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Full Length Research Paper

Microbiological quality of crude milk along the rural and peri-urban dairy systems of Nakuru county

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Abstract

The study aimed at profiling the microbiological quality of raw milk from the udder to the cooling centers in rural and peri-urban. Samples were collected directly from the udder, at the farm gate, from transporters delivering to cooling centers and from the bulking centers. A total of 461 raw milk samples were collected. Microbiological analysis were done following standard procedures of ISO and American Public Health Association, these included Total Viable Count (TVC), Coliform Counts (CC), Thermophilic bacteria counts (ThBC) and Psychrophillic bacteria counts (PBC). Indicator microorganisms enumerated were *Streptococcus*, *Staphylococcus, Enterobacteriaceae E. coli* and *Bacillus spp*. For both nodes the collection centers recorded the highest in TVC (Rural 10^5cfu/ml, Peri urban 10^6cfu/ml) with transporters at both nodes recording the highest percentage for gram negative rods (rural 63.3%, peri urban 62.5%). ThBC was significantly different at the farm and bulking center in both dairy systems. PBC recorded highest counts at cooling centers in both dairy systems. Given the high counts recorded at all nodes (up to 10^7 CFU/ml), hygiene need to be high from milk production (farms) throughout the value chain. Cooling points along the value chains need to be introduced and use of food grade equipment to handle and transport milk would help in reducing microbial load in raw milk.

Keywords: Microbiological quality, raw milk, value chain, rural, peri-urban.

INTRODUCTION

Milk is a highly nutritious product and therefore facilitates the growth and multiplication of a wide range of microorganisms (Worku et al., 2012). When secreted within the alveoli it is basically sterile. Contamination however begins within the udder in an infected animal with mastitis. Microorganisms may also enter the udder through the teat of the udder and cause milk contamination. Studies have recorded counts of up to 100 CFU/ml in milk aseptically drawn from the udder (Limond and Griffiths 1991). Microorganisms isolated from the udder which also cause sub-clinical mastitis include staphylococcus. Mastitis causing bacteria are largely gram positive commensal or pathogenic microorganisms.

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Milk has also been categorized as a high risk product in terms of shelf life after harvesting. If not cooled immediately after harvesting and in the absence of proper hygiene practices milk spoilage occurs very fast (Dey and Karim, 2013).

Microorganisms are capable of breaking down milk components to various by products hence rendering the milk unfit for processing or consumption depending on the extent of spoilage leading to losses. Psychrotrophic bacteria once in milk, they are able to grow and multiply at cooling temperatures. At these temperatures, they produce heat stable enzymes. These enzymes withstand pasteurization and persist in the subsequent dairy product. The heat stable enzymes reduces the shelf life of milk products like UHT, butter and ghee (Arslan et. al., 2011, Ray, 2004, Chen et al., 2003). Thermophillic bacteria are capable of growing under a wide range of

temperature. Thermophiles which have been isolated from milk originate mainly from the bacillus and pseudomonas family (Abdul-Hadi et al., 2014). These are mainly spore formers and in their vegetative state they can withstand Ultra heat treatment (140^{o}C/ 30min) of milk during UHT milk production (De-Jonghe et al., 2010). UHT milk is expected to have a shelf life of not less than six months under normal room temperature. When contaminated with psychrotrophic bacteria, UHT milk will not attain its shelf life due to the germination of the bacterial spores of these microorganisms. In the germination stage, the spores utilize the milk components to grow. Studies have reported the presence of spore forming bacteria in UHT milk (Abo-Elnaga et al., 2002; Scheldeman et al., 2005; Abdul-Hadi et al., 2014).

Total viable counts (TVC) have been used to grade milk by standard developing organizations like Kenya Bureau of Standards (KEBS). Raw milk containing total viable counts greater than 2 x 10^6 CFU/ml is not considered for processing (KS EAS 163:2007) due to protein instability. TVC (Mesophilic bacteria) also assess the general microbiological quality and safety of a food product or sample under investigation. Coliforms have long been used as hygiene indicators in the food industry. This is because they have been majorly isolated from sewer systems and waste of fecal origin. When coliforms are found in milk then the milk is labeled as one produced under unhygienic conditions. Some of the common coliforms and other bacteria from fecal contamination isolated from milk include; *Enterobacteria, E.coli*, *Samlmonella* and *Shingella*. Coliforms cause milk spoilage due to their ability to breakdown lactose to produce lactic acid and gases (Kornacki and Johnson, 2001).

