

Original Article

Microbiological safety and hygienic quality of camel meat at abattoir and retail houses in Jigjiga city, Ethiopia

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Abstract

Introduction: Camel meat is a relatively new, emerging meat type that may serve as sources of foodborne pathogens to the consumer. Methodology: A cross-sectional study was conducted to determine the microbiological safety and quality of camel meat from an abattoir and retail houses in Jigjiga city, Ethiopia. A total of 140 camel carcass and retail meat samples (70 each) were examined for the presence and load

retail houses in Jigjiga city, Ethiopia. A total of 140 camel carcass and retail meat samples (70 each) were examined for the presence and load of *Staphylococcus aureus*, *Escherichia coli* O157: H7, *Listeria monocytogenes*, *Campylobacter* spp., aerobic bacteria, fecal coliforms (FCs), and yeast and molds (Y&Ms). Presumptive isolates were confirmed using biochemical tests.

Results: *S. aureus* and *E. coli* O157: H7 populations varied widely between carcasses at the abattoir and retail meat samples. *S. aureus* and *E. coli* O157:H7 were detected in 12.1 and 4.3% of the samples, respectively. *E. coli* O157:H7 counts were significantly higher in retail meat (4.21 ± 0.02) compared to the carcasses (3.99 ± 0.00) at the abattoir (P < 0.05). Out of 140 samples analyzed, 5% were positive for *Campylobacter* spp. The mean fecal coliforms, and yeast and molds counts were significantly higher in retail meat samples $(6.17 \pm 0.067 \text{ and } 4.95 \pm 0.067 \log 10 \text{ cfug}^{-1}$, respectively). *L. monocytogenes* (11 cfug⁻¹) were detected below the permissible limit (100 cfug⁻¹).

Conclusions: This study indicated that the further the process progress, the greater the risk of contamination to the product. Therefore, good hygienic practices at the abattoir and retail houses and strict slaughtering process should be prompted to enhance the overall safety and quality of camel meat.

Key words: Camel carcass; hygienic quality; Jigjiga; meat; microbial safety.

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Introduction

Meat, an excellent source of protein in the human diet, is highly susceptible to microbial contaminations that can cause food spoilage and foodborne infections to the consumer [1,2]. Camel meat is a relatively new, emerging meat type that is gaining increasing popularity in the international meat markets [3]. It contributes significantly to the food security of the Ethiopian nomadic pastoral households including the Afar, Somali and Borena [4]. From the nutritional point of view, camel meat is considered healthier with lesser overall fat content and richer in polyunsaturated fatty acids compared to beef [3]. However, any sector that promotes camel meat production and consumption need to ascertain its public health safety. In Ethiopia, studies were carried out on the microbiological quality and

public health safety of beef, mutton and goats' meat [5-7]. However, information on microbiological safety of camel meat destined for human consumption are scarce.

In Ethiopian Somali region, camels are slaughtered in the open air, on bare ground, without any roof and wall to provide protection from dust and the sun. Hence, there is a high possibility of microbial contamination of carcasses and meat during processing. To this end, it is important to elucidate the state of contamination of meat with pathogens of public health importance such as *Staphylococcus aureus*, *Escherichia coli* O157:H7, *Listeria monocytogenes*, and *Campylobacter* spp. It is also equally crucial to address the hygienic status of the meat production and distribution in the region as such information will be beneficial in designing preventive strategies and as baseline data for related researches.

With the above motives, the present study was undertaken to assess microbiological safety/quality of camel carcasses and meat at the municipal abattoir and retail houses, respectively in Jigjiga city, Ethiopian Somali Regional State, eastern Ethiopia.

Methodology

Microbiological Sample Collection and Preparation

A total of 140 samples (70 carcass samples from one abattoir and 70 meat samples from four different retail houses) were analyzed. Each sample contained 200g of pooled meat. Each pooled carcass sample was collected from distinct parts of an individual slaughtered camel. Similarly, from retail houses, meat cuts were collected from different camel meat types and were pooled. The municipal abattoir and each retail house were visited two times per week for nine consecutive weeks. In each visit, a total of eight samples; four carcass samples from the abattoir and four meat samples one sample from each retail house were taken. During each sampling, samples were obtained from all the retail houses and the abattoir. All samples were collected under aseptic conditions using individual sterile surgical blades and containers.

