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Journal of Environmental Science and Water Resources
Vol. 3(1), pp. 015 - 25, January 2014

ISSN 2277 0704
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Changes in the densities of faecal and organic matter contaminants from upstream to downstream along Nyangores River of Mara catchment, Kenya

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Accepted 9 January 2014

Changes in land use for development purposes in the upper catchment of the Mara River Basin have threatened the water quantity of its major tributaries. This study investigated the effect of human settlement and development on the microbial water quality at various points along the channel of Nyangores River using Membrane Filtration Technique (MFT) to determine the densities of total coliforms, *Escherichia coli*, intestinal enterococci and *Clostridium perfringens.* Pollution with easily biodegradable organic matter was detected by Heterotrophic Plate Count (HPC) procedures and BOD_5 determination. Temperature, dissolved oxygen (DO), conductivity, turbidity, total dissolved solids and pH of the water sources were also measured at the time of sampling using appropriate measuring Meters. The collected data was analyzed using Statistical Package for Social Sciences (SPSS) version 17 software with a confident level of 95%. The results indicated spatial variation in the densities of faecal contamination and easily degradable organic matter indicators, $p<0.05$. Physico-chemical parameters studied also showed significant spatial variation except DO, $p<0.05$. In conclusion, the presence of anthropogenic activities along Nyangores River have impacted negatively on quality of its water and therefore appropriate corrective mechanisms are necessary to help improve and restore its water and uphold its ecological integrity.

Key words: Anthropogenic activities, BOD_5, faecal indicators, organic matter, water quality, Nyangores river.

INTRODUCTION

Human development which entails land clearing, urbanization and poor waste disposal measures along the tributaries of most rivers as in the case of the Mara River has significantly degraded the biological and chemical quality of its water. The consequence of this is to triggerthe occurrence of point and non-point sources of pollution which have been found in other Rivers too (Yillia et al., 2009).

River Nyangores flows through an area with intensive anthropogenic activities (Mati et al., 2005). Human activities such as settlement, urbanization and poor farming methods have not only been perceived to be the major cause of degradation to the quality of water in this river, but also to both River Mara and Lake Victoria where water from the tributary is emptied (Dadwell, 1993). Faecal pollution to water sources is a serious threat to the quality of water with a negative impact on the integrity of aquatic ecosystems and therefore is a risk to the health of the community utilizingwater from such sources. It is believed that 80% of all diseases in the world are caused by inadequate sanitation, polluted water or unavailability of water (WHO, 2002). Both direct contact and consumption of water contaminated with faeces of ill individuals can lead to human illness and even death (United State Environmental Protection agency (USEPA), 1995).

To test for the microbial quality of any water source, faecal contamination indicator organisms are preferred as the approach is fast and cheap (APHA, 2005). While a variety of pathogenic indicators have been proposed, the mostly commonly used estimator of faecal pathogenic bacteria presence is faecal coliforms and faecal streptococci abundance (Dadwel, 1993, Ford and Colwell, 1996). Traditionally, indicator micro-organisms

have been used to suggest the possibility of presence of pathogens (Berg and Metcalf 1978). Other useful indicators include intestinal enterococci and *Clostridium perfrigens*. Organic matter loading from catchment activities results in vigorous consumption of oxygen attributable to large oxygen requirement by heterotrophic microbes in oxidative degradation processes. High Biological Oxygen Demand (BOD) is experienced in such systems and oxygen deficit is greatly increased often leading to destruction of other aquatic organisms. Thus BOD_5 is used as a measure of oxygen consumption and aerobic heterotrophic activities (Rheinheimer, 1991).

Inorganic nutrients (PO_4 and NO_4) from agricultural activities also affect microbial flora of streams (Yuan et al., 2001).This study was thereforeinitiated to determine the influence of human settlement and development on the microbial quality of the water within Nyangores River through the use offaecal contamination and easily degradable pollutant indicator organisms.

MATERIALS AND METHODS

Study area

The Mara River is located in Mau escarpment with its source mainly in Kenya and flow through Tanzania and drains into Lake Victoria at Musoma bay. The Mara River covers a surface area of 13,504km^2 and distributed in the two countries in proportion of 60% Kenyan and 40% Tanzania. The basin is located between longitudes 33° 53" 14' and 35° 54" 28' west and latitude 00° 19" 54' and 01° 58" 30' South (Mati et al., 2005).The major catchment is Mau-Complex Forest which borders Nakuru, Kericho, Bomet, and Narok Counties in Kenya and flows for a distance of 395 Km.Thebasin is characterized by different land cover and land uses. Some of the land uses include urban settlement and villages, subsistence and large scale agriculture, forestry, livestock, fisheries, tourism, conservation areas and mining.

