The gut microbiota and its metabolites in mice are affected by high heat treatment of Bactrian camel milk

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ABSTRACT

Heat treatment is the most common method used to make milk safe; however, it leads to changes in the organoleptic and nutritional properties of milk. This study aimed to investigate the effects of different heat treatments on nutrients and microbiota of camel milk. The results showed that the nutrient composition of camel milk could be influenced by heat treatment. Ultra-high-temperature treatment of samples significantly reduced levels of camel milk proteins, vitamin C, and lactose, but did not significantly alter the amino acids content. Analysis of 16S rRNA amplicon sequences demonstrated that the composition of the intestinal microbiota of mice fed different heat-treated camel milks changed, as did the production of short-chain fatty acids as determined by gas chromatography–mass spectrometry. High temperature/short time treatment had similar effects to UHT treatment on microbial diversity of camel milk; however, the low temperature/long time treatment had different effects. In addition, higher-temperature treatments changed the abundance of key bacteria at the genus level. These results demonstrated that different heat treatments not only resulted in some nutrient loss, but also changed the proliferation of some probiotic genera. Our results could provide the basis for the potential industrial application of camel milk processing technologies.

Key words: heat treatment, camel milk, nutrient, short-chain fatty acid, microbiota

INTRODUCTION

Milk is rich in macronutrients, such as proteins, lipids, sugar, vitamins, minerals, and enzymes. Especially, milk is an important source of high-quality protein in the human diet and the most important source of nutrition in infancy. The richness in nutrients of raw milk means that it could harbor pathogens and putrefying microorganisms, making it a threat to human health. Hence, the processing of milk, such as by homogenization and heat treatment, ensures microbial safety and extends shelf life (Claeys et al., 2013). However, the heat treatment of milk not only ensures milk safety, but can also change the primary sensory and nutritional properties of raw milk (Melini et al., 2017). For example, heat treatment can cause irreversible damage, including lactose degradation, protein denaturation, and inactivation of functional components (Felfoul et al., 2016).

In arid and semi-arid regions, inhabitants gain an important part of their nutrition from camel milk. In terms of essential nutrients, camel milk is very similar to cow milk (Elhadi et al., 2015; Nongonierma et al., 2017). However, their relative compositions and protein fractions differ. β -Casein is the main casein fraction in camel milk. Camel whey is rich in immunoglobulins, lactoferrin, serum albumin, α -LA, and lysozyme; however, it has no β -LG (Khalesi et al., 2017). It also contains higher levels of PUFA and antimicrobial components than other ruminant milk (He et al., 2019). In addition, camel milk has certain medicinal properties and is used to treat different human diseases in some countries (Sawaya et al., 1984; Mihic et al., 2016; Mati et al., 2017).

To ensure camel milk safety and extend shelf life, heat treatment is a key technology. In recent years, a few studies have investigated the changes in contents and functional differences in camel milk samples after different heat treatments. Recent studies showed that

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camel whey proteins were affected by treatment at 80°C for 1 h; however, the casein fractions remained intact (Laleye et al., 2008; Lorenzen et al., 2011; Felfoul et al., 2017). Furthermore, camel milk whey showed better thermal stability than bovine or buffalo whey (Farah and Atkins, 1992). Another study found that some nutrients were lost, which affected milk quality, after heat treatment at 100°C for 30 min (Elagamy, 2000). Moreover, the functional features of the intestinal microbiota were altered by changes in the nutrients of camel milk (Shao and Wang, 2018). However, little information is available on the changes in gut microbiota and their metabolites following UHT treatment of camel milk. Consequently, in the present study, we aimed to determine the effects of camel milk that had undergone different heat treatments on fecal short-chain fatty acids (SCFA) and changes in gut microbiota of mice. Our results could provide useful information for the dairy industry.