Microbiological Safety and Quality Assessment

The microbiological safety and hygiene quality were assessed using the methods recommended by the International Commission on Microbiological Specifications for Foods (ICMSF) [8]. All the samples were analyzed for the presence and loads of *S. aureus*, *E. coli* O157:H7, *L. monocytogenes*, *Campylobacter* spp., aerobic bacteria, fecal coliforms, and yeast and molds (Y&Ms).

A 25g of meat sample was aseptically minced and stomached using Stomacher-400 (Seward, Norfolk, UK) for 2 min at 230 rpm in 225 mL of 0.1% sterile peptone water (BPW) (Oxoid, CM0509, Basingstoke, Hampshire, UK) [9]. Subsequently, 10-fold serial dilutions ranging up to 10⁻⁶ were prepared by adding 1 mL of sample in 9 mL 0.1% peptone water. An appropriate portion of dilution (0.1 mL of the homogenates) from 10⁻⁴ to 10⁻⁶ were transferred to specific culture media agar plates.

Detection and Enumeration of S. aureus

An appropriate portion of dilution (0.1 mL of the homogenate) were transferred to Baird Parker agar (BPA) plates (Oxoid, CM0275, Basingstoke, Hampshire, UK) and distributed over the surface using sterile, bent glass rods. The inoculums were incubated at 37°C for 48 hours. Plates having 30-300 colonies

were examined and typical *S. aureus* colonies were counted using Stuart SC6PLUS colony counter (Bibby scientific Limited, Staffordshire, UK). *S. aureus* produce black, shiny, convex colonies with entire margins and clear zones, with or without an opaque zone [10]. Biochemical tests including gram stain, coagulase, catalase and DNase tests were used for confirmation.

Detection and Enumeration of E. coli O157: H7

An appropriate portion of dilution (0.1 mL) was transferred onto Sorbitol-MacConkey agar (SMA) (Oxoid, CM0813, SR0172, Basingstoke, Hampshire, UK) and incubated at 35 °C for 20 to 22 hours. Presumptive *E. coli* O157:H7 colonies were counted using colony counter. *E. coli* O157:H7 does not ferment sorbitol and produces colorless, smooth, circular, entire edge colonies with brown center. In contrast, most other *E. coli* strains ferment sorbitol and form pink colonies [11]. Biochemical tests such as indole production, latex agglutination, and methyl red and citrate tests were used for confirmation.

Detection and Enumeration of L. Monocytogenes

For the detection and enumeration of *L. monocytogenes*, 0.1 mL of the dilution was spread onto *Listeria* selective agar (LSA) (Oxford, CM0856, SR0140, Basingstoke, Hampshire, UK). After incubation for 48 hours at 37 °C, presumptive *L. monocytogenes* colonies were counted. *L. monocytogenes* produce special brown color colony with black zone due to the formation of phenolic compounds derived from the aglucon [12]. For confirmation, gram stain and CAMP tests were conducted.

Test for Campylobacter species

One gram of each of the collected samples was suspended in 9 mL of Bolton selective enrichment broth (Oxoid, CM0983, SR0183, Basingstoke, Hampshire, UK) and incubated at 37°C for 4 hours, followed by further incubation at 41.5°C for 44 hours. Subsequently, the sample was sub-cultured to Campylobacter selective agar (CCDA; Oxoid, CM739, SR0155, Basingstoke, Hampshire, UK) at 41.5°C for 48 hours. A typical Campylobacter colony on CCD-agar has a gray, moistening and effuse appearance. Campylobacter jejuni has a green or gray appearance that can be very dry. At the same time, the appearance can be with or without a metallic sheen. A creamy grey, moistening and raised colony is a typical Campylobacter coli [13]. For confirmation, oxidase and

Table 1. Bacterial species detected from camel carcass and meat sampled from Jigjiga municipal abattoir and retail houses.

