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Microbiological quality evaluation of goat milk supplemented with different napier treatments

Nadiawati Alias[1*], Zakiah Mustapha[1], Abd Jamil Zakaria[1], Wan Rohani Wan Taib[2], Aryati Ahmad[2], Napisah Hussin[2], Zarinah Zakaria[1], Siti Nuriah Mohd Noor[1]and Noor Aini Mohd Yusoff[2]

[1]School of Agriculture Science and Biotechnology, Faculty of Bioresources and Food Industry, University Sultan Zainal Abidin, Besut Campus, 22200 Besut, Terengganu, **Malaysia**
[2]Faculty of Health Sciences, University Sultan Zainal Abidin, Gong Badak Campus, 21300 Kuala Terengganu, Terengganu, **Malaysia**

***Correspondence:** nadiawati@unisza.edu.my **Received 13-02-2020, Revised: 14-07-2020, Accepted: 15-07-2020 e-Published: 20-07-2020**

In Malaysia, increasing number of small scale dairy goat farms have been observed due to the demand for dairy goat products. Studies on milk quality and its safety at local farms may have been carried out. However, it may not be documented leading to lack of information on the standard management of dairy goat. From this point of view, a study was carried out at a community farm in Besut, Terengganu to evaluate the microbiological quality and safety of raw and pasteurized goat milk supplemented different Napier treatments. Methylene Blue Reduction Test (MBRT) carried out on all raw milk samples showed excellent hygienic condition with no color change after five hours of incubation. There were significant variations in Total Plate Count (TPC) for all raw milk samples tested and reduced TPC counts were observed for pasteurized milks. Nevertheless, all milk samples were found free from *E. coli* after pasteurization process and no contamination by yeast/moulds and *Streptococcus aureus* were observed. However, the presence of *Salmonella* or *Shigella* spp was detected in raw milk samples with the highest in RT4 (2.42 log cfu/mL) which may indicate cross contamination during milking. The presence of Lactic Acid Bacteria (LAB) was found highest in RT5 at 6.33 x 10^2 cfu/mL after treatment with goat fodder consisted of 45 days-old Napier supplemented with dolomite (60 g/clump). Overall microbiological quality of raw and pasteurized goat milks produced from the community farm showed good quality milk which is compliance to Malaysia Veterinary Services (not exceed 10^6 cfu/mL) and Food & Drug Administration standard (not exceed 20,000 cfu/mL) for dairy milk products..

Keywords: microbiological quality, Napier treatments, pasteurized goat milk, raw goat milk, safety.

INTRODUCTION

In recent years, goat milk has been served as surrogates to cow milk to provide a pivotal human nutrition. Many studies have shown the greater nutritional advantages of goat milk compared to the cow milk especially for its hypoallergenic potential, good digestibility, higher alkalinity and higher buffering capacity (Lad et al. 2017). In addition, it gives the most mimic and provides greater similarity to human milk. Therefore, it is suitable for people or infants who are allergic to cow milk.

Goat milk production in most part of Malaysia is much a cottage industry where the milking process uses hand and local retailing through farm gate sales (Shahudin et al. 2018) . Most of the milk is sold untreated either in the form of fresh liquid or frozen (Roberts 1985). Noteworthy, milk drawn from a healthy goat is almost bacteria-free.

However, the microorganisms might be traced in the milk from various routes such as the environment and the milk operative production from milking to distribution (Banik et al. 2014; Piotrowska et al. 2015). The microorganisms can be transmitted through endogenous route such as mastitic agents including the coagulase-negative *Staphylococcus* species and *Streptococcus* species which enter *in vivo* to the milk. In regard to faecal material, they produce a dry faecal pellet compared to large volume and moist dung produced by a cow. This form of pellet might less likely to introduce contamination to the milk in which the goats are considered as browsers that less potentially pick up infection from pasture contaminated with faecal material (Roberts 1985). Any problem related to illness with goat milk consumption is most related to poor hygiene rather than microorganism transmission from the goat itself. The most common pathogens in goat milk are *Staphylococci*, *Streptococci*, *Corynebacteria*, coliforms and Mycoplasms which may cause salmonellosis, tuberculosis, brucellosis, listeriosis, Q fever, toxoplasmosis to human (Clark & Mora García 2017; Suguna et al. 2012).