MATERIALS AND METHODS

Treatment of Camel Milk

Twenty fresh samples of camel milk were obtained from Bayannur (Inner Mongolia, China). All samples were mixed and stored on ice in sterile containers during transportation to the laboratory. The untreated samples were used as control (raw control milk, **RCM**), and other samples were treated using different heat processing methods. Heat treatment conditions were as follows: 65°C for 30 min (low temperature/long time; **LTLT**), 85°C for 15 s (HTST), and 135°C for 5 s (UHT). Whole milk samples were stored at -20°C in a refrigerator.

Animal Experiments

A total of 24 C57BL/6J male mice (6–8 wk old) were provided by Weitonglihua Experimental Animal Tech Co. (Beijing, China). The mice were reared at 22 ± 2°C with a 12-h light/dark cycle and fed a standard chow diet during experimental period. After acclimatization for 1 wk, the mice were divided randomly into 4 groups (n = 6 per group): RCM, LTLT, HTST, and UHT groups. All mice received 10 mL of camel milk/kg of BW daily for 4 wk via intraperitoneal injection. On d 28, the colon and fecal contents of all animals were collected.

This study was approved by the Review Committee for the Use of Human or Animal Subjects of the Food Science and Engineering College of Inner Mongolia Ag-

ricultural University (Hohhot, China). All procedures were conducted according to the National Institutes of Health *Guidelines for the Care and Use of Laboratory Animals* (Publication No.85–23, revised 1985).

Determination of Nutrients in Heat-Treated Camel Milk

The composition of different heat-treated camel milks, including protein, fat, lactose contents, ash, and vitamin C, were determined according to international standard methods (Zhang et al., 2005). Total amino acids were detected using a previously established method (He et al., 2019). The determination of the main nutrients was performed in triplicate.

Determination of SCFA Contents

Concentrations of SCFA in fecal samples were determined using GC-MS analysis. Sample quantification was obtained by means of acetic, propionic, butyric, and valeric acid standard curves.

16S rRNA Sequencing

Twenty-four cecal samples were collected for 16S rRNA gene amplicon sequencing. The 16S rRNA gene (V3–V4 variable region) was amplified using primers 338F/806R. Specifically, a QIAamp Fast DNA stool Mini Kit (Qiagen, Valencia, CA) was used to extract total DNA from mouse feces, according to the manufacturer's instructions. A Phusion High-Fidelity PCR Master Mix Kit (catalog no. M0541, New England Biolabs, Ipswich, MA) was used to carry out all the PCR reactions. After purification and quantification of the PCR products, they were subjected to DNA sequencing using the Illumina MiSeq (Illumina Inc., San Diego, CA) platform, according to the manufacturer's recommendations, which generated 250-bp paired-end reads. Using QILME version 1.9.1, the sequences were further demultiplexed and analyzed (Zhang et al., 2005). We used the SILVA 16S rRNA reference database to classify taxonomic abundance (<https://www.arb-silva.de>). Operational taxonomic unit (**OTU**) clustering was then performed at 97% sequence identity (Edgar, 2010).

Statistical Analysis

All data were expressed as the mean ± standard error of the mean (SEM). The Kruskal-Wallis test with Dunn's multiple comparison test analysis was used to assess significant differences among different groups.

The β -diversity was calculated using weighted UniFrac distances with principal coordinate analysis and non-metric multidimensional scaling, and by hierarchical cluster analysis and Bray-Curtis distance heatmap analysis to illustrate the similarities and differences among the microbial communities. The unweighted pair group method with arithmetic mean (UPGMA) was used to prepare the hierarchical cluster tree. The algorithm linear discriminant analysis of effect size (LEfSe) was used for discovering biomarkers and differences in the taxonomic feature of the 4 groups.