The main tributaries are Amalaand Nyangoresrivers which are both facing a serious threat as a result of change in land use for various purposes like settlement, urban development among others in the catchment. This has led to drastically reduced forest cover which has hampered the recharge of the river with faster surface runoff leading to water pollution. The river meanders through open savannah grasslands that are mostly governed by Maasai group ranches and eventually into Maasai Mara National Reserve and Serengeti National and finally drains into Lake Victoria in Tanzania.

This study mainly focused on Nyangores River from the source where pollution was least expected to the confluence of Amala River (Figure 1). Eight sampling stations were systematically established considering the presence of points and non-points pollution sources, as well as the intensity of anthropogenic activities. These were distributed as follows; Site 1 at the source before forested portion near Kiptagich (S 00° 34′ 55.8″, E 035° 36′ 13.0″), Site 2 located at at Masese point (S 00° 42′ 25.7″, E 035° 25′ 24.5″) Site 3 located at the upstream of Tenwek Mission hospital (S 00° 44′ 15.9″ E 035° 21′ 45.2″), Site 4 located at the downstream of Tenwek Mission hospital (S 00° 44′ 53.2″ E 035° 21′ 52.8″), Site 5 located at the upstream of Bomet municipality at Raiya village (S 00° 46′ 30.6″, E035° 21′ 05.0″), Site 6 located at the downstream of Bomet Municipality near St. Michael secondary school (S 00° 47′ 44.8″, E 035° 20′ 18.5″), Site 7 located at Olbutio trading centre at the bridge (S 00° 51′ 30.0″, E 035° 16′ 44.8″) and finally Site 8 located after the confluence of Amala and Nyangores river at Tuiyobei (S 00° 56′ 14.6″ , E035° 14′ 30.4″).

Sampling

Water samples were collected in triplicates from the eight selected sites within the river as indicated in the study area. Sampling was conducted two times a month from each station for six months (February to July) covering both wet and dry months during the year 2012. The dry season was on the months of February and March while wet season was on the months of April, May and June. Sterilized glass sample bottles were used to collect samples from the river 30 centimetres below the surface and at the middle of the river channel. The following physico-chemical parameters were measured on site; Temperature, pH, Electrical Conductivity (EC), Total Dissolved Solutes (TDS) by use of H1 991301 portable pH/EC/TDS/Temp meter. Dissolved Oxygen (DO) was measured by the use of H1 9143 microprocessor and also Turbidity was measured using 2100 isoTurbidimeter. These were all measured *in-situ* at the time of sampling from each site. All samples were marked appropriately, placed in a cool box packed with ice and transported to laboratory for analysis.

Sample analysis

Analysis of microbiological parameters was conducted according to guidelines outlined in APHA (2005) and Scott et al. (2002). This was done within 6 to 24 hours after sampling to avoid changes of the bacteria count due to growth or die off. To avoid contamination during sampling and analysisaseptic technique was strictly observed at all the stages. Methods of analysis involved the use of Heterotrophic Plate Count (HPC) procedure to estimate the number of live heterotrophic bacteria. Membrane Filtration Technique (MFT) was also used in the analysis of samples for the presence of indicator organisms. The nutrients and selective media were prepared in advance for each procedure as per the manufacturer's instruction and kept in a refrigerator at 4°C