Livestock GDP contributes about 50% to the agricultural GDP in Kenya with dairy production contributing up to 33% of this (Lore et al., 2005). Smallholder dairy farmers dominate the dairy industry by accounting for over 75% at the production level (FAO, 2011). In 2014, the Agricultural sector recorded mixed performance mainly attributable to erratic rains with some regions experiencing depressed rainfall. The lower levels of rainfall resulted in a decrease in production for some crops as well as pasture regeneration for livestock. For small holder dairy farmers, this was a big challenge in terms of milk production (Economic Survey, 2015).

In Kenyan highlands, dairy farming is largely practiced and is a source of food and money for many households (FAO, 2011). Farmers however face the challenge of lack of skills to handle milk hygienically during and after milking. This has contributed to milk contamination with spoilage microorganisms. Previous studies have focused on the microbiological quality of milk at the farm. There is a gap of information on the microbiological quality of this milk as it moves along the dairy value chain. This work therefore, aims at documenting the microbial quality of milk at the farm, transporters and cooling centers of the informal value chain. The information generated is expected to inform appropriately on the best mitigation measures towards milk spoilage by microorganisms. This is expected to improve on the food security of dairy farmers and improve their financial status by reduction of microbiological milk spoilage.

MATERIALS AND METHODS

Study area

The study was carried out in Nakuru county Kenya where dairy farming is thriving and small scale farmers were targeted because they are the majority (FAO, 2011). Two locations were selected to capture rural and peri urban farm characteristics. Olenguruone is a rural setting which lies about 35^{0}40' 60''E and 0^{0}34' 60''S while Wanyororo is a peri-urban setting which lies about 36^{0} 40'60''E and 0^{0}40' 60''N.

Sample collection

Stratified random sampling was used in collecting samples from the farm since dairy farmers were targeted in the two population settings. The sampling procedure used by Bonfoh et al., (2003) was used in setting at the nodes as the critical control points for sample collection along the sub value chain. Milk samples were picked from the cow udder directly, at the farm gate, from transporters and at the collection centers. From the cow, milk from all the four teats was drawn into a sterile sampling bottle. At the farm gate, milk bulked from different cows within the farm was sampled from. Milk samples delivered to the cooling center by different methods of transportation was picked on arrival. At the collection center, the tap of the bulk tank was opened and milk allowed running for a few seconds before picking samples in a sterile 100ml containers. All the samples collected were immediately transferred into a cool box maintained at 4^{o}C with cooling elements and transported to the lab at Egerton University within four hours. A total of 342 milk samples were collected from the Rural (167 cows, 51 farms, 120 transporters and 4 cooling centers) and119 (157 cows, 30 farms, 30 transporters and 2 cooling centers) samples from the Peri urban dairy systems.

Microbiological analysis

Total viable counts (TVC) indicate the initial bacterial load representing the level of contamination of the sample. Coliforms are hygiene indicators on handling practices along the value chain. Thermophilic bacterial count represent microorganisms capable of growing within a wide range of temperature even past HTST (High Temperature short time) and LTLT (Low temperature long

Table 1. Standard procedures for milk analysis for TVC, CC, ThBC and PBC.

Type of microorganism	Type of media	Temperature/ time	Colonies counted
Total Viable counts (TVC)	Standard plate count agar (SPCA)	37^{O}C/ 24hrs	All colonies
Thermophillic bacterial Count	Standard plate count agar (SPCA)	42^{O}C/ 24hrs	All colonies
Psychrophilic bacterial count (PBC)	Standard plate count agar (SPCA)	8^{O}C/ 10days	All colonies
Coliform counts (CC)	Violet red bile agar (VRBA)	37^{O}C/ 48hrs	Typical dark red colonies

Where TVC- Total Viable Counts; CC- total coliform counts; ThBC; Thermophillic bacterial count and PBC- Psychrophillic bacterial counts.

TABLE 2. Range of different microbial counts in Rural and Peri-urban dairy systems %(N).