The quality and quantity of milk are also determined by manure of grass. Napier grass (*Pennisetum purpureum*) has been widely used as a fodder crop. The young and dark green leaves of Napier grass contain highly nutritious contents with good palatability. Treated manure for Napier grass would be beneficial in producing higher yield of quality and quantity of goat milk (Mohamad Nasir et al. 2018; Kari et al. 2019). Introducing several treatments to the Napier grass would give a better quality and quantity of milk produced by goats (Sembiring et al. 2015). Therefore, this study aimed to assess the microbiological quality of both raw and pasteurized local goat milk supplemented with different Napier treatments. This study also provides information on microbiological and safety risk assessment associated with raw goat milk consumption.

MATERIALS AND METHODS

Sample sampling and storage

Milk samples were collected from *Saanen* goats from a community farm at Kampung Kubang Depu, Besut, Terengganu that were given treated 45 days-old Napier, *Pennisetum purpureum* with five different treatments (assigned as T1, T2, T3, T4 and T5) as their fodder. All treatments were given with a standard NPK fertilizer and goat dung at the same rate of 80 g and 20 kg respectively for a clump of Napier that consisted of 200 plants at day 7 after replanting. T1 was a control with NPK and goat dung whilst T2 was enriched with Calcinit at 80 g/clump, T3 with Powerfeet and Seasol at 30 mL/10 L respectively, T4 with Keical at 40 g/clump and T5 with Dolomite at 60 g/clump. Fertilizer enrichment for T2, T4 and T5 were done on day 7 and day 30 after replanting whilst T3 treatment (foliar spray) was given on weekly basis starting from day 7 until day 35. Each treatment involved three goats which were fed with the Napier for three days prior to milking. The milk from three goats for each treatment were collected aseptically, homogenized and processed immediately as per the standard protocols. In the laboratory, the milk was pasteurized using low temperature-slow heating at 60°C for 20 minutes and kept in the chiller at 4°C for further analysis. All raw and pasteurized milk samples from each treatment (T1 to T5) were tested for microbiological test to determine its quality.

Methylene Blue Reduction Test

Methylene Blue Reduction Test (MBRT) was carried out according to the method described by Atherton & Newlander (1977). An amount of 10 mL milk sample was pipetted into a clean test tube and added with 1 mL of methylene blue. The tube was shaken to homogenize prior to incubation in water bath at 37°C. All procedures were carried out in aseptic technique and decolourization of blue colour milk was recorded. The time taken for decolourization indicated the milk quality. Milk decolourization stage as stated in Table 1 was used to indicate the quality of the milk tested.

Table 1: Milk decolourization phase by Methylene Blue Reduction Test (MBRT).

Time taken for decolourization	Milk Condition
5 hours and above	Excellent
3 to 4 hours	Good
1 to 2 hours	Fair
Less than ½ hours	Poor

Standard Total Plate Counts

Standard plate count was carried out using the Tryptone Glucose Yeast Extract Agar (himedia). The milk sample was serially diluted up to 10^{-3} dilution in 0.85% sterile saline water and enumeration of total bacteria was done using the spread plate method. The plates were incubated at 37˚C for 24 h for total aerobic mesophilic counts. While thermophilic count was obtained from the incubation for 24 h at 60˚C and psychrotropic count was obtained at low temperature incubation of 5˚C

for five days. The colonies appeared on the agar were counted and Colony Forming Unit (CFU) was calculated according to Sutton (2011).

Coliform Count

Presumptive Coliforms count was done by using MacConkey's agar. A serially diluted milk sample was spreaded on MacConkey's agar and incubated at 37˚C for 48 h. The dark red colonies appeared were counted and the Colony Forming Unit (CFU) were calculated according to Sutton (2011).