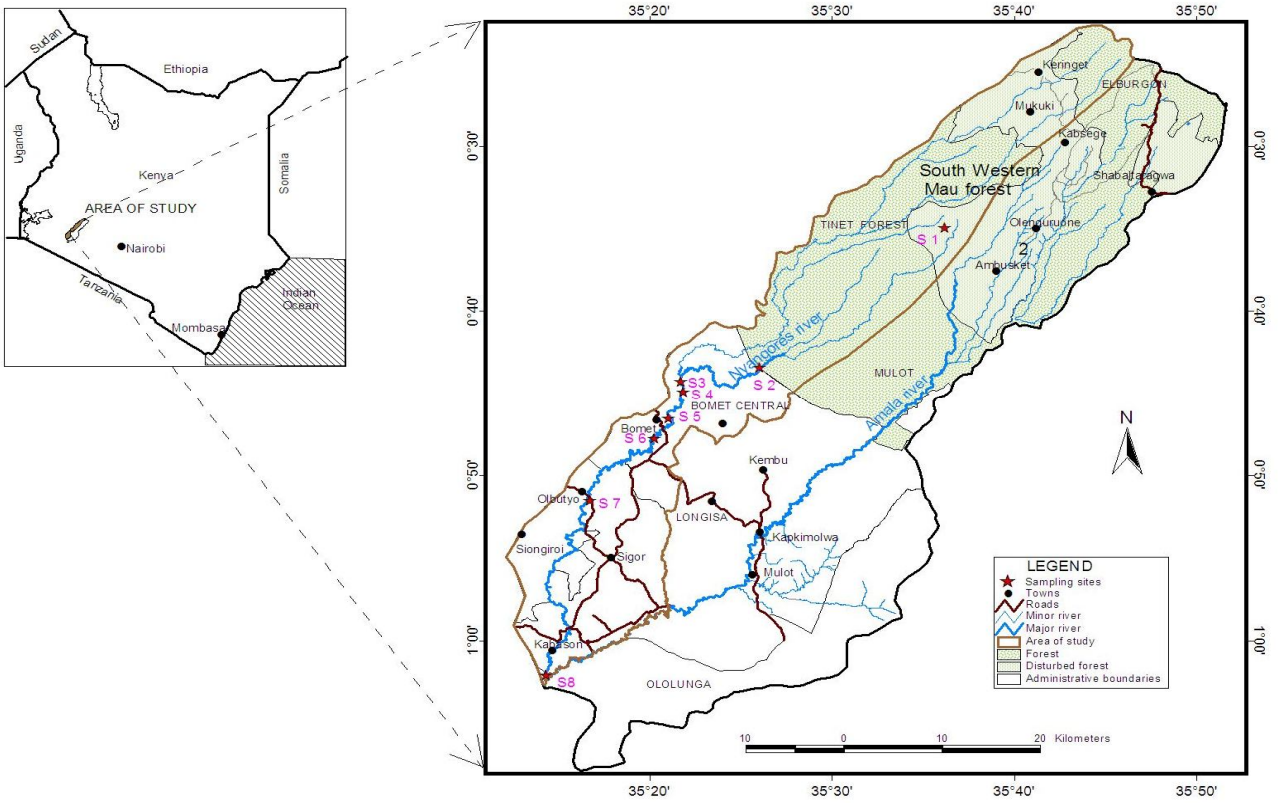

Figure1. Map of study area (Constructed by Geofrey Maina- Senior GIS Technologist at Environmental Science Department of Egerton University).

apart from HPC which was prepared afresh. Serial dilutions of samples were also made as appropriate for each test depending on the water source. Details for each method are given in following sections.

Heterotrophic plate count (HPC) procedure

One ml of each sample or dilutions of it was placed onto 80mm diameter plates and mixed with molten plate count agar and incubated at 37°C for 48 hours in triplicates. Counting was made on the dilution with plates containing 30 to 300 colonies. The numbers of HPC bacteria per ml of water sample were estimated by multiplying mean numbers of CFU's recorded with the reciprocal of the dilution.

Membrane filtration technique

Aseptic filtration was done separately for each dilution. Sterile funnel was detached, a sterile filter membrane placed on sterile filtration device using a pair of forceps, flamed for a short while and the funnel reattached. Known volume of water and or its dilutions where necessary were filtered starting with the highest to the lowest dilution.

After sucking off the whole samples, the tap or pump was turned off and the funnel detached. The membrane filter was gently taken off using a pair of sterilized forceps and placed on the surface of the corresponding culture media. For total coliforms and *E. coli* counts, filters were placed onto chromocult agar plates and incubated at 37°C for 18 to 24 hours.

Typical colonies appearing pink and dark blue were counted as total coliforms. For *E. coli* only blue colonies were counted on the same plate as for total coliforms. For all colonies forming units (CFU) counted, total numbers per 100ml was expressed as; No/100ml = (CFU's × Dilution/Volume filtered) × 100 (APHA 2005). For intestinal enterococci counts, filters were placed onto enterococci agar (Merck) plates and incubated at 44°C for 24 to 48 hours.

Typical colonies appearing pink were counted as intestinal enterococci. For all colonies forming units (CFU) counted, total numbers per 100ml were expressed

as; No/100ml = (CFU's × Dilution/Volume filtered) × 100 (APHA, 2005).For *C. perfringens* counts, filters were placed onto Tryptose Sulphite Cyclocerine (TSC) agar plates.

The plates were then placed in an anaerobic jar with an anaerocultstrip and incubated at 44°C for 18 to 24 hours. Black fluorescent counts of *C. perfringens* were then observed under 360nm UV light. For all colonies forming units (CFU) counted, total numbers per 100ml were expressed as; No/100ml = (CFU's × Dilution/Volume filtered) × 100 as stipulated in (APHA, 2005).For *Salmonella typhi* filters were placed on HiCrome ™ Salmonella agar improved plates and incubated at 37°C for 24 hours.

Typical colonies appearing light pink were identified and recorded (APHA, 2005; Al-Wasify et al., 2011).

Measurement of biochemical oxygen demand

Samples were collected in 250ml aluminium foil-coated BOD bottles and transported to the laboratory for BOD analysis using BOD OxiTop® meter(Yuan et al., 2001).450 mls of sample was put into dark BOD bottles with magnetic stirrer. Two pellets of sodium hydroxide were placed in the bottles and tightly corked. They were then put into BOD meter and incubated at 20°C for 5 days. After which the BOD_5 results were obtained directly from the metre reading.

