

$$n = \frac{56315}{1 + 56315\,(0.05)^2} = 398 \text{ samples.}$$

100ml of water was collected for each of the 398 samples from river water, pan water and water tanks (66 samples per water source, per season) using sterile Duran bottles, covered and kept in an ice box then transported to the Maasai Mara University Biological Sciences laboratory for analysis within 6 hours.

Presumptive Test

Samples of treated water were inoculated into Mac Conkey broth double strength and single strength media with Durham tubes as per standard methods (Lenore *et al.*, 1989). Incubation was done at 35°C for 24 and 48 hours. Samples from non- treated water sources were diluted (1: 10) then inoculated into double and single strength Mac Conkey broth media. Undiluted samples were also inoculated into double and single strength Mac Conkey broth media. Incubation was done at 35°C for 24 and 48 hours. The tubes were checked for presence of growth and gas production. The Most Probable Number (MPN) was determined using the MPN index (Lenore *et al.*, 1989).

Confirmatory Test

Inoculums from positive tubes (growth and gas production) in the presumptive test were inoculated into Brilliant Green Lactose (Bile) Broth (BGLB) (incubated at 35°C) and Tryptone water (incubated at 44°C). After 24 hours, each broth tube was examined for growth and presence of gas in the Durham tube. To each tube of tryptone water, approximately 0.1ml of Kovacs reagent was added and mixed gently. Presence of indole was indicated by a red colour forming a film over the aqueous phase of the medium and the MPN was determined as described by Lenore *et al.*, 1989.

Completed Test

From Brilliant Green Lactose Bile (BGLB) broth tube of the highest dilution showing growth and gas production, a plate of Eosin Methylene Blue (EMB) agar was streaked then incubated at 37°C for 24 hours and the Gram Stain technique (Cheesbrough, 2004) was done on each colony after incubation. Thereafter, those colonies which were Gram negative were inoculated into TSI agar, Simmons Citrate agar, Urea media, MR-VP broth then incubated for 24–48 hours at 37°C. The media was then observed for changes in colour, appearance and reaction to added reagents. Results obtained were compared to the reactions expected for typical coliforms and the bacterial isolates were then identified according to the procedure described by Arlington (1992).

Results and Discussion

From this study, it was found that the MPN (Most Probable Number)/100ml values for total coliform bacteria in the study areas were beyond WHO recommendations. During the dry season, total coliform count of 0.9×10^1 MPN/100ml was recorded in the water tanks and 4.6×10^2 MPN/100ml in the rainy season (Table 1). These findings correspond to a study by Abok *et al.*, 2018 on microbiological quality and contamination of water sources in Isiolo town where ground and surface water sources were contaminated with microorganisms beyond national regulatory standards levels. Similar findings were obtained by Mbaka *et al.*, (2017) in a study on the water quality of shallow wells in Keiyo Highlands, Kenya where mean levels of faecal coliforms during the dry and wet season ranged between 4.04 MPN/1ml

and 31.56 MPN/100ml respectively. In Enkare Narok and Ewaso Ng'iro rivers, the total coliform count recorded was 2.3 x 10^1 MPN/100ml and 1.1x10^3 MPN/100ml during the rainy season (Table 1). These findings were lower than those obtained by Ombaka and Gichumbi (2012) and Shittu *et al.*, (2008) on Irigu River Meru South where the total coliform concentration was found to be more than 2.42 x 10^3 MPN/100ml in the dry and wet season and Sokori stream and Lafenwa river in Nigeria where analysis of bacteria in drinking water and water used for swimming purposes were found to have a total coliform count of 1.8 x 10^3 MPN/100ml respectively. Opisa *et al.*, (2012), in a study on faecal contamination of public water sources in informal settlements of Kisumu City, Kenya found the water sources to be highly contaminated. Findings from this study also indicated the presence of faecal coliform bacteria in the water samples collected from all of the water sources under study. The concentrations ranged between 0.9 x 10^1 MPN/ 100ml in the water tanks, 3.9 x 10^1 MPN/100ml in the water pans during the dry season and between 2.3 x 10^1 MPN/100ml in the water tanks and 2.4 x 10^2 MPN/100ml in Enkare Narok river during the rainy season (Table 1). The increase in numbers during the rainy season can be attributed to contamination from surface run off resulting from rainfall.