Yeast and Mould Count

Potato Dextrose Agar (PDA) was used for the cultivation of yeast and mould in the milk sample using the spread plate method. A serially diluted sample in 0.85% sterile saline water was pipetted and spreaded onto the PDA agar and incubated at room temperature (28 ± 2^{o}C) for five days. The colonies appeared on agar were counted and the Colony Forming Unit (CFU) were calculated according to Sutton (2011).

Bacterial enumeration using selective and differential media

Selective and differential media were used to isolate and identify particular organisms. Selective media allow certain types of organisms to grow while inhibit the growth of other organisms. A serially diluted milk samples in 0.85% sterile saline water were aliquoted and spreaded on different agar media for detection of different type of microorganisms. The colonies appeared on agar were counted and the Colony Forming Unit (CFU) were calculated according to Sutton (2011).

Violet Red Bile Agar (VRBA)

Violet Red Bile Agar was used as the selective medium for the detection and enumeration of coliform organisms in water, milk and other dairy products (Wehr & Frank 2004). Plates were incubated at 37˚C for 48 h. The Lactose-fermenting microorganisms produced pink to red colonies surrounded by a reddish zone of precipitated bile and non-lactose-fermenting microorganisms resulted in colourless colonies.

Xylose Lysine Deoxycholate (XLD) Agar

Xylose Lysine Deoxycholate (XLD) Agar was used as the selective medium for the isolation of *Salmonella* and *Shigella* spp from clinical specimens and food samples (Widodo et al. 2019). Plates were incubated at 37˚C for 24 h. The *Shigella* species appeared as red colony on the agar while *E. coli*, *Citrobacter* and *Proteus* spp appeared yellow.

Tryptone Bile X-Glucuronic Agar (TBX)

Tryptone Bile Glucuronic Agar was used as the selective medium for detection and enumeration of *E. coli* in food, animal feed and water (Cupáková et al. 2012). Plates were incubated at 44˚C for 24 h. The *E. coli* colony appeared in turquoise to blue colour, *Citrobacter* and *Pseudomonas* colonies appeared in white to green-beige colour.

Mannitol Salt Agar (MSA)

Mannitol Salt Agar (MSA) was used as the selective medium for the isolation of pathogenic *Staphylococci* genus (Omar et al. 2018). Plates were incubated at 37˚C for 48 h. *Staphylococcus aureus* produced small yellow colonies surrounded by yellow zones on this media while other types of *Staphylococci* produced small pink or red colonies with no colour change to the medium.

MRS Agar

MRS Agar was used as the selective medium for the isolation of LAB strains and the plates were incubated unaerobically at 37˚C for 48 h (Sule et al. 2014). *Lactobacillus* appeared as white colony on the agar.

Data Analysis

The experiments were arranged in a completely randomized design (CRD). Data were analyzed using Analysis of Variance (ANOVA) from SPSS version 21. Multiple comparisons were done using Tukey's multiple comparison test.

RESULTS AND DISCUSSION

Improper handling at farm levels including poor hygienic conditions, inadequate storage, inefficient transport system would encourage contamination to goat milk. These factors are mostly related to poor handling and management by farmers in Malaysia (Chye et al. 2004; Abdullah et al. 2015). Therefore, poor goat milk quality has often been considered as one of the major reasons for losses and reduced income for the smallholder dairies in Malaysia (Shahudin et al. 2018). Presence of multi nutrients in goat milk is however may be the factor which encourages the growth and accumulation of microorganisms (Lima et al. 2018; Malik et al. 2019). Thus, by providing adequate details on the microbiological quality of the goat milk and prevalence of pathogenic and spoilage microorganism in the milk, it might be useful to identify appropriate HACCP (Hazard Analysis

Critical Control Point) and implement better Good Agricultural Practices (GAP) and Good Manufacturing Practices (GMP) at the farm level. This in a long run would provide benefit to consumers and the dairy industry in Malaysia.