RESULTS

Nutrient Composition of Camel Milk Under Different Heat Treatments

The nutrient composition of camel milk in the 4 treatment groups is shown in Table 1. We found that the concentration of certain camel milk nutrients was significantly reduced by heat treatment ($P < 0.05$). We detected significant differences in vitamin C and lactose contents among the RCM, HTST, and UHT milk samples ($P < 0.05$). Protein content also decreased when camel milk was subjected to HTST and UHT treatment ($P < 0.05$). However, no differences in the amounts of amino acids were observed among the 4 groups.

Taxonomic Annotation of the Gut Microbiota in Camel Milk Under Different Heat Treatments

In the present study, 24 fecal samples (from the 4 groups) were collected and further evaluated for the effect of heat treatment on the intestinal microbiota from Bactrian camel milk, as assessed by sequencing the 16S rRNA V3–V4 region. An average of 54,462 high-quality sequences were acquired for each of the samples, which varied in length from 401 to 405 bp (Supplemental Figure S1A; <https://doi.org/10.3168/jds.2020-18657>). Eventually, we obtained 573 OTU at 97% similarity. The rank-abundance curve showed that for each sample, sufficient sequencing depth had been achieved for the analysis of gut microbiota diversity (Figure S1B).

The taxon-based analysis was performed on the OTU to identify changes in the gut microbiota in all groups. At the phylum level, in the intestinal tract of the mice, the dominant phyla were *Firmicutes*, *Bacteroidetes*, *Actinobacteria*, and *Patescibacteria*. *Firmicutes* were dominant in UHT and HTST samples (62.53 and 66.37%, respectively), whereas *Bacteroidetes* were dominant in the RCM and LTLT samples (70.86 and 58.08%, respectively; Figure 1A). At the family level, *Lactobacillaceae* (24.00 and 23.00%), *Lachnospiraceae* (22.90 and 30.49%), and *Muribaculaceae* (21.88 and 21.76%) predominated in the gut of UHT and HTST

Table 1. Nutritional variation in different heat treatments of camel milk¹

Item	Heat treatment ²			
	RCM	LTLT	HTST	UHT
Fat (%)	4.05 ± 0.04 ^a	3.89 ± 0.10 ^a	3.98 ± 0.10 ^a	3.87 ± 0.03 ^b
Protein (%)	4.15 ± 0.08 ^a	3.94 ± 0.06 ^a	3.93 ± 0.03 ^b	3.91 ± 0.03 ^b
Lactose (%)	5.06 ± 0.12 ^a	4.85 ± 0.10 ^a	4.81 ± 0.07 ^a	4.63 ± 0.07 ^b
Ash (%)	0.73 ± 0.01 ^a	0.73 ± 0.01 ^a	0.72 ± 0.01 ^a	0.72 ± 0.01 ^a
Vitamin C (mg/100 g)	30.54 ± 0.90 ^a	27.17 ± 0.65 ^a	26.99 ± 0.40 ^a	25.70 ± 0.47 ^b
Aspartic acid (g/100 g)	0.26 ± 0.02 ^a	0.27 ± 0.01 ^a	0.27 ± 0.02 ^a	0.24 ± 0.03 ^a
Threonine (g/100 g)	0.19 ± 0.01 ^a	0.20 ± 0.01 ^a	0.19 ± 0.02 ^a	0.17 ± 0.02 ^a
Serine (g/100 g)	0.20 ± 0.01 ^a	0.21 ± 0.01 ^a	0.21 ± 0.02 ^a	0.18 ± 0.02 ^a
Glutamic acid (g/100 g)	0.82 ± 0.06 ^a	0.87 ± 0.04 ^a	0.87 ± 0.09 ^a	0.78 ± 0.10 ^a
Glycine (g/100 g)	0.05 ± 0.01 ^a	0.05 ± 0.01 ^a	0.04 ± 0.02 ^a	0.04 ± 0.01 ^a
Alanine (g/100 g)	0.09 ± 0.01 ^a	0.09 ± 0.02 ^a	0.09 ± 0.01 ^a	0.08 ± 0.01 ^a
Valine (g/100 g)	0.24 ± 0.02 ^a	0.25 ± 0.01 ^a	0.25 ± 0.03 ^a	0.22 ± 0.03 ^a
Methionine (g/100 g)	0.10 ± 0.01 ^a	0.11 ± 0.01 ^a	0.11 ± 0.02 ^a	0.10 ± 0.01 ^a
Isoleucine (g/100 g)	0.21 ± 0.02 ^a	0.22 ± 0.01 ^a	0.23 ± 0.02 ^a	0.20 ± 0.03 ^a
Leucine (g/100 g)	0.37 ± 0.03 ^a	0.39 ± 0.02 ^a	0.40 ± 0.04 ^a	0.35 ± 0.04 ^a
Tyrosine (g/100 g)	0.15 ± 0.01 ^a	0.16 ± 0.01 ^a	0.16 ± 0.02 ^a	0.14 ± 0.02 ^a
Phenylalanine (g/100 g)	0.17 ± 0.02 ^a	0.18 ± 0.0 ^a	0.18 ± 0.02 ^a	0.16 ± 0.02 ^a
Histidine (g/100 g)	0.11 ± 0.01 ^a	0.12 ± 0.01 ^a	0.12 ± 0.01 ^a	0.11 ± 0.01 ^a
Lysine (g/100 g)	0.29 ± 0.02 ^a	0.31 ± 0.01 ^a	0.31 ± 0.03 ^a	0.28 ± 0.03 ^a
Arginine (g/100 g)	0.14 ± 0.02 ^a	0.15 ± 0.01 ^a	0.15 ± 0.01 ^a	0.14 ± 0.02 ^a
Proline (g/100 g)	0.42 ± 0.02 ^a	0.42 ± 0.02 ^a	0.43 ± 0.05 ^a	0.38 ± 0.05 ^a