Tracking of faecal contamination sources

Faecal contamination source identification was achieved through *E. coli*: intestinal streptococci ratio determination based on their CFU values. It was based on the knowledge that a ratio of above 4 was to indicate high levels of human faecal contamination while below 0.7 was to indicate contamination by faeces from non-human sources (Scott et al., 2002).

Data analysis

Data analysis was done using Statistical Package for Social Sciences (SPSS) version 17 software.In all the analysis, 95% level of significance was used as the critical point (P= <0.05). The collected data on the density of indicator organisms and HPC from the water sources were statistically analysed. Data on physicochemical parameters (pH, Temperature, DO, TDS, Turbidity, BOD, and Conductivity) were also computed for all the water sources to calculate their mean values. One way Analysis of variance (ANOVA) was used to compare means recorded at different sampling sitesfor various variables. The means were separated using Least Significance difference (LSD) as the *post hoc* test.

RESULTS

Physical and chemical parameters

Physicochemical parameter values recorded in this study are represented in Table 1. Temperature values showed significant spatial variation, F= 21.239, P=0.001 and df= 7,239. Dissolved Oxygen (DO) values had no significant variation between sites, F=1.752 at P=0.098 and df= 7,239.pH values showed significant variation with respect to sites, F= 90.769 at P=0.001 and df= 7,239. TDS also showed significant spatial variation, F=30.560 at P=0.001 and df= 7,239.Turbidity values showed significant spatial variation, F= 6.893 at P= 0.001 and df = 7, 239. Electrical Conductivityvalues ranged between 100 to 900 µs/cm with Sites 3, 4, 5 and 6 recording the highest mean values.

Spatial variation in faecal contamination indicator densities

The results on mean densities of microbiological indicators of pollution are shown in Figure 2. Total Coliforms (TC) had values ranging between0-3 log units of Colony Forming Units per 100ml (CFUs/100ml), with Site 1 which was the furthest upstream recording mean density value of zero while Site 6 giving the highest mean density value in 3 powers of magnitude. TC showed significant variation with respect to sites, F= 31.972, P= 0.001 and df= 7, 239. *E. coli* had values ranging between 0.0 to 6900.0 cfu/100ml, with Site 1 recording a mean value of zero while Site 6 recording the highest mean value. *E. coli* also showed significant spatial variation, F= 19.253, P=0.001 and df= 7, 239.

Intestinal enterococci had values ranging between 0.0 to 1400.0 cfu/100ml. Site 1 had a mean value of zero while Site 6 recorded the highest mean value. With respect to IE, there was significant spatial variation, F= 46.244, P= 0.001 and df= 7, 239.*C. perfringens* had values ranging between 0.0 to 1830.0 cfu/100ml with Site 6 recording the highest mean value. *C. perfringens* also indicated significant variation with respect to sampling sites, F= 38.461, P=0.001 and df= 7, 239.

Pollution level by easily degradable organic matter

Values of indicators for easily degradable organic matter are shown in Figure 3. Biological Oxygen Demand (BOD_5) had values ranging between 0.0 to 4.0 mg/l. BOD showed significant variation with respect to sampling sites, F= 215.695 at P=0.001 and df= 7, 239. Site 1 recorded the lowest mean values than the other remaining six sites.

Heterotrophic Plate Count (HPC) had values ranging between 2-5 log units cfu/1ml. Sites 1 recorded the lowest mean value while Sites 4 and 5 recorded the

Table1. Mean values for physic-chemical parameters recorded at different study sites on Nyangores River.

Sites	Temperature (°C) Mean±SE	DO (mg/l) Mean±SE	pH Mean±SE	TDS (ppm) Mean±SE	Turbidity (NTU) Mean±SE	Conductivity (µs/cm) Mean±SE
1	16.7±0.1	6.3±0.2	5.4±0.0	0.0±0.0	6.8±0.1	153.0±13.3
2	14.9±0.2	7.2±0.2	6.8±0.1	39.5±7.2	41.1±4.8	284.4±20.8
3	20.2±0.4	6.9±0.2	7.1±0.1	210.3±20.6	71.1±7.2	517.2±36.3
4	18.7±0.5	6.7±0.2	7.0±0.1	268.434.8	92.0±6.1	538.4±42.3
5	18.4±0.7	6.5±0.2	6.8±0.0	245.7±18.9	110.5±8.3	715.9±190.0
6	18.9±0.4	6.8±0.2	6.5±0.1	256.7±19.1	125.6±16.7	554.0±34.6
7	19.6±0.4	7.3±2.0	7.1±0.1	232.3±21.9	147.7±44.3	541.7±46.7
8	20.2±0.2	7.6±0.1	7.3±0.1	107.0±3.8	112.6±8.3	305.5±19.3

DO (dissolved Oxygen), TDS (Total Dissolved Solids) and n=30.