Fourty four milk samples were collected from *Saanen* goats after underwent different fodder treatments at local community farm at Kampung Kubang Depu, Besut, Terengganu, Malaysia. Results obtained from Methylene Blue Reduction Test (MBRT) for all the samples tested showed excellent quality of the raw milk products where all samples showed no color change after five hours of incubation. The test was based on the decolourization of methylene blue dye solution which correlated to the microbial activity that consume dissolved oxygen in the sample. The test employed enzymatic reduction of methylene blue during bacteria metabolism turning the dye colorless (Nandy & Venkatesh 2010; Sudhasaravanan & Binukumari 2015). The sooner the time taken for the decolourization, the greater the amount of microbial content in the milk which related to poor quality of milk (Bapat et al. 2006).

According to Chye et al. (2004), generally, fresh raw milk collected from farms were heavily contaminated by bacteria with a mean TPC of 12 x 10^6 cfu/ml. Limit of bacteria count set by Malaysia Veterinary Services must not exceed 10^6 cfu/ml (Chye et al. 2004). In order to estimate TPC for all milk samples, Tryptone Glucose Yeast Extract agar was used. This media is known as standard media for cultivation and enumeration of bacteria in milk and dairy products as stated by Wehr & Frank (2004).

Results obtained for microbial population in goat milk samples collected from the community farm is shown in Figure 1. TPC in samples collected from RT1 (1.98 x 10^4 cfu/ mL) showed the highest bacterial count followed by RT3 (1.1 x 10^4 cfu/mL), RT2 (6.92 x 10^3 cfu/mL), RT5 (2.33 x 10^3 cfu/mL) and RT4 (1.83 x 10^3 cfu/mL) respectively. For pasteurized samples, major reductions in TPC were exhibited for all the samples with up to 20X reduction for sample PT1.

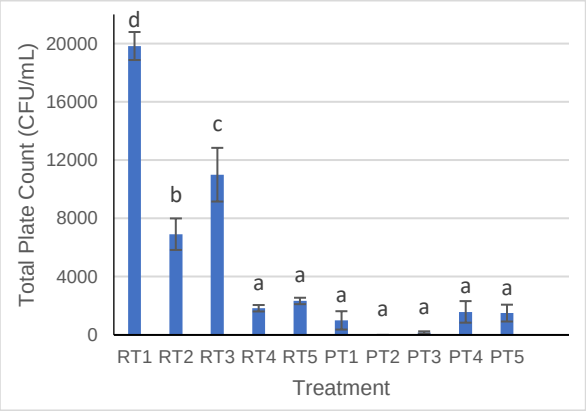

Figure 1. Total Plate Count (TPC) for all goat milk samples after different fodder treatments. RT; raw treatment milk; PT; pasteurized treatment milk. Each value is expressed as a mean ± SE of triplicates. Means with the same letters are not significantly different at *P*≤ 0.05 Tukey's multiple comparison, n=3.

No bacteria count was shown for sample PT2 after pasteurization. While for sample PT4 and PT5, TPC were still under the minimum CFU stated by Food and Drug Administration (FDA) (not exceed 20,000 cfu/ml). High number of microorganism presence in milk indicated that these microorganism not only contaminated the milk but also multiplied and grew in it. This is due to the fact that milk is a good nutritive medium for the growth of the microorganism especially with unhygienic condition. Variety of milk compositions (fats, proteins, amino and fatty acids) in raw goat milk may contribute to the presence of mixed microflora in the milk (Lai et al. 2016). Meanwhile, a study done by Lima et al. (2018) mentioned that different feeds formula given to the goats was also one of the major factors contributed to the presence of different nutrients found in goat milk leading to presence of mixed microflora in milk. Besides, other factors such as genetics (breed/species), stage of lactation, health status and environmental factors (climate & season) and method of milking also play important roles in determining milk compositions (Lima et al. 2018).