		Bacterial species detected						
Cample	No of	of C	E!: 0157117	L. monocytogens —	Camplyobacter spp.			
Sample	sample	S. aureus	E. coli O157H7		C. coli	C. jejuni	Total	
		No (%)	N <u>o</u> (%)	No (%)	No (%)	N <u>o</u> (%)	No (%)	
Carcass	70	6 (8.57)	2 (2.86)	0 (0)	1 (1.43)	3 (4.29)	4 (5.71)	
Meat	70	11 (15.71)	4 (5.71)	1 (1.43)	2 (2.86)	1 (1.43)	3 (4.29)	
Total	140	17 (12.14)	6 (4.28)	1 (0.71)	3 (4.29)	4 (2.89)	7 (5.00)	

microaerophilic growth tests were used. *Campylobacter* shows positive oxidase reaction. For microaerophilic growth test, suspected colonies were sub-cultured from *Campylobacter* Selective Agar into two Colombia blood agar plates. One of the plates was incubated in microaerophilic condition and the other aerobically at $41.5 \pm 1^{\circ}\text{C}$ for 22 ± 1 hour. Growth in microaerophilically incubated plates and no growth in aerobic conditions, in line with other tests confirm the result [14].

Aerobic Plate Count (APC)

For aerobic bacteria count, 0.1 mL of homogenate was plated onto the surface of plate count agar (Oxoid, CM0325, Basingstoke, Hampshire, UK). Plates were incubated at 35°C for 48 hours and plates containing between 30 and 300 colonies were counted [9].

Fecal Coliforms Count (FCC)

Fecal coliforms were enumerated using violet red bile (lactose) agar (VRBL) (Oxoid, CM0107, Basingstoke, Hampshire, UK); 0.1 mL of the homogenate were spread onto agar plates and incubated at 44 ± 1 °C for 24 hours, typical and atypical colonies were enumerated [15].

Yeast and Mold Count (Y&MC)

Enumeration of yeasts and molds was done using potato dextrose agar (PDA) (Oxoid, CM0139, Basingstoke, Hampshire, UK). The inoculums (0.1 mL of the homogenate) were spread on PDA and incubated for 2-7 days at 30-32°C. Yeast grows as creamy to white colonies whereas molds have filamentous colonies of diverse colors. The numbers of colonies were counted, and the dilution factors were considered

to determine the yeast and/or mold counts per gram of meat [16].

Statistical Analysis

The results of microbial counts (CFU/cm²) were converted into log10 and descriptive statistics were used to calculate mean, standard error, minimum and maximum values considering the type of sample and origin. Percentages were calculated to express the frequency of contamination. Microbial counts were compared by ANOVA. P-value < 0.05 was considered statistically significant with 95% level of confidence. All data were analyzed using SPSS (Statistical Package for Social Science) software version 20.

Results

Bacterial Profile and Load of Camel Carcass and Meat from Abattoir and Retail Houses

Pathogenic bacteria detected from camel carcass and meat sampled from the municipal abattoir and retail houses are summarized in Table 1. In the present study, 12.14% of the samples revealed typical colonies of S. aureus on BPA. S. aureus positive samples were higher in retail houses compared to the abattoir. However, there was no statistically significant difference (P > 0.05) in mean counts between the abattoir and retail house samples (Table 2). E. coli O157:H7 was detected in 4.28% of samples and the mean count was statistically higher in retail houses (P < 0.05). The overall occurrence of L. monocytogenes was low and detected only from a retail house in a single sample. Out of 140 analyzed samples, 5 % were positive for Campylobacter spp. Based on the results obtained, both, abattoir and retail house samples were Campylobacter-positive. The most common

Table 2. Pathogenic bacteria load of camel carcass and meat from Jigjiga abattoir and retail houses.

		Bacterial colonies log10 cfug-1						
Sample	No of sample	S. aureus			E. coli O157H7			
		Mean	Min	Max	Mean	Min	Max	
Carcass	70	6.19 ± 0.10	5.85	6.46	$5.99\pm0.00_a$	5.99	5.99	
Meat	70	6.33 ± 0.04	6.13	6.47	$6.21\pm0.02_a$	6.19	6.23	

a = the means indicated with the same letter are significantly different at the P value < 0.05.

Table 3. Indicator organisms detected from camel carcass and meat sampled from Jigjiga municipal abattoir and retail houses over the three-month period.

		Organisms detected					
Sample	No of sample	FCs	AB	Y&Ms			
	_	No (%)	No (%)	No (%)			
Carcass	70	13 (18.57)	12 (17.14)	4 (5.71)			
Meat	70	19 (27.14)	12 (17.14)	6 (8.57)			
Total	140	32 (22.86)	24 (17.14)	10 (7.14)			

FCs: fecal coliforms, AB: aerobic bacteria, Y&Ms: yeast and molds.