NODE/VARIABLE	RURAL (%)					PERI URBAN (%)				
	≤30	≤10^5	>10^5≤ 10^6	>10^6- 2 x10^6	>2 x10^6	≤30	≤10^5	>10^5≤1 0^6	>10^6	>2 x 10^6
Farm gate										
TVC	0	33.3	33.3	15.3	15	19	8	33	20	20
CC	41	25	17	8	9	28	11	44	1	7
TBC	8	25	50	10	7	52	14	24	5	5
PBC	0	8	42	25	25	42	0	11	27	20
Transporters										
TVC	4	44	20	16	16	4	5	52	9	30
CC	44	8	16	16	16	26	22	30	12	10
TBC	4	64	20	8	4	14	27	27	30	2
PBC	4	24	32	20	20	9	9	18	50	14
BULKING										
TVC	0	50	12	30	8	0	20	33	40	7
CC	25	12	13	40	10	0	12	0	80	8
TBC	0	12	63	20	5	0	0	25	60	15
PBC	0	12	38	30	20	0	0	12	70	18

Where TVC- Total Viable Counts; CC- total coliform counts; ThBC;Thermophillic bacterial count and PBC- Psychrophillic bacterial counts.

time) pasteurisation. Psychrotrophic bacterial counts represents spoilage microorganisms that are capable of growing at cooling temperature and produce heat stable enzymes which withstand pasteurization and would shorten the shelf life of the resulting milk products. The analysis of Total Viable counts, Coliform counts, Thermophillic bacterial count and psychrotrophic bacterial count followed the guideline of ISO 4833-1: 2013 and ISO 4832: 2006 methods. A summary is in the Table 1. Enumeration of selected colonies from the total plate count (E.coli, Staphylococcus, streptococcus and bacillus) were carried out as described by the standard methods of the American Public Health Association (2000).

Data analysis

Log transformation was done on data from counts before any analysis was done. General descriptive statistics was done (means). Means and standard error were done by SAS procglm, mean comparison was done by Fisher's test. Counts between the nodes was done by linear contrasts. Probability of occurrence of indicator microorganisms was according to Matofariet. al., (2007).

$$\text{Incidence (\%)} = \frac{\text{Number of positive samples} \times 100}{\text{Total samples collected}}$$

RESULTS

In the rural farms, none of the samples had counts less than 30CFU/ml while in the peri urban farms 19% of the samples had counts less than 30CFU/ml. the range of microbial counts for CC increased towards 10^6 in the rural dairy value chain. The same scenario was observed in the peri urban value chain. Psychrophilic bacteria counts were recorded in high values at the cooling centers in both dairy systems (Table 2).

Mean comparison of microbial counts of milk at Nodes, Dairy systems and nodes within the dairy systems

Analysis of variance (ANOVA) showed that there was no significant difference in TVC between the two dairy systems. However, a significant difference was observed in CC, ThBC and PBC between the Rural and Peri urban

Table 3. The analysis of variance (ANOVA) for the milk microbial contamination in the rural and peri-urban dairy systems and dairy value chains nodes within the two systems.

		Mean squares of the microbial load (log_{10}cfu/ml)			
S.O.V	**DF**	TVC	CC	ThBC	PBC
System	1	0.080^{ns}	30.234^{*}	75.699^{***}	83.480^{***}
Node(System)	6	8.704^{*}	11.463^{ns}	26.763^{***}	14.128^{**}
Error	457	3.685	7.096	4.924	4.892
C.V		3.745	6.396	5.466	4.477
R^2		96.78	87.70	72.940	91.03

S.O.V; Source of variation, DF; Degree of freedom, C.V; Coefficient of variation, R^2; Coefficient of determination, TVC; Total viable counts, TCC; Total coliform count, ThBC; Thermophilic bacterial counts, PSYCH; Psychrophilic bacterial counts, ns; not significant at P>0.05, *significant at P<0.05, **significant at P<0.01 and ***significant at P<0.001.

Table 4. Means comparison of milk microbial loads for the rural and peri-urban dairy systems and for the dairy value chains nodes within the two systems.