Pasteurized milks (PT1 – PT5) were treated with low heat (60°C) for 20 minutes in order to guarantee significant reduction of spoiling microorganism and destruction of all pathogenic bacteria, without damaging the product. This technique, if performed correctly, would prolong the shelf life and quality of the milk (Hoffmann et al. 2006). Figure 1 depicts all pasteurized milk showed

very low in TPC count which were less than 2,000 cfu/mL. Fodder enriched by 40 g/clump keical (T4) and 60 g/clump dolomite (T5) showed the highest in TPC after pasteurization at 1.58 x 10^3 cfu/mL and 1.5 x 10^3 cfu/mL, respectively. The standard TPC stated by FDA Pasteurized Milk Ordinance for pasteurized milk must not exceeds 20,000 cfu/mL eventhough the pasteurization process may vary from one country to another according to the state national legislation (PMO 2017). The natural bacteria flora of goat as well as those associated with mastitis are generally not thermoduric, although there may be a few exceptions. Higher microbial contents presence in raw milk could also be due to infection of the udder arise from the teat duct (Msalya 2017). But if high count of bacteria found after pasteurization, this could normally be associated with a serious cleaning failure. The exterior of the teat and udder must be carefully washed to remove residues of manure and dirt, which contain large numbers of microorganisms. In addition, milking process especially the equipments associated with it such as utensils, rubbers, pails, cans and pipelines of the milking equipments could also introduce microorganisms proportion into the raw milk (Granado et al. 2014; Msalya 2017). In order to reduce the milk contamination, utensils used for milking should be properly cleaned and rinsed using suitable detergents and must be disinfected immediately after use (Noordhuizen et al. 2008; Tormo et al. 2011).

Comparison data on thermophile and psychrotroph contamination in raw and pasteurized milk are shown in Table 2. All data show a reduction in bacteria count after pasteurization was performed on the milk samples. The highest thermophiles presence was in raw milk RT1 (4.75 x 10^2 cfu/mL) but after pasteurization, PT1 showed about 59 folds reduction in thermophile count to 0.08 x 10^2 cfu/mL. While for raw sample RT2, approximately 2.0 x 10^2 thermophiles were counted but after pasteurization, no thermophiles were found. It is noteworthy that the thermophilic bacteria were still present but in reduced number for other treatments. No psychrotrophic bacteria was found for all samples tested. Normally, milk which undergo heat treatment would result in reduced psychrotrophic and mesophilic bacteria population, however the two main groups of bacteria known as thermoduric microorganism and bacteria introduced may remain through post-pasteurization stage (Quigley et al. 2013). Thermoduric bacteria is a miscellaneous group of bacteria that is capable to survive during pasteurization or other heat treatments (Tamine & Robinson 1999). During pasteurization, some bacteria may enter a 'viable but nonculturable' state which they may be underestimated by traditional culture methods (Wesolowska & Bartoszcz 2009). As a general rule, all thermoduric and thermophilic bacteria are gram-positive and some are spore-forming bacteria (such as *Bacillus*, *Paenibacillus*). This spore forming microorganisms usually enter the milk chain from soil, silage, bedding material and significantly are resistant to pasteurisation (Driehuis 2013).

Table 2. Bacterial load of milk samples collected from local dairy farm in Besut, Terengganu.

Treatments	Bacteria count (cfu/mL)		
	Total Plate Count (TPC)	Thermophiles	Psychrotrophs
	(x 10^4)	(x 10^2)	(x 10^2)
RT1	$1.98^{d} \pm 0.09$	$4.75^{c} \pm 1.04$	NP
RT2	$0.69^{b} \pm 0.11$	$2.00^{a,b} \pm 0.25$	NP
RT3	$1.10^{c} \pm 0.18$	$3.83^{b,c} \pm 0.83$	NP
RT4	$0.18^{a} \pm 0.02$	$1.42^{a} \pm 0.08$	NP
RT5	$0.23^{a} \pm 0.02$	$1.83^{a,b} \pm 0.22$	NP
PT1	$0.10^{a} \pm 0.06$	$0.08^{a} \pm 0.08$	NP
PT2	$0.00^{a} \pm 0.00$	$0.0^{a} \pm 0.00$	NP
PT3	$0.02^{a} \pm 0.01$	$0.17^{a} \pm 0.08$	NP
PT4	$0.16^{a} \pm 007$	$0.67^{a} \pm 0.08$	NP
PT5	$0.15^{a} \pm 0.06$	$0.83^{a} \pm 0.17$	NP

[abc]Different letters within the counts in the same column indicate significant different (P<0.05). NP: not present.