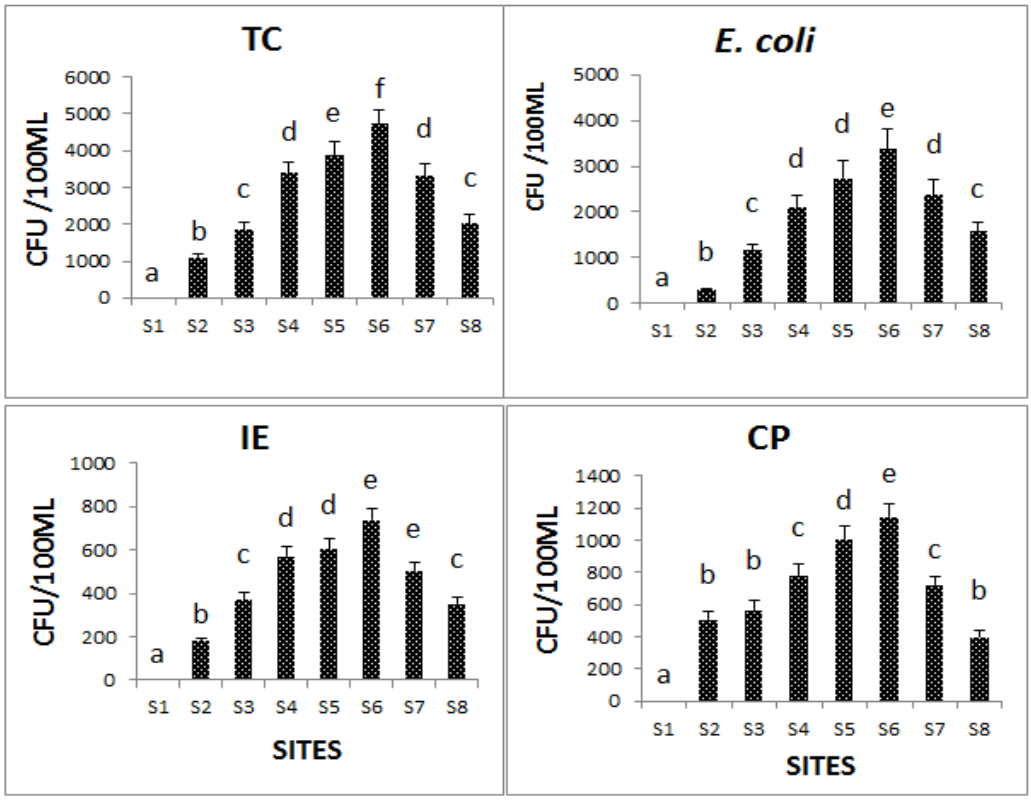

Figure 2. Graphs of mean values of microbiological contamination indicator parameters from all the sites. *Sites are S1 to S8. Vertical bars indicate standard error of mean and sites with significant mean differences are shown by different letters at P<0.05. n= 30. TC= total coliforms, CP= C. perfringens and IE= intestinal eneterococci.*

highest values. There was significant spatial variation in HPC values, F= 44.996, P= 0.001 and df= 7, 239.

Correlation between microbiological and physicochemical parameters

The relationship between various physicochemical parameters and microbiological parameters were as in Table 2. Most of the parameters showed significant positive correlation. There was significant correlation within microbial parameters as well as between microbial parameters and physicochemical parameters. *E. coli*, total coliforms, intestinal enterococci and *C. pefringens* showed positive significant correlation between themselves. All these microbiological parameters also

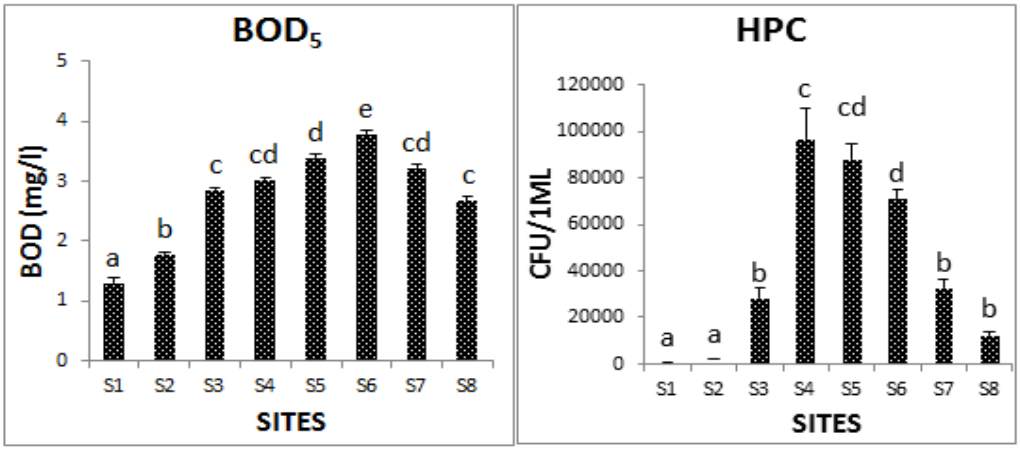

Figure 3: Graphs showing the mean values of organic pollution indicator parametersfrom all the sites. *Organic pollution indicators are BOD and HPC. Vertical bars indicate standard error of mean, sites with significant mean differences are shown by different letters at P<0.05 and n= 30).*

Table 2. Correlation between physical, chemical and microbiological parameters.