			Mean milk microbial loads (log_{10} CFU/ml)			
Factor	**Level**	**N**	TVC	CC	ThBC	PBC
System	Rural	342	5.10 ± 0.2^{a}	3.66 ± 0.3^{b}	4.87 ± 0.2^{a}	5.79 ± 0.2^{a}
	Peri-urban	119	5.14 ± 0.2^{a}	4.51 ± 0.2^{a}	3.51 ± 0.3^{b}	4.36 ± 0.3^{b}
Node (Rural)	Cow	167	4.46 ± 0.6^{b}	3.05 ± 0.7^{b}	4.41 ± 0.6^{b}	6.12 ± 0.3^{a}
	Farm gate	51	5.09 ± 0.3^{ab}	3.18 ± 0.8^{b}	4.73 ± 0.5^{b}	6.04 ± 0.2^{a}
	Transporters	120	5.72 ± 0.3^{a}	3.39 ± 0.6^{b}	4.98 ± 0.2^{ab}	5.47 ± 0.3^{b}
	Cooling centers	4	5.58 ± 0.3^{a}	5.19 ± 0.7^{a}	5.81 ± 0.2^{a}	5.66 ± 0.2^{ab}
Node (peri-urban)	Cow	57	4.63 ± 0.3^{b}	3.93 ± 0.4^{c}	2.65 ± 0.4^{b}	4.21 ± 0.4^{c}
	Farm gate	30	4.84 ± 0.5^{b}	4.33 ± 0.5^{bc}	2.68 ± 0.6^{b}	4.61 ± 0.7^{c}
	Transporters	30	5.60 ± 0.3^{a}	4.78 ± 0.5^{b}	4.98 ± 0.4^{ab}	5.30 ± 0.5^{b}
	Cooling centers	2	6.61 ± 0.2^{a}	6.03 ± 0.7^{a}	5.63 ± 0.7^{a}	6.91 ± 0.2^{a}

Means with the same letter along the columns are not significantly different at P>0.05. TVC; Total viable counts, CC; Coliform count, ThBC; Thermophilic bacterial counts, PBC; Psychrophilic bacterial counts and N; Sample size

dairy system. Mean comparison of coliform counts (CC) in the nodes within the dairy systems was not significantly different. Significant difference was recorded in TVC (P<0.05), PBC (P<0.01) and ThBC (P<0.001) in nodes within the system (Table 3).

There was a significant (P<0.05) difference in microbial quality of milk at the cow node compared to microbial mean counts at the cooling center in TVC, CC and ThBC in the rural dairy system. In the Peri urban dairy system, there was no significant (P>0.05) difference in the mean microbial quality of milk at the cow's node and farm gate in TVC, CC, ThBC and PBC (Table 4).

Percent colony morphology and Microbial types

In bacterial morphology, gram positive cocci was highest at the farm gate, slightly higher than that of milk drawn directly from the udder. The number was significantly lower ($p < 0.05$) at the transporters node. Gram negative rods recorded the highest at the transporters node while gram positive rods were most at the bulking centers. Gram negative rods were high in transporters node in peri urban location, with gram positive cocci recording the lowest at the same node (Figure 1). There was a thirty two percent incidence of *Enterobacteriaceae* occurring in rural milk with the highest probability in the milk drawn directly from the udder. Nine samples were positive for *E.coli* at the transporters node. *Streptococcus* and *staphylococcus* recorded highest positive samples in milk drawn from the udder in rural dairy system (Table 5). There was a significant fall in all microbial types enumerated in at the cooling center compared to other noded of the value chain in Rural.

There was 82% incidence of *staphs* occurring in peri urban milk. *E.coli* had an incidence of 76% while *Enterobacteriaceae* recorded a 54% incidence of occurrence in the peri urban dairy value chain. Farm gate milk recorded relatively high positive samples for almost all groups of microorganisms sorted during the study (Table 6).