Coliform count from the raw goat milk sample was found highest in RT1 sample as 2.67 log cfu/mL followed by RT5 (1.92 log cfu/mL) and RT4 (2.12 log cfu/mL). Coliform bacteria concentration was gradually decreased after pasteurization with PT1 (2.22 log cfu/mL), PT4 (1.96 log cfu/mL) and PT5 (1.62 log cfu/mL) as stated in Table 3. Unfortunately, these coliform counts exceeded coliform ratio stated by Malaysian Food Act (1983) and Food Regulations Act (1985) which is supposed to be below 1.7 log cfu/mL. Presence of *E. coli* (Enterobacteria) was also observed in raw goat milk RT4 (1.90 log cfu/mL), RT1 (1.72 log cfu/mL) and RT5 (1.70 log cfu/mL). Nonetheless, all milk samples were found free from *E. coli* after pasteurization process. Presence of coliform mainly indicates fecal contamination during milking (Jayarao et al. 2004). Meanwhile, high coliform counts are more often resulted from dirty equipments and unsanitary milking proceduces (Lai et al. 2016). Coliforms including *Escherichia coli*, *Klebsiella* spp, *Enterobacter* spp and *Citrobacter* spp are found ubiquitous in feces,

manure and soil which allow easy dispersal of pathogens in the farm (Martin et al. 2016; Lingathurai & Vellathurai, 2013). In addition, this milk contamination could be attributed to the cumulative contamination at different levels (Worku et al. 2012). Some milk samples may be held up a bit longer after milking, this may become a major source of milk contamination while milk is transported and stored before sold. Eventhough global risk of *E. coli* as a causative agent for diarrheal illness has decreased over the past 50 years, but the risk is still accountable especially in under-developed countries (Qadri et al. 2005).

All goat milk samples were found to be free from yeast, moulds and *Streptococcus aureus* infection as depicted in Table 2. *S. aureus* is widely recognized as a major causative agent for clinical and subclinical mastitis in dairy industry (Petersson-Wolfe et al. 2010). The prevalence of pathogens in the goat milk has been widely associated with the occurrence of diseases in the animals including goat mastitis (Ondiek et al. 2018) and brucellosis (Nofal et al. 2017). The presence of *Salmonella* or *Shigella* spp was observed in all raw milk samples. The highest was in RT4 (2.42 log cfu/mL) and the lowest in RT2 (1.03 log cfu/mL) respectively. Both strains are major foodborne pathogens associated with consumption of raw milk and milk products that affect humans causing foodborne illness like salmonellosis and shigellosis with serious health implications (Omar et al. 2018; Younis et al. 2018). Microbiological study carried out indicated that the strains were heat sensitive and not able to survive under pasteurization treatment as shown in Table 2. However, inadequate heat treatment and post-processing contamination of dairy products could be among factors that need to be attained (Chye et al. 2004). It is important to reassure the implementation of hygienic measures during milking and manufacturing of dairy products to minimize the risk of human infections with these pathogens (Lanzas et al. 2010; Younis et al. 2018).