	EC	TC	IE	CP	TEMP	DO	pH	COND.	HPC	TURB	TDS	BOD
EC	1											
TC	.818**	1										
IE	.809**	.879**	1									
CP	.796**	.885**	.894**	1	.							
TEMP	.113	.207**	.214**	.156*	1							
DO	.140*	.129*	.045	.061	.079	1						
pH	.012	.160*	.201**	.135*	.392**	0.053	1					
COND.	-.094	.105	.091	.098	.271**	-.01	.291**	1				
HPC	.595**	.571**	.613**	.586**	-.009	-0	.005	.052	1			
TURB	.415**	.410**	.352**	.355**	.085	.803**	.131*	.07	.284**	1		
TDS	.028	.337**	.335**	.296**	.414**	-.02	.494**	.497**	.186**	.093	1	
BOD	.673**	.737**	.781**	.720**	.365**	.060	.392**	.278**	.582**	.389**	.533**	1

****** Correlation is significant at 0.01 level (two tailed)
*****Correlation is significant at 0.05 level (two tailed)

showed positive significant correlation with physicochemical parameters like temperature, TDS, turbidity, and BOD. There was also significant correlation between some of the physicochemical parameters as well as between physicochemical parameters and microbiological parameters. Indicators of pollution by easily degradable organic matter (BOD and HPC) also showed significant correlation.

Faecal contamination source tracking

Source tracking for faecal contamination was done through *E. coli* and intestinal enterococci ratio determination. Results are shown in Table 3. The values from all the sites except sites 1 and 2 were closer to a ratio of 4.0 than 0.7.

DISCUSSION

Physical and chemical parameters

Apart from point sources of pollution, diffused sources of pollution such as agricultural pollution and various in stream anthropogenic activities such as cattle watering, bathing, open defeacation and cloth washing pose an additional contribution to the deterioration of river water quality(Yilia et al., 2009).The results from this study to a greater degree concurwith such findings and reasoning. Temperature exhibited spatial variation with the upper-most/upstream site (site 1) giving the lowest values. This could be attributed to the density and canopy coverage of riparian vegetation that determined the shading effect on the stream at Site 1.The lowest temperature values was noted to be at the area with the highest riparian

Table3. Mean values of *E. coli* and intestinal enterococciand ratios of *E. coli* to intestinal enterococci from all the sites.

Sites	1	2	3	4	5	6	7	8
E. coli(cfu/1ml)	0	284.2	1144.4	2075.6	2731.0	3369.3	2356.3	1555.8
IE(cfu/1ml)	0	182.8	370.2	571.6	605.1	739.7	505.0	353.0
Ratio	-	1.6	3.1	3.6	4.5	4.6	4.7	4.4

vegetation cover which kept the water underneath cool for a long time. The amount of shading at various sites contributed to differences in stream temperature (Sherri, 2004). In general the mean temperature values increased downstream with an exception of Site 3 which was not significantly different from Site 8(Furthest downstream).

This was because both site 3 and 8 lacked canopy cover resulting to direct warming of water within the channel at those particular sites by the heat from the sun's radiation.

The colder spring water from underground that is dominant at site 1 contributed to low DO as has been observed elsewhere (Nicholes et al., 2013).The high volume of water at the downstream sites was able to trigger high flows which resulted to aeration as a result of waterfalls hence increased the amount of DO downstream.

An additional point to note in this case is the nature of the stream gradient at different points. High gradient triggers fast flow of water within the channel and high flow may result to aeration hence high DO values (Harrelson et al., 1994). Increase in deforestation downstream contributed to warming up of water as it flows downstream (Sherri, 2004) thus increasing microbial respiration and consequently low DO(Kerr, 2008).

The absence of spatial variation in DO values could be attributed to the balancing effects of the water temperature as well as flow regime as a factor of the channel topography. This factor could have also been contributed by the presence of cataracts and waterfalls along the channel at the downstream sites which resulted to unexpected increase in DO values downstream. However significant variations may be evident on prolonged or increased frequency of sampling (Craig and Brian, 1994).

Site 1 showed the lowest pH values than all the other sites, probably because the water at that particular site was noted to be very clean with minimum anthropogenic activities. This trend was also noted for TDS, turbidity and conductivity values. The study was able to show the existence of "self-purification" of a river. From physicochemical parameters point of view, it was noted that the water from site1 was of good quality but as it moves down stream through Sites 2 to 3upto 6, this quality deteriorated. But as the flow continues further downstream beyond Site 6 through Site 7 and 8 the quality again starts to improve, this was due to self-purification as one of the functions of rivers and stream in water quality maintenance (Maddock, 1999).

