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DETERMINATION OF MILK COMPOSITION, BACTERIOLOGY AND SELECTED BLOOD PARAMETERS OF DAIRY GOATS UNDER DIFFERENT FEEDING SYSTEMS

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ABSTRACT

This research was carried out at two farms located in the Karacabey region of Turkey: an extensive goat farm (A) and a semi-intensive goat farm (B). A total of 32 Saanen goats (3 years old) at an early stage of their second lactation were selected from Farm A and Farm B. The total DM intake (TDM) values were 1.89 and 1.86 (kg d^{-1}) for goats housed on the A and B farms, respectively. Compared with Farm A, Farm B produced more milk each day ($P<0.05$; 1.38 -. 1.76 kg day^{-1}). The milk samples taken from Farm A had a higher ($P<0.05$) milk fat content than the samples from Farm B (milk fat=4.40 and 1.89 %, respectively). The serum creatinine values were significantly higher ($P<0.05$) in the blood of goats from farm A compared with farm B (1.11 and 0.56 mg dl-1, respectively). Comparison of glucose levels from both farms showed a significantly higher level of glucose in the blood samples from goats at Farm B ($P<0.05$; 24.23 and 61.43 mg dl^{-1}). Serum parameters for cholesterol, GGT and urea were not affected by the feeding system ($P > 0.05$).

Keywords: Extensive or semi-intensive, Goat, Dry matter intake, Milk composition, Bacteriology, Blood.

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Contribution/ Originality

This study is one of very few studies which have investigated the milk composition, bacteriology and selected blood parameters of dairy goats under different feeding systems.

1. INTRODUCTION

The efficiency of goat production depends on the type of feeding system and the availability of nutrients for high productivity. Feeding systems are divided into the following categories: extensive systems, semi-intensive systems and very intensive systems [1]. In the extensive system, goat flocks are kept at or close to the village or farm year-round. During the day they are grazed either on the common village range or on privately-owned or hired grazing areas. The extensive system is common in village farms within Turkey. Village flocks managed under this system may consist of 200–300 goats. Some farms feed straw or hay to their goats during winter, and several of the flock owners feed their goats approximately 100 to 200 g of barley daily per head toward the end of pregnancy and during early lactation [2]. However, the productivity of goats under this traditional production system is very

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low [3]. Previous studies have reported that semi-intensive feeding improved milk yield in dairy ewes, goats and Anatolian water buffaloes [4-8]. Grazing animals in an extensive rearing system can cause a nutritional imbalance during the summertime. These animals may show decreased milk production [4]. The aim of the present work was to study the effects of different forms of management on feeding, milk quality and selected blood parameters at existing goat farms.

2. MATERIALS AND METHODS

This research was carried out at two farms located in the Karacabey region of Turkey: an extensive goat farm (A) and a semi-intensive goat farm (B). A total of 16 three-year-old Saanen goats at 30-35 days of their second lactation were selected from Farm A. During March, the goats had access to the natural pasture ad libitum and were provided with 2.0 kg of oat hay and salt blocks for licking. An equivalent number of Saanen goats (3 years old; stage of second lactation, 30-38 days) were selected from Farm B. On Farm B, goats received *ad libitum* pasture as well as corn silage (1.5 kg d^{-1}), alfalfa hay (1000 g), 0.40 kg of barley hay, 0.20 kg of a concentrate feed mixture (CFM, 180 g CP kg DM^{-1}) and 2600 ME (Kcal kg DM^{-1}). The individual consumption of roughage was not determined because a group feeding protocol was used in this study. The dry matter, organic matter, crude protein, crude fat and ash content of the diets were analyzed according to AOAC [9]. Neutral detergent fiber (NDF) and acid detergent fiber (ADF) values were determined using the methods outlined by Robertson and Vansoest [10]. The metabolizable energy (ME) content was also estimated [11]. The animals were milked once a day with a milking machine at both the A and B farms. The milk production of each goat was measured daily. Raw milk samples were collected monthly. Each sample was taken aseptically directly from the udder of individual goats after discarding the foremilk and was stored at 4 °C and analyzed within 2 hours.