^{a,b}Values within a column with different superscript letters indicate significant differences ($P < 0.05$).

¹Data are shown as the mean ± SEM.

²RCM = raw camel milk (untreated); LTLT = low temperature/long time (65°C for 30 min); HTST = 85°C for 15 s; UHT = 135°C for 5 s.

Figure 1. Taxonomic annotation of the gut microbiota at the phyla and family levels. RCM = raw camel milk (untreated); LTLT = low temperature/long time (65°C for 30 min); HTST = 85°C for 15 s; UHT = 135°C for 5 s.

mice, respectively. However, *Muribaculaceae* (52.37 and 43.56%), *Lachnospiraceae* (16.63 and 17.96%), and *Prevotellaceae* (8.31 and 7.27%) were the main communities in the gut of RCM and LTLT mice (Figure 1B). The relative abundances of bacteria from the families *Muribaculaceae* and *Prevotellaceae* were significantly lower in the RCM and LTLT samples, whereas those in the *Lactobacillaceae* and *Streptococcaceae* decreased significantly in UHT and HTST mice ($P < 0.05$). Hence, the abundance of certain phyla and families differed significantly (Figure 2).

At the genus level, 103 genera were detected in all mice gut microbiota, including *norank_f_Muribaculaceae*, *Lactobacillus*, *norank_f_Lachnospiraceae*, *Lactococcus*, and *Bacteroides*. The community heatmap and circus plot showed that the different heat-treated camel milks had altered abundances of specific bacterial taxa at the genus level (Figure 3). *Muribaculum*, *Butyrivibrio*, and *Papillibacter* were the main communities in the gut of the HTST group. *Alloprevotella*, *Muribaculum*, *Odonbacter*, and *Bifidobacterium* were enriched in the gut of the LTLT group, while *Lactobacillus*, *Lactococcus*, and *Candidatus_Arthromitus* were the key communities in the UHT group (Figure 4). These results indicated that the different heat treatments could inhibit certain bacteria in the mouse gut microbiota.