Campylobacter spp. isolated from meat samples was C. *jejuni* followed by C. coli (Table 1).

Hygienic Quality of Camel Carcass and Meat from Abattoirs and Retail Houses

Aerobic bacteria were detected in 17.14% of the samples (Table 3). There was no significant difference (P > 0.05) in mean APCs between samples from the abattoir and retail houses (Table 4). Fecal coliforms were detected and enumerated irrespective of pathogenicity of the strain to estimate the level of hygiene. Out of 140 samples, fecal coliforms were detected in 22.86% of the samples. Though not statistically significant, more samples from retail houses tested positive for FCs than the abattoir samples. The detection rates of Y&Ms obtained from retail house samples were also higher than samples from the abattoir (Table 3). In addition, a significant difference (P < 0.05) in the mean count of Y&MCs between camel carcass from the abattoir and retail houses meat were observed (Table 4).

Discussion

Detection of *S. aureus* from camel meat indicates the poor sanitary quality of the abattoir and retail houses. *S. aureus* positive samples were higher from retail house samples compared to the abattoir (15.71% vs 8.57%). Similar findings were reported by previous studies. A higher level of *S. aureus* contamination of poultry and beef 'Kitfo' from retail markets has been reported by Voidarou *et al.* and Tassew *et al.* respectively [17,18]. The mean *S. aureus* count detected in this study was greater than the study conducted in Addis Ababa (1.1×105 cfug⁻¹) [19] and Mekele city (2.33×104 cfug⁻¹) abattoirs [20]. This could be

attributed to the availability of hot water, detergents, adequate uniforms and regulations governing hygienic practices of meat handlers at all levels in Addis Ababa and Mekelle abattoirs. According to Kadariya *et al.* total *S. aureus* counts above 5 log cfug⁻¹ in food results in the production of toxins to elicit food poisoning [21]. In this study, *S. aureus* counts were moderately elevated than 5 log cfug⁻¹. Therefore, detection at such concentrations shows that camel carcass and meat could be potential sources for staphylococcal food poisoning in the study area.

In the previous studies, the low detection rate of E. coli O157:H7 than the current finding (4.28%) were noted from beef carcasses i.e. 2/370 (0.54%) [22]. Nevertheless, there are also evidences showing an increasing trend of E. coli O157:H7 in meat production systems in Ethiopia [23,24]. In recent studies, the detection of higher proportions of E. coli O157:H7 most probably is associated with the wider use of sensitive detection methods [25]. Considering the very low infective dose (10-100 cfug⁻¹) of this pathogen, detecting at such concentrations poses significant public health risks [26]. It is assumed that most retail camel meats will be adequately cooked before consumption, leading to the destruction of the pathogen. However, the presence of contaminated meats at retail and consumer levels places consumers at risk of acquiring E. coli O157:H7 due to the possible persistence of the pathogen in undercooked meat products [11,25,27]. This finding shows the importance of camel meat as potential sources of E. coli O157:H7 for human infection.

The microbial load of L. monocytogenes detected in camel meat samples was calculated using the data obtained from the culture method. One sample that

Table 4. Microbial loads of indicator organisms on camel carcass and meat.

Sample	No of sample	Bacterial colonies								
		FCCs			APCs			Y&MCs		
		Mean	Min	Max	Mean	Min	Max	Mean	Min	Max
Carcass	70	5.73 ± 0.07 a	5.54	6.00	6.06 ± 0.09	5.78	6.47	$4.64 \pm 0.07 \textbf{b}$	4.53	4.77
Meat	70	$6.17 \pm 0.07\mathbf{a}$	5.89	6.47	6.06 ± 0.09	5.79	6.46	$4.95 \pm 0.07 \textbf{b}$	4.69	5.05

FCCs: fecal coliform counts, APCs: aerobic plate counts, Y&MCs: yeast and mold counts; a,b = the means indicated with the same letter are significantly different.

turned out positive for *L. monocytogenes*, the estimated count was 11 cfug⁻¹. According to the European Commission Regulation (EC) No 2073/2005 on microbiological criteria for foodstuffs, the acceptable level of *L. monocytogenes* in ready to eat food is less than 100cfug⁻¹. In the current study, the relatively low concentration of *L. monocytogenes* in camel meat was detected. Nonetheless, when exposed to temperature abuse and given enough time, *L. monocytogenes* is able to multiply exponentially to a level where high-risk groups are particularly threatened upon consumption of the undercooked camel meat [28].