Lactic acid bacteria (LAB) is known as an indigenous microflora in raw milk. But the species composition of LAB varies and inconsistent when isolated from different sources of milk (Rinkinen et al. 2003). LAB isolated from milk, milk-based and non-milk based fermented foods have been labelled as GRAS (Generally Recognized As Safe) status and have widely been used in food and medicine because of their probiotic attributes (Mahalot & Mandal 2018). Figure 2 demonstrates raw goat milk from RT5 which yielded the highest in LAB count which at 6.33 x 10^2 cfu/mL followed by RT4 (4.42 x 10^2 cfu/mL) and RT3 (3.17 x 10^2 cfu/mL). Treatment 5 of goat fodder contained 45 days-old Napier supplemented with dolomite (60 g/clump) whilst Treatment 4 contained 45 days-old Napier supplemented with keical (40 g/clump). Napier grass (*Pennisetum purpureum*) is a robust perennial grass that has been widely used as tropical forage. This grass produces more dry matter yield compared to other tropical grasses (Kahindi et al. 2007; Turano et al. 2016). Eventhough it has low protein concentration, it can provide a satisfactory forage source for goats and cows, if supplemented with legumes, protein and other minerals (Shahudin et al. 2016). Dietary fibre contributes significantly towards balance nutrient requirements in goats especially for lactating dairy goats which require fibre to maintain a normal milk fat content (Lu et al. 2005, Asmad et al. 2015).

Fibre is also important as prebiotics which constitutes as substrate for desirable bacteria in the gut (Lima et al. 2018). Various feed additives have been used in livestock such as fructooligosaccharide (FOS), galactooligosaccharide (GOS), inulin, isomaltooligosaccharides (IMO), xylo-oligosaccharides (XOS), lacticol, lactulose and cereals fibre (Crittenden & Playne 2009; Rahman et al. 2018). When formulating composition of prebiotics for animal feed, determination of accurate dosage is essential. Over usage of prebiotics may lead to flatulence and diarrhoea (Olveira & Gonzalez-Molero 2016). This action would equilibrates microflora within the intestines and consequently improve feed conversion efficiencies.

After pasteurization, most milk samples showed reduction in LAB counts. Sample T5 showed the biggest reduction in LAB to 1.67 x 10^2 cfu/mL from 6.33 x 10^2 cfu/mL. Sample T4 showed reduction in LAB count to 1.17 x 10^2 cfu/mL after pasteurization procedure. Meanwhile, for T3 sample, no LAB was present after pasteurization stage. During pasteurization, low heat treatment at 60°C was used to pasteurize all raw milks.

The indigenous LAB population has to cope with pasteurization and heat stress, particularly in spontaneous fermentations. (Papadimitriou et al. 2016). LAB is considered as “thermotolerant” strains if abundantly grow (>300 cfu/mL) after thermal treatment (Pérez-Chabela et al. 2008). But most of the samples showed less than 300 cfu/mL LAB counts after pasteurization process which is not indicative for thermotolerant LAB strains. Previous studies have identified a few LAB strains presence in goat milk such as *Lactobacillus*

plantarum (Sridevi et al. 2015), *Lactococcus garvieae* (Morea et al. 1999) and *L. paracasei* (Badis et al. 2004; Widodo et al. 2016). In addition, research carried out by Marroki et al. (2011) managed to isolate three different species of LAB such as *Lactobacillus plantarum, Lactobacillus rhamnosus* and *Lactobacillus fermentum* from goat's milks.

Table 3. Contamination of raw and pasteurize milk samples by coliform, *Escherichia coli*, *Streptococcus aureus, Salmonella* and *Shigella* spp.

Treatments	Bacteria count (log cfu/mL)				
	Coliform	Enterobacter/ *E. coli*	Yeast/ mould	*S. aureus*	*Salmonella*/ *Shigella* spp.
RT1	2.67^{c} ± 0.09	1.72 ± 0.12	NP	NP	1.99 ± 0.10
RT2	NP	NP	NP	NP	1.03 ± 0.13
RT3	NP	NP	NP	NP	1.66 ± 0.11
RT4	2.12 ± 0.11	1.90 ± 0.08	NP	NP	2.42 ± 0.07
RT5	1.92^{ab} ± 0.18	1.70 ± 0.27	NP	NP	2.41 ± 0.14
PT1	2.22^{b} ± 0.11	NP	NP	NP	NP
PT2	NP	NP	NP	NP	NP
PT3	NP	NP	NP	NP	NP
PT4	1.96^{ab} ± 0.19	NP	NP	NP	NP
PT5	1.62^{ab} ± 0.93	NP	NP	NP	NP

^{abc}Different letters within the counts in the same column indicate significant different (P<0.05). NP: not present.