Diversity of the Gut Microbiota of Camel Milk Under Different Heat Treatments

We compared the α -diversity of the microbiota in all samples using the Chao, ACE, Shannon, and Simpson indices, and found that all 4 indices showed significant differences. For community richness, feeding mice

with HTST and UHT camel milk significantly lowered the Sobs (total number of species observed) and Ace indices compared with that of the LTLT group, suggesting that bacterial richness was reduced by high-temperature treatment, especially in the UHT group. However, LTLT treatment of camel milk had only slight and nonsignificant effects on microbial community richness. For community diversity, bacterial diversity was reduced in the HTST and UHT groups compared with the other groups (Figure 5).

The β -diversity in intestinal microbiomes between all 4 groups are shown in Figure 6. The principal coordinate analysis based on weighted, normalized Unifrac indicated that the gut microbiota had a different distribution of microbes among the groups, and that the bacterial communities of (1) the UHT and HTST samples, and (2) the RCM and LTLT samples were spatially separated. Similar results were found using nonmetric multidimensional scaling analysis. The distances between the RCM and LTLT group samples were shorter than the distance between the UHT and HTST groups, indicating that the RCM and LTLT groups were more similar to each other compared with the other groups. The sample distance heatmap and Bray-Curtis distance cluster analyses also showed differences and similarities between the different samples (Figure 7).

Effects of Heat Treatment on SCFA Production

The SCFA contents in mice were altered by different heat treatments (Table 2); contents of acetic acid, isobutyric acid, and butyric acid were significantly different among groups ($P < 0.05$). After supplementation of mice with different camel milks, the SCFA contents

Figure 2. Richness of particular families in the camel gut. RCM = raw camel milk (untreated); LTLT = low temperature/long time (65°C for 30 min); HTST = 85°C for 15 s; UHT = 135°C for 5 s.

were significantly increased in the HTST and UHT groups compared with those in the other groups. There were no significant differences between the HTST and UHT groups. Notably, the concentration of butyric acid in the HTST group was much higher than that in the other groups ($P < 0.05$). However, the HTST and LTLT groups showed no significant differences.

DISCUSSION

The main aim of heat treatment of milk is to ensure its microbiological safety. However, heat treatment causes changes in the nutritional and organoleptic properties of camel milk. High-temperature heat treatment (e.g., UHT treatment) can induce the formation

of lactulose, via isomerization, and of Maillard reaction compounds, formic acid, and lactic acid (Van Boekel, 1998; Law et al., 2010). In this study, we observed that lactose content of camel milk was remarkably lower in the UHT group than in the other groups. Heat treatment decreased the vitamin C content in camel milk, likely because vitamin C is heat degradable and may be affected by packaging and storage (MacDonald et al., 2011). Heating, especially UHT and HTST, also decreased the amount of protein, possibly because whey proteins are heat labile and easily undergo heat denaturation (Anema and Li, 2003). Extensive heat treatment also leads to whey proteins becoming associated with casein micelles by interactions with κ -casein (Anema and Li, 2003; Zhang et al., 2018). Therefore,

Figure 4. Plot from linear discriminant analysis effect size (LEfSe) analysis indicating enriched bacterial genera (*g__* = genus; *f__* = family). LDA score = linear discriminant analysis score; RCM = raw camel milk (untreated); LTLT = low temperature/long time (65°C for 30 min); HTST = 85°C for 15 s; UHT = 135°C for 5 s.

heat treatment can alter not only the physicochemical properties but also the nutritional functionality of milk (Barbé et al., 2013; Ye et al., 2016). For amino acid contents, similar to previous findings, heat resulted in 1 to 4% loss of lysine but had little effect on levels of

other amino acids (Claeys et al., 2013; Melini et al., 2017).