DISCUSSION

Milk from the cow udder directly had counts higher than 30cfu/ml in rural. Contamination sources for this milk are; the udder and hands of milking personnel and also the air from the milking environment. The animal's udder is a contamination source of milk with spoilage microorganisms. In this study microorganisms isolated

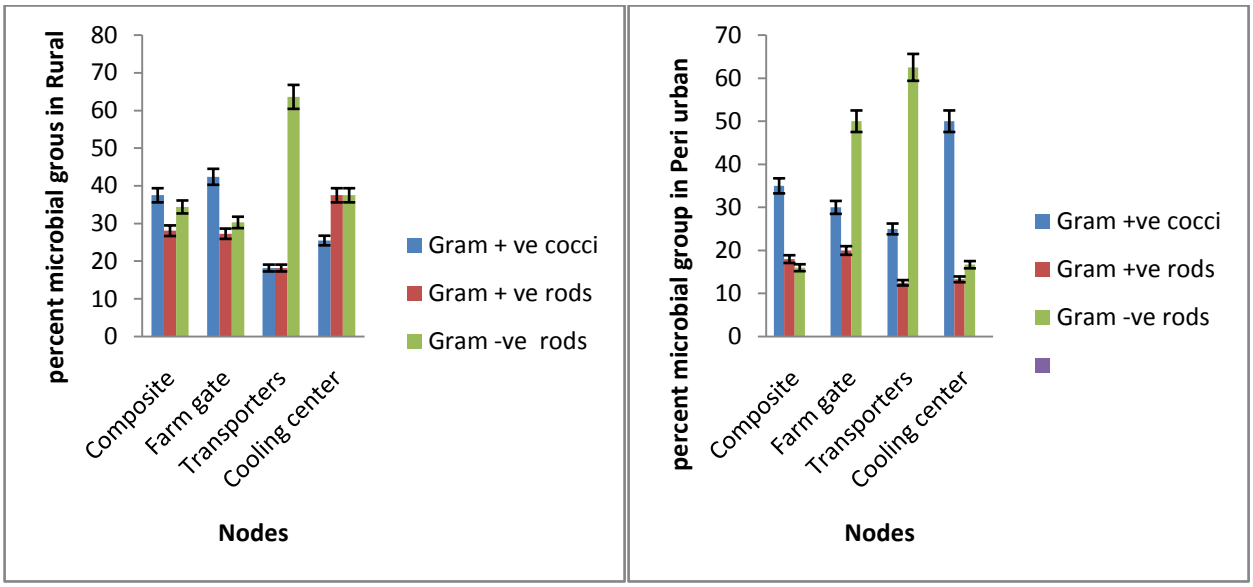

Figure 1. Percentage microbial morphology at each node in both dairy systems.

Table 5. Incidence of occurrence of different groups of microorganisms along the Rural dairy value chain.

Node	N	*Staphs.*	*Streps.*	*Bacillus*	*E.coli*	*Enterobacteriacea*
Udder milk	167	37	18	58	55	58
Farm Gate	51	7	15	7	15	7
Transporters	120	43	8	17	9	43
Cooling center	4	1	7	5	1	4
Total	341	88	42	83	80	109
Incidence (%)		26	13	26	23	32

Staphs – Staphylococcus spp, Strep. – Streptococcus fecalis E.coli – Escherichia Coli.

Table 6. Incidence of occurrence of microbial groups in Peri urban dairy value chain.

Node	N	*Staphs.*	*Streps.*	*Bacillus*	*E.coli*	Enterobacteriaceae
Composite	57	28	13	16	10	15
Farm Gate	30	30	20	20	10	20
Transporters	30	20	30	20	28	20
Cooling center	2	20	14	4	43	10
Total	120	98	77	104	91	65
Incidence (%)		82	64	87	76	54

Staphs – Staphylococcus spp, Strep. – Streptococcus fecalis E.coli – Escherichia Coli

from milk drawn directly from the udder had *staphylococcus, streptococcus, bacillus and entrerobacteriacea*. Other studies have isolated gram positive bacteria (*staphylococcus, streptococcus, Yeast and Moulds)* in milk asceptically drawn from the udder (Worku et al., 2012; Debela, 2015) Contamination of milk at this point is through the duct opening into the udder, soiled udder from contaminated sleeping material and the milking environment (Vissers, 2007) . The air around the milking parlour has been reported to contribute <5 CFU/ml of the total bacterial counts in milk. Out of these 20% have been reported to be spore forming bacteria especially the Bacillus *spp* (Vacheryou et al., 2011). Milk drawn directly from the udder has recorded counts of up to cfu/ml in other studies (Malese et al., 2015).