In this study, the bacteria isolated from the water sources were *Escherichia coli, Shigella* spp, *Proteus* spp, *Salmonella* spp, *Enterobacter* spp, *Klebsiella* spp and *Citrobacter* spp (Table 2). These are pathogenic bacteria and they pose health risks to the residents who consume without any form of treatment. The water analysed from the rivers in the present study was found to contain *E. coli*, *Shigella* spp, *Proteus* spp and *Salmonella* spp. These findings concur with studies by Musyoki *et al.*, (2013) where bacteria isolated from the Nairobi River and Athi River included *Shigella flexneri, Salmonella typhi, Salmonella paratyphi,* and *E. coli* and those of Silas *et al.*, 2011 on Njoro River where it was reported that the river was heavily contaminated with *Salmonella typhimurium, S. typhi,* and *E. coli*. The water samples collected from the water tanks in the study area were found to contain *E. coli, Enterobacter* spp, *Klebsiella* spp and *Citrobacter* spp. However, from some of the water storage tanks, there was no growth observed. The findings from the current study correspond with those of Nwachukwu and Ume (2013) who isolated *E. coli, Klebsiella* spp, and *Enterobacter aerogenes* from various drinking water sources in a local area of Eastern Nigeria. Ngwa and Chrysanthus (2013) analysed bacterial composition of well water sources in Bambui student residential area, Cameroon, and found out that the well water samples from the locations under study were highly contaminated with *E. coli, Klebsiella* spp and *Enterobacter* spp. Katiyar *et al.*, (2013) analysed drinking water samples in Delhi, NOIDA and Meerut and identified various kinds of bacteria. They revealed that *E.coli* and *Pseudomonas* were more abundant when compared with *Enterobacter* and *Klebsiella*. A study of bacteriological quality of drinking water sources of Hail, Saudi Arabia conducted by Abdullah *et al.*, 2016 found out abundance of *E. coli* (26.66%), *P. aeruginosa* (12.22%), *Klebsiella* (8.88%) and *Salmonella* (6.66%) from the samples analysed. In the current study, bacteria isolated from the water pans were *Enterobacter* spp and *Shigella* spp during the dry and rainy season respectively. These results are similar to a study carried out in Abeokuta in Nigeria by Shittu *et al.*, 2008 where the water samples from surface water sources were found to contain *E. aerogenes* and *Shigella* spp. The findings in this study

were higher than those recommended by the WHO, EPA and KEBS for irrigation and drinking water. This study has provided evidence on water quality status of water sources used by local community members that can inform public health interventions to safeguard public health in Narok. The public should be educated against direct consumption of water from the rivers and water pans. Efforts should be made to protect the water sources from pollution by instituting community based water resource management for example by strengthening existing Water resource User Associations (WRUAS).

Conclusion

The water sources widely used in Narok are heavily contaminated with faecal and total coliform bacteria and not suitable for direct consumption. Possible sources of water contamination include disposal of human waste into the water and contamination with rain water runoff from shallow pit latrines. Some of the treated water was found to be contaminated at the point of use but not at the source. This could be an indication of leakage of old and unrepaired pipes, bursts along water pipelines and unhygienic handling of water at the point of use. Most of the residents used underground concreted tanks that were refilled periodically but were also prone to contamination from rainwater runoff and seepage from pit latrines because they were on the same level as the ground. Water pans could have been polluted mostly via animal and human excreta through rain water runoff and direct defecation. Bacterial contamination was higher during the rainy season than the dry season which can be attributed to contamination of the water sources through rain water runoff. Proper solid and liquid waste management, separation of water pans meant for human and animal consumption and use of hygienically placed and maintained water tanks should be implemented in order to improve drinking water quality at the point of use and protect water sources from contamination. Exploration of climate smart environmentally sustainable sources of drinking water such as rainwater harvesting and shallow wells will be a major step towards achieving water security in Narok.

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Table 1: ***Faecal Coliform and Total Coliform Diversity during the Dry and Rainy Seasons in Water Sources in Narok Town and its Environs.***

	Faecal coliforms MPN/100ml	Faecal coliforms MPN/100ml	Total coliforms MPN/100ml	Total coliforms MPN/100ml
	DRY SEASON	RAINY SEASON	DRY SEASON	RAINY SEASON
Enkare Narok	2.3×10^1	2.4×10^2	1.1×10^3	1.1×10^3
Ewaso Ng'iro	2.3×10^1	2.1×10^2	1.1×10^3	1.1×10^3
Water Pans	3.9×10^1	7.6×10^1	2.4×10^2	1.1×10^3
Water Tanks	0.9×10^1	2.3×10^1	2.3×10^1	4.6×10^2
Katakala	1.5×10^1	1.25×10^2	2.13×10^2	8.7×10^2

Table 2: Microbial Diversity (%) in Water Sources during Dry and Rainy Season in Water Sources in Narok Town and its Environs.

	Katakala		Water Pans		Water Tanks		Enkare Narok		Ewaso Ng'iro	
Bacterial Isolates	Dry Season (%)	Rainy (%)	Dry Season (%)	Rainy (%)	Dry Season (%)	Rainy (%)	Dry Season (%)	Rainy (%)	Dry Season (%)	Rainy (%)
E. coli	100	0	0	0	30	19	63	36	59	0
Shigella spp	0	100	0	100	0	0	37	32	0	50
Enterobacter spp	0	0	100	0	16	15	0	0	0	0
Klebsiella spp	0	0	0	0	45	13	0	0	0	0
Citrobacter spp	0	0	0	0	0	29	0	0	0	0
Proteus spp	0	0	0	0	0	0	0	32	41	17
Salmonella spp	0	0	0	0	0	0	0	16	0	33
No Growth Observed	0	0	0	0	45	24	0	0	0	0

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