The occurrence of *Campylobacter* spp. may be due to cross-contamination during manual skinning, evisceration, and processing in the slaughterhouse or insufficient hygiene during processing in the retail houses. Campylobacter present in the intestinal tract of animals represents a potential risk for the contamination of carcasses depending on shedding patterns and hygienic slaughtering practices [29]. The most common Campylobacter spp. isolated from meat samples was C. *jejuni* (57.14%), the remaining (42.86%) isolates were C. coli. The results are comparable with those reported from beef carcasses in Ethiopia [30] and lower than the report from Tanzania [31]. However, the present detection rates were higher than the reports from Australia [32]. To our knowledge, this is the first report on the detection of Campylobacter from camel meat in Ethiopia.

APC is a measure of the microbial quality of the meat. Presence of microbes in high numbers (APC > 5log cfug⁻¹) is a fast pathway to the spoilage of the meat. According to the International Standard Organization (ISO 4833), APC of 80% of analyzed samples must not exceed 5 log cfug⁻¹, whereas 20% of the samples may have counts of up to 5 log cfug⁻¹ [33]. In this study, 17.14% of samples had APCs more than 5 log cfug⁻¹. The level of aerobic plate count in this study was comparable to previous studies [27,34,35]. The microbial contamination level of abattoirs and retail house meat were higher and do not conform to EU specifications [36]. There was no significant difference (P > 0.05) in mean APCs between samples from abattoirs $(6.06 \pm 0.092 \log 10 \text{ cfug}^{-1})$ and retail houses $(6.06 \pm 0.091 \log 10 \text{ cfug}^{-1})$ (Table 4). In another study, however, a significantly higher level of contamination in the meat shops as compared to the abattoir was reported [37]. The higher aerobic plate count enumerated from meat $(6.06 \pm 0.092 \log 10 \text{ cfug}^{-1})$, indicates the elevated level of contamination and/or growth of aerobic bacteria on camel meat in retail houses.

Fecal coliforms (FCs) count was significantly higher (P < 0.05) in meat samples from retail houses $(6.17 \pm 0.067 \log 10 \text{ cfug}^{-1})$ compared to carcass samples from the abattoir $(5.73 \pm 0.066 \log 10 \text{ cfug-1})$. This finding agrees with previous findings of Karama et al. who reported FCCs from butchers (4.57 log10 cfug⁻¹) and abattoir (4.32 log10 cfug⁻¹) [37]. The numbers of fecal coliforms enumerated from camel meat $(6.17 \pm 0.070 \log 10 \text{ cfug}^{-1})$ were higher than established limits (10-100 cfug⁻¹) that are assumed to be an indicator of fecal contamination [34]. The results of FCCs in the current study were of practical significance as camel carcasses could be contaminated at different processing points during the slaughter process. The high detection rate of FCs is an indication of contamination at the abattoir from intestinal contents and unhygienic meat handling in retail houses. In the present study, all Y&M positive sample (7.14%) were found above the permissible level which is more than 3 log cfug⁻¹, hence, unacceptable from the quality point of views.

Conclusion

This study provides valuable information on microbiological safety/quality of camel carcass and meat at the abattoir and retail houses in the study area. Furthermore, it can be used as a baseline for additional studies and to develop practical guidelines. To our knowledge, the current study is the first report on the occurrence of L. monocytogenes, Campylobacter spp., and E. coli O157:H7 on camel carcasses and/or retail camel meats in Ethiopia. The overall loads of the pathogenic and indicator bacteria in raw camel meat were high which can be attributed to unhygienic conditions at the abattoir and retail houses. In addition, higher levels of contamination were observed for retail house samples as compared to abattoir samples indicating further contaminations during transportation and handling at retail houses. Therefore, camel meat could be a significant source of food-borne pathogens to the consumer unless good hygienic practices and slaughtering process are implemented in the abattoir. It is also suggested that municipal authorities should monitor and regulate the hygienic practices of camel meat retail markets to safeguard the consumer and reduce the public health risk to the minimum.

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