Spatial variation in faecal contamination indicators

All the other Sites except Site 1 had values of faecal contamination indicators far much above the values by WHO for drinking water guidelines (WHO, 2002).The significant variation in total coliforms between different sampling sites was an indication of the existence of different degree of the anthropogenic activities which also impacted differently onto the quality of Nyangores River.The same trend was also observed in *E. coli*values, Site 6recorded highest values for both TC and *E coli* counts. A study result byCooperative Research Centre for Fresh Water Ecology(CRCFW, 2001)which involved the monitoring offaecal coliform levels in a stream also found higher values similar to what was achieved in some sites in this study.

A study on bacteriological water quality status of River Yamuna in Delhi had indicated increased bacterial total countfrom upstream to downstream stretch of river Yamuna (Chetna et al., 2006). Down-stream increase in feacal pollution in River Awach in Nyanza region of Kenya was also attributed to increase in settlements in middle reaches of the River (Okoko et al., 2012).

The influence of anthropogenic activities on the bacteriological water quality has also been evidenced on Kenyan borehole waters (Donde et al., 2013). Within Nyangores River, the high pollution levels recorded were attributed to contamination by sewage or stormwater discharges from Bomet Municipality at site 6. Similar study by Stoimir and other researchersontheassessment of the microbiological quality of the River Tisa in Serbia at selected sites was also attributed mainly to a large amount of raw or improperly treated urban wastewater, organic pollutants loads and increased agricultural activities in that area (Stomir et al., 2011).

Although instream regrowth of *E.coli* can serve as the source of high faecal coliform levels Byamkhama *et al.,* (2005) showed that *E. coli* is still a dependable indicator of faecal when comparing feacal pollutions from different sites.On the other hand, other studies have highlighted that surface waters are always poor in water quality due to their openness. This exposes them to various forms of pollution. A study within Khamis Mushait Governorate in South Africa showed that water derived from traditional

sources (shallow wells) showed high values for most of the investigated bacteriological parameters, followed by surface water as compared to bottled or desalinated water. This may be highly attributed to the fact that shallow wells and surface water of Khamis Mushait Governorate being open and exposed to numerous pollution sources are highly at risk of contamination as indicated by the higher levels of bacteriological parameters (Eed et al., 2009).

Faecal pollution of rivers used as source of drinking water pose health risk to humans not only through direct infection by pathogens, but such water if used for irrigation can transmit pollutants through vegetables/fruits consumed by man. A study byLabanit*et al.,* (2005) had indicated that river water wasof the poorest quality with high densities of faecal coliforms. That finding was the same as that of another study by Marijke (2010), who concluded thatthe rivers he had investigated during his study contained high levels of faecal contamination.

According to the results on an assessment of the microbial quality of river water sources in rural Venda communities in South Africa, where modern membrane filtration technique was used, it was also concluded that the microbial quality of the water sources was poor and unacceptable for human consumption due to faecal pollution. This indicated the potential risk of infection to consumers and calls for prompt intervention to mitigate the socio-economic and health impact of water-borne diseases in these rural communities (Obi *et al.,* 2002).

Based on the densities of total coliforms and *E. coli*, the Nyangores river water was found to be unfit for human consumption without proper purification. This finding was also in agreement with the values of total coliforms and *E. coli* indrinking water sources used by the Cree community of Mistissini area in Canada (Jean-Luc et al., 2009).

Use of intestinal enterococci for feacal pollution detection gave similar results as those for coliforms making this test a valuable alternative parameter for water quality monitoring. Values of *C. perfringens* also had a similar trends as for coliforms and intestinal enterococci.

This makes *C. perfringens* to be considered as a backup indicator for faecal contamination alongside other parameters. For instance, a study by Medema et al. (1997) showed that the rapid die-off of *E. coli* and faecal enterococci makes them less suitable as indicators of oocyst presence in water. *C. perfringens*being able to survive longer than oocystsinuntreated river water,it may prove useful as indicator for the presence of *C. parvum*.

This was also similar to the conclusion by Florence et al. (2012) who had studied Malaysian tropical rivers and found out *C. perfringen*s as being a potential indicator of the influence of high human population along the bank of these Malaysian Selangor River to its water quality (Florence et al., 2012). The poor microbiological water quality is impacted by anthropogenic actities as has been attributed to poor water quality for other countries of the world (Ouattara et al., 2009).

Pollution level by easily degradable organic matter

Nyangores River has high levels of pollution with easily degradable organic matter as depicted by high values of HPC and BOD. The pattern of the values of these parameters from Site 1 to the last site 6 and significant spatial variation also shows that the intensity of organic loading into Nyangores river increases from upstream to downstream upto site 6 and reduces thereafter. This trend is linked to the trend in the density of riparian vegetation which was noted to reduce from upstream to downstream.