The characteristics of gut microbes depend on the host's genome, nutrition, and lifestyle (Nicholson et al., 2012). A balanced gut microbiota composition benefits

Figure 5. Comparison of the α -diversity (in operational taxonomic units, OTU) of gut microbiome among the 4 treatment groups using boxplots. Boxes span interquartile range; midlines indicate median; whiskers indicate minimum and maximum. RCM = raw camel milk (untreated); LTLT = low temperature/long time (65°C for 30 min); HTST = 85°C for 15 s; UHT = 135°C for 5 s. Sobs level = total number of species observed. * $P < 0.05$; ** $P < 0.01$.

the host, whereas abnormal changes in the gut microbial community are associated with many metabolic disorders. The microbiome is related to the host's diet and metabolism (Krumbeck et al., 2016; Vaiserman et al., 2017). In this study, we observed different effects of heat-treated camel milk on the gut microbiota of mice. The different heat treatments had significantly different effects on the mouse microbiome structure and composition. The α -diversity of the mouse microbiota is typically reduced in response to heat-treated camel milk (Shao and Wang, 2018; Wang et al., 2018), which

is consistent with the results of the present study. The gut microbiota of mice fed HTST- and UHT-treated milk clustered closer than that of the mice fed untreated milk and LTLT-treated milk. The loss of certain nutrients in milk treated at higher temperatures might have affected the function of the host microbiome.

Consistent with our findings, *Bacteroidetes* and *Firmicutes* have been reported as the most abundant phyla in the mouse microbiota (Shao and Wang, 2018; Wang et al., 2018). We found that the relative abundances of bacteria changed after mice ingested different

Figure 6. β -Diversity (in operational taxonomic units, OTU) among the 4 groups based on principal coordinate analysis (PCoA) and non-metric multidimensional scaling (NMDS). PC = principal component; RCM = raw camel milk (untreated); LTLT = low temperature/long time (65°C for 30 min); HTST = 85°C for 15 s; UHT = 135°C for 5 s.

heat-treated camel milks. Feeding UHT milk caused a dramatic change in the mouse gut microbiota by decreasing the population of *Firmicutes* and increasing that of *Bacteroidetes*. The *Firmicutes* proportion is higher in obese individuals, thus the *Firmicutes* are considered an obesity-related factor (Ley et al., 2006). Thus, high heat treatment of camel milk might reduce the risk of obesity by decreasing *Firmicutes* levels. At the family level, the *Muribaculaceae* were drastically decreased in the gut of mice receiving UHT and HTST camel milk compared with mice in the RCM and LTLT

groups. *Muribaculaceae* is a key bacterial marker that is abundant in the microbiota of healthy mice (Lagkouravos et al., 2019). Dietary changes negatively affect the relative abundance of *Muribaculaceae*. Moreover, treating camel milk with UHT and HTST can destroy some nutrients, which could induce gut microbiota changes with negative effects.

At the genus level, the abundance of *Bifidobacterium* was lower in the UHT group than in the LTLT group. This might have resulted from the unchanged content of lactose and protein in the LTLT group, which would be

Figure 7. Differences and similarities among 4 groups based on hierarchical clustering and distance on an operational taxonomic unit (OTU) level. RCM = raw camel milk (untreated); LTLT = low temperature/long time (65°C for 30 min); HTST = 85°C for 15 s; UHT = 135°C for 5 s.

Table 2. Changes in the concentrations ($\mu\text{mol/g}$) of short-chain fatty acids (SCFA)¹