Between the udder and the farm gate, TVC increased by 0.1 log cycle (rural) and 0.3 log cycle (Peri urban). Contamination sources for this milk are the hands of milking personnel, udder surface, milking container, water, the sieve as well as the bulking container (Islam et. al., 2009; Kaindi et. al., 2011; Matofari et al., 2013). External udder contamination is a major risk to milk

contamination during milking. It has been reported that bedding material and feces, soil, mud are significant contributors to external udder contamination. Several studies have incriminated containers used at the farm and for milk storage and transportation to be most responsible for milk contamination (Bonfoh et al., 2003, Worku et al., 2012, wafula et al., 2016).

Water used during udder preparation and hand washing just before milking poses a risk to milk contamination. If the water is untreated and is used to wash and rinse equipment surfaces, then milk will be contaminated when it comes into contact with these surfaces. This type of untreated water can introduce a number of bacteria in milk including *Pseudomonas spp., coliforms Salmonella and Bacillus spp (*Al-Hubeaty et al, 2013; Matofari et al., 2003). Milking personnel are likely to contaminate milk with commensal bacteria if hand washing and sanitation is not practiced prior to milking. Microorganisms from human hands contamination are mainly gram positive *Staphylococcus spp, Streptococcus spp, Bacilluss pp* and gram negative *E. coli*. The extent of contamination also depends on the health of the milk handling personnel. It has been proven that water and sanitation are very significant in avoiding food contamination with both spoilage and pathogenic microorganisms (Gran et al., 2002).

Increase in total viable counts from the time the transporter picks milk from the farm gate to the time it is delivered to the collection center is the highest for both value chains. The value increases by 0.3 log cycle for rural and 0.5 log cycle for peri urban. The time that milk takes to move from the farm gate to the cooling center is the longest in the dairy systems. This is because the transporters not only pick milk from one farm, they move from one farm gate to the next. The transporters may take almost thirty minutes moving from one farm to the next before they make the journey to the cooling center. The modes of transport used to transport milk in Kenya vary from use of donkey, bicycle, motor cycles, vehicles and foot (Wafula et al., 2016). This hurdle coupled with poor roads allows microorganisms to multiply faster since no cooling is applied at this node (Lore et al., 2005; Kaindi et. al., 2011; Bareda et. al., 2012,). Due to poor roads which would increase chances of milk spillage during transportation, most transporters prefer to use containers with narrow openings to reduce the spillage. These types of containers are majorly plastic and are also light in weight compared to their metal counterparts. However, The narrow opening of the container makes it difficult to clean and therefore act at risk factors to milk contamination with microorganisms (Mesfine et. al., 2015; Wafula et al., 2016). Plastic materials have macro pores which hide biofilms and act as contamination sources (Bareda et. al., 2012; Mesfine et. al., 2015,).

The difference in TVC between the transporter and the cooling center was not significant, however there was a slight increase. Psychrotrophic bacterial counts were recorded the highest in both locations at the cooling center. The psychrotrophic bacterial count standard has been set at 100,000 CFU/m (Regulation No. 853/2004) by the European (EC) parliament of the Council. High processed dairy products need the limits before milk processing due to the stability of proteins and lipids (Cempirkova, 2007). Milk is cooled to 4^{o}C in the rural and to 7^{o}C in the peri urban. These temperatures slow down the growth of mesophiles and thermophiles due to the reduction in metabolic rate but have no effect on the control of Psychrotrophic bacteria.

Psychrotrophic bacteria represent a large group of microorganism in raw milk. Majority are aerobic, rod shaped and gram positive mainly pseudomonas. Other psychrotrophs isolated from raw milk include genera; *Micrococcocus, Aerococcus, LactococcusBacillus* and the family *Enterobacteriaceae*. Psychrotrophs have the ability to grow at low temperatures (3-7^{o}C) and utilize the large molecules of lipids and proteins for growth. During growth they produce heat resistance enzymes; lipases, phospholipases and proteases which persist after the enzyme producing microorganism has been destroyed (Herrera, 2001; Burdova et. al, 2002; Chan et. al., 2003; Arslanet.al., 2011). These enzymes are capable of spoiling milk products such as UHT, cheese, ghee, butter, skim milk powder among others (Bhunia, 2008; Ray 2004; Arslan, et. al., 2011).