However, sudden drop from Site 6 to Site 8 may have resulted from dilution effect by other emerging small tributaries. This couldalso be due to the fact that the organic material in these sites not being easily degradable. In addition, other in stream activities like nitrification could have also led to reduced oxygen concentration, which had an ultimate influence on the values of HPC and BOD.

This was comparable to a study by Etleva et al. (2012) onVjosa River, Masedonia and whose preliminary results, as it was expected, had high load of heterotrophs in sample stations near urban areas. Domestic sewage loading from settlements along the river and farming activities are also responsible for pollution with easily degradable organic matter.

Regular monitoring of river and taking suitable remedial measures like collection of domestic sewage and setting up the common treatment plant; before discharge of sewage into river system, is a good way to control pollution and prevent the depletion of the quality of river waters (Usharani et al., 2010).

Correlation between physicochemical and microbiological parameters

The significant correlation between *E. coli*, total coliforms, intestinal enterococci and *C. perfringens* was good evidence that all these parameters can be used as perfect indicators of organic pollution. It also showed that at the time of this study, there existed both the recent and the persistent faecal pollution into Nyangores River. Significant correlation between faecal contamination indicators (*E. coli*, total coliforms, intestinal enterococci and *C. perfringens*) and organic pollution indicators (HPC and BOD) also showed that human development activities along Nyangores River do contribute to both faecal and organic pollution into the river.

The result is also comparable to studies by Desmarais et al. (2002); Kei et al. (2004) and Olag et al. (2006). In all the studies, there was strong relationship between *E.*

coli, total coliforms, intestinal enterococci and *C. perfringens*) and organic pollution indicators.Another study of base-flow conditionsindicated that the turbidity in the Stock Creek watershed correlates most strongly with *E. coli* load rates and there was a spatial dependency of the *E.* on precipitation. The persistence of *E. coli* in faster draining sub-basins may be tied more directly to the antecedent storm events and elevated base-flow response (Randall et al., 2006).

On a different perspective, wastewater effluents discharge has also been found to pose an influence not only to the microbiological parameters but also to the physico-chemical properties of water and vice versa (Jakhrani et al., 2009).

Faecal contamination source tracking

The ratios of *E. coli* to intestinal enterococci at different sites within Nyangores River were closer to a ratio of 4.0 than 0.7. This showed that the major source of faecal pollution into the river was probably of human (Weaver et al., 2005) and not livestock in the area as noted for a river in North Area of Wigry National Park where it was found that source of faecal contamination was majorly coming from flows arising from other arable-forestry-pasture-meadowcatchments as expressed by a larger number of streptococci than *E. coli*, (Niewolak, 1999).

Generally, the source of microbial pollution into Nyangores River could be different and hence need to be determined. Indeed, all current methods and those in progress require additional investigation. However, all have merit and are important constituents of the constantly expanding microbial source tracking toolbox. With Environmental Protection Agency-mandated total maximum daily loads being calculated throughout the United States, the need for current and future source tracking technologies is increasing.

These methods are certain to play a pivotal role in identifying point and nonpoint sources of fecal pollution in the nation's impaired water systems as in the case of Nyangores River (Troy et al., 2002).

Conclusion and recommendation

The densities of faecal contamination indicators vary significantly between various points within Nyangores River. The river water is of good quality as it comes from the source at Kiptagich. The water quality deteriorates as the water flows downstream due to human activities on the quality of this Nyangores River as the water flows downstream. Pollution with easily degradable organic matter in Nyangores River is rampant and levels are significantly influence by anthropogenic activities. For the better management of Nyangores River to maintain the quality of its water as well as its ecological integrity there is need to educate the community on issues of environmental integrity, proper agricultural practices and to supply them with adequate and effective sanitary facilities in addition to safe and clean drinking water a requirement of fulfilling MDGs. There is also a need to put in place coordinated and continuous pollution monitoring strategy for sustainable management and use of this resource.

Interestingly, since the scientific data obtained in this study also supported the traditional community perception that a limited number of environmental sites constituted safer water sources. In this regard even if water harvesting practices mitigate risk, boiling water therefore remains the best and reliable simple method to inactivate pathogens before consumption.

ACKNOWLEDGEMENT

The authors are grateful to USAID Mara Basin Water Scholars Program through the Trans-boundary Water for Biodiversity and Human Health in the Mara River Basin, Kenya and Tanzania (TWB-MRB) Global Water for Sustainability (GLOWS) Program, Florida International University for financing this study.

The smooth coordination and running of the GLOWS Mara Basin project by Mr. Yazdani Iman and Dr. Nzula Kitaka of Egerton University Department of Biological Science are highly appreciated.

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