SCFA	Heat treatment ²			
	RCM	LTLT	HTST	UHT
Acetic acid	8.74 $\pm$ 0.68 ^a	6.54 $\pm$ 1.02 ^a	27.96 $\pm$ 7.20 ^b	26.81 $\pm$ 9.85 ^b
Propionic acid	47.39 $\pm$ 28.22 ^a	27.99 $\pm$ 5.97 ^a	30.33 $\pm$ 19.97 ^a	31.52 $\pm$ 13.19 ^a
Isobutyric acid	0.25 $\pm$ 0.10 ^{ab}	0.21 $\pm$ 0.07 ^a	5.71 $\pm$ 1.74 ^c	3.94 $\pm$ 2.17 ^c
Butyric acid	0.22 $\pm$ 0.07 ^a	0.24 $\pm$ 0.09 ^a	5.82 $\pm$ 0.99 ^b	4.38 $\pm$ 1.11 ^a
Isovaleric acid	0.58 $\pm$ 0.33 ^a	0.38 $\pm$ 0.08 ^a	0.39 $\pm$ 0.24 ^a	0.26 $\pm$ 0.09 ^a
Pentanoic acid	0.24 $\pm$ 0.21 ^a	0.14 $\pm$ 0.02 ^a	0.29 $\pm$ 0.11 ^a	0.23 $\pm$ 0.08 ^a

^{a-c}Values within a row with different superscript letters indicate significant differences ($P < 0.05$).

¹Data are shown as the mean $\pm$ SEM.

²RCM = raw camel milk (untreated); LTLT = low temperature/long time (65°C for 30 min); HTST = 85°C for 15 s; UHT = 135°C for 5 s.

beneficial to the growth of *Bifidobacterium*. However, in the UHT group, *Lactobacillus*, a probiotic bacterium that influences host health (Delgado et al., 2020), was dominant. The relative abundance of *Lactobacillus* was reduced by UHT, in contrast to results of a previous study (Shao and Wang, 2018). Moreover, the lactic acid-producing *Lactococcus* was a key member of the community after UHT milk intake in this study. Additionally, these results led us to speculate that UHT treatment may not be suitable for camel milk (Felfoul et al., 2017). Previous studies showed that camel milk has natural antimicrobial activity because of the presence of lactoferrin, lysozyme, immunoglobulin, and partially digested or fermented peptides, which can inhibit bacteria in the gut (Beermann and Hartung, 2013; Ahamad et al., 2017; Mati et al., 2017). However, at 65°C, these antimicrobial compounds mostly retain their activity, whereas at 80°C, their activity decreases significantly (Felfoul et al., 2017). In this connection, we hypothesize that HTST and UHT heat treatment might reduce antimicrobial components in camel milk.

The present study demonstrated that feeding mice a UHT and HTST milk diet increased the fecal concentration of SCFAs, suggesting that the effect of UHT camel milk on the gut microbiota was to promote the growth of SCFA-producing bacteria. In the intestines, resident bacteria degrade nondigestible food components, including resistant proteins, resistant starches, oligosaccharides, and dietary fibers, and produce SCFA (Morita et al., 1998; Den Besten et al., 2013). Importantly, SCFA modulate host health by affecting glucose homeostasis, maintaining the balance of the epithelial barrier, and regulating energy metabolism (Maslowski et al., 2009; Liu et al., 2019; Tamura et al., 2019). However, recent studies have shown that butyrate is not universally beneficial for intestinal health (Singh et al., 2019; Vancamelbeke et al., 2019). It is possible that the degradation of lactose, protein, vitamin C, and some natural antimicrobial components in camel milk

changes functional features in the intestines (Shao and Wang, 2018). However, the mechanisms by which these changes in microbial structure and increased concentrations of SCFA, under UHT conditions, affect host health remain unclear.

CONCLUSIONS

We observed changes in the physicochemical properties of camel milk induced by different heat treatments and these changes were thought to be key factors in altered diversity in gut microbiota of mice receiving the different milks. The change in microbiota induced production of SCFA. Different heat treatments have different effects on the nutritional value of camel milk. In particular, treating camel milk with UHT can destroy some nutrients, which could induce gut microbiota changes with negative effects on the growth of gut probiotics. The LTLT treatment preserved some nutrients and did not induce changes in the diversity or composition of the gut microbiota community. Our results indicate the importance of selecting an appropriate heat treatment for camel milk that will preserve its functional advantages while ensuring its safety.

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