Thermophilic bacteria from the study was significantly different in between the dairy systems. The temperatures in the rural locations were slightly lower during milking time compared to relatively high temperatures in Peri urban at milking. Peri urban location, milking was done when the sun had risen (6:00 am – 8:00 am) while Rural location milked in the wee hours of the morning (3:00 am – 600 am). Thermophillic bacillus are major contaminants of raw milk and dairy products (Janstova et al., 2006). They persist in dairy products which undergo elevated heat treatment of upto 65^{o}C (Cempirkova 2007). Facultative thermophiles can grow at both thermophilic and mesophilic temperatures. Some of the most common strains include *Bacillus licheniformis*, *Bacillus coagulans*, *Bacillus pumilus*, bacillus *sporothermodurans* and *bacillus subtillis* (Scheldeman et al., 2006). These thermophillic microorganisms do not pose a health risk to humans but they are used as hygiene index set in processing industries. Dairy processing industries adopt their own specifications of thermophilic index in their products to be able to attain marketability of these products (Rueckert et al., 2004).

Microbial groups and indicator microorganisms

The steady increase in gram negative rods along the chain with the highest recorded at the transporters' node shows the level of contamination at this point. *E. coli* and other *enterobacteriacea* might have entered milk through fecal sources like udder. The udder is in close proximity

with the cow's anus and is likely to be contaminated with coliforms and related microbes (Islam et al., 2009; Kumar et. al., 2012). These results are similar in finding the presence of enterobacter, Coliforms and E.coli in raw milk (Belli et al., 2013; Malese et al., 2015; Debela, 2015). This poses a public health risk to subsequent milk uses. Other isolated bacteria in milk with fecal source were *Streptococcus fecalis*. Initially these counts were lower in milk drawn directly from the udder and at the farm gate. At the transport node there is more time for proliferation and lack of cooling facilitating their growth. Milk leaving the animal is approximately 37^{o}C but arrives at the collection center at 34^{o}C-29^{o}C; these temperatures range is still suitable for the growth and proliferation of coliforms and most spoilage microorganisms. This finding is different from that of Malese et al., (2015) where staphylococcus as indicator microorganism was increasing in number as milk moved along the value chain. Staphylococcus has the ability to cause Staphylococcus food poisoning (SFP) and in other studies it has recorded an incidence of 38.7% (Tarekgne et al., 2015) which is higher than our findings in rural but lower than findings in peri urban. A study by Anueyiangu and Isiyaku (2015) however reported the incidence of *Staph aureus* at 21.8% in raw milk.

Gram positive cocci were falling steadily along the value chain in peri urban. Microorganisms such as *Staphylococcus* contaminated the milk most at the farm level but as they moved through the value chain, the gram negative coliform, *E. coli* and other *Enterobacteriaceae* competed favourably for the substrates hence affecting the rate of growth for the gram positive cocci. Gram negative bacteria were represented by *E.coli and enterobacteriaceae* for this study. The sum of the two groups was significantly different between the milk drawn directly from the udder and at the transporters node. Coliforms are used as indicator organisms for hygiene practice. They are capable of breaking down lactose to lactic acid and gas (Kornacki and Johnson, 2001,). At the cooling center the rate of growth of the gram negative cocci fell due to the fall in temperature. However the mean count for TVC was high due to the growth of Psychrotrophic bacteria. The cooling of milk at the cooling centre plays a significant role in microbial count differences compared to farm gate milk.

CONCLUSION AND RECOMMENDATIONS

Microbiological quality of milk in Rural and Peri urban is very low. This indicates poor hygiene in milk post-harvest practices. There is a risk of milk spoilage as a result of the extent of milk contamination with spoilage microorganisms in these dairy systems. Dairy products processed from this milk are likely to fall short of the expected shelf life due to contamination with high numbers of Psychrotrophic and Thermophilic microorganisms. This work recommends further studies to identify the microorganisms isolated up to the species level. It is also recommended that farmers should undergo informal training on pre milking and post harvesting hygiene practices.

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