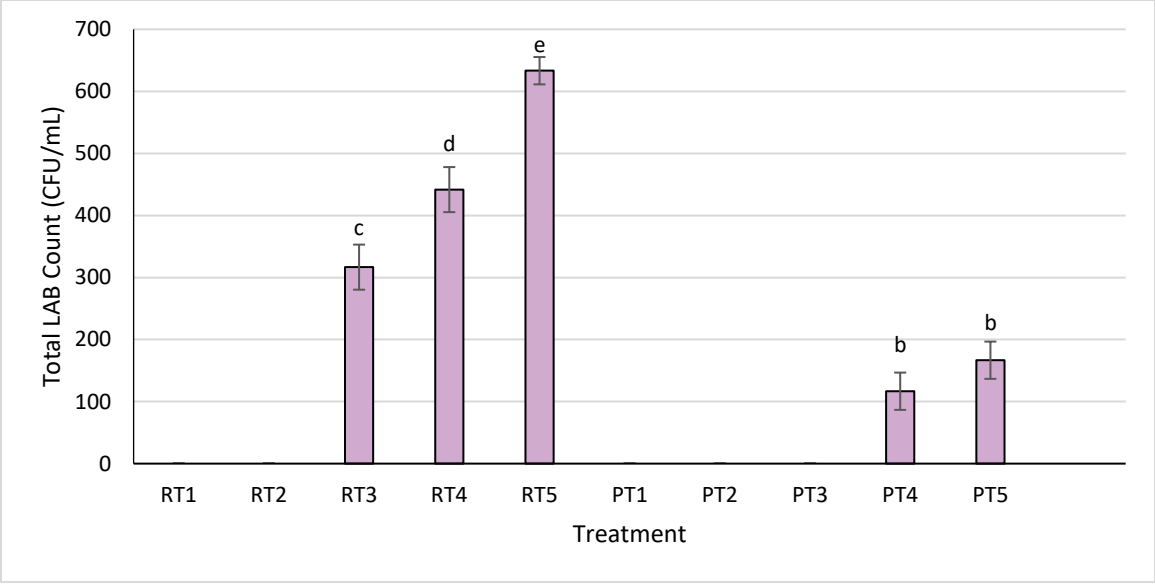

Figure 2. Total Lactic acid bacteria (LAB) count from raw and pasteurize goat milks. Means with the same letters are not significantly different at *P*≤ 0.05 Tukey's multiple comparison, n=3.

CONCLUSION

This study has clearly indicated that microbiological quality of raw and pasteurized goat milk produced by community farm in Kampung Kubang Depu, Besut, Terengganu are in compliance with Malaysia Veterinary Services limits as well FDA standard (FDA Pasteurized Milk Ordinance) for dairy milk products. No yeast or moulds and pathogenic *Streptococcus aureus* were found in both raw and pasteurized milk. However, the presence of *Salmonella* spp and *Shigella* spp were notified but at low level in raw goat milk indicating poor hygiene and sanitation during milking which need to be improved. After pasteurization, both strains were not present in both raw and pasteurize milk. It is interesting to annotate that, Lactic Acid Bacteria (LAB) was found present in both raw and pasteurized goat milk. This indicates good feeds and optimum formulations were given to the goats which are essentials to boost milk quality and productivity.

CONFLICT OF INTEREST

The authors declared that present study was performed in absence of any conflict of interest.

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AUTHOR CONTRIBUTIONS

NA designed the experiments, performed data analysis and wrote the manuscript. ZM, AJZ and SNMN performed field & laboratory experiments and data analysis. WRWT, AA and NAMY carried out manuscript editing. NH and ZZ performed final revision and reviewed the manuscript. All authors read and approved the final version.

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