The somatic cell count (SCC) was determined with a Somacount 150 (Bentley Instruments, Chaska, MN, USA). The total bacterial count was measured as the number of bacteria in a sample that were able to grow and form countable colonies on Standard Methods Agar after being held at 32°C (90°F) for 48 hours [12]. The non-fat solids (SNF), fat, protein and lactose contents of milk were analyzed using a Milkoscan FT-120. For bacteriological analysis, the initial milk samples were incubated at 37°C for 24 hours on thioglycolate agar and then cultured on blood agar (BBL; 297876) and EMB agar (eosin-methylene blue-lactose-saccharose) (BBL; 221355). The samples were then incubated again for 24 hours at 37°C. Colonies were identified based on colony morphology and Gram staining. To identify the bacteria, direct cultures were performed using BBL Crystal Gram-positive and Gram-negative ID system kits and the associated database (Becton-Dickinson, Sparks, USA). All milk samples were inoculated with tenfold serial dilution in modified Hayflick broth (Oxoid, UK). Following serial dilution of milk samples in the broth medium, several drops were spread on Hayflick Mycoplasma agar (Oxoid, UK) and incubated at 37 ^{0}C under a 5-10 % CO_2 atmosphere (Oxoid CO_2Gen, UK) for 3-7 days [13]. Plates were examined daily for pH change and opalescence, and the agar media were examined under a stereo microscope (Olympus SZ2-ILST Zoom Stereo Microscope, Japan) for typical 'fried-egg' colonies. If bacterial contamination was detected, milk was sterilized by filtering with a 0.45 µm Minisart filter (Sartorius AG, Goettingen, Germany) [13]. If mycoplasma growth was not observed on solid media or broth, the subculture interval was extended to 7 days. If there was no growth after this period, the result was considered negative [14]. Blood samples were drawn from the jugular vein of 6 goats from each farm at 2 h post-feeding. The samples were centrifuged to obtain serum (2800 rpm × 10 min) after resting for 10 min to allow coagulation. The glucose, total cholesterol, urea, GGT and creatinine (CRE) of the blood serum were analyzed using a Reflotron at the Central Laboratory of the Faculty of Veterinary, Uludag University. Hemogram values were counted manually.

An analysis of variance was conducted using the SPSS version 15.0 statistical package SPSS [15] and means were compared using the t-test models described by Cochran and Cox [16]:

$Yijkl = \mu + Ti + Pj + Eijk$, where $Yijkl$=observation, μ = population mean, Ti = farming (extensive and semi-intensive), Pj = animals (j = 1, 2, 3…31 or 32) and $Eijk$ = residual error.

3. RESULTS AND DISCUSSION

The chemical composition of the diets, oat hay, alfalfa hay, corn silage and barley hay are presented in Table 1. Average total dry matter intake (TDM) was 1.89 and 1.86 kg day^{-1} at A and B Farms, respectively (Table 2). Farm A fed lactating goats 1.89 kg DM of oat straw (per head per day). The goats also had access to the natural pasture ad libitum. Farm B fed lactating goats 0.47 kg DM of maize silage, 0.94 kg DM of alfa hay, 0.26 kg DM of barley straw and 0.18 kg DM of CFM (per head per day). The TDM of Farm A was similar to that of farm B. However, goats fed the semi-intensive diet had a richer nutrient intake than goats fed the extensive diet. The average milk yield of goats was higher for Farm B than for Farm A (21.59 %; $P<0.05$) (Table 2). The difference in mean milk production between farm A and farm B was significant ($P<0.05$). This reduced milk production on farm A was probably associated with limited body reserves and a reduction in energy intake associated with the consumption of straw [4, 7]. These results are consistent with previous reports [3, 17] which stated that goats under a traditional production system had very low milk yield; however, the mean milk yield for Farm B was 1.76 kg d^{-1} (Table 2). This value is significantly lower than the 2.5 kg d^{-1} reported by Pridolova, et al. [17] similarly; Degirmencıoglu [18] reported that the mean daily milk yield was approximately 2.1 kg d^{-1} at a semi-intensive goat farm. Cabbidu, et al. [19] reported that the level of energy was important for milk production of goats. The observed response of milk yield may be due to a lower total intake of ME (CFM rate of 0.5 - 0.2 kg milk^{-1}). Milk fat content was lower on Farm B compared with the milk fat content at the extensive farm (milk fat=4.40 and 1.89 %, respectively). In the present study, the 2.51 % reduction in milk fat at farm B ($P<0.05$) was probably due to either greater milk production or lower forage intake [8]. In addition, Sales-Duval, et al. [20] reported that fat content was lower when the proportion of natural pasture in feeding systems was lower. Bacterial differences were observed among raw milk samples from the 2 farms. *Bacillus cereus* was the most common isolate (47.8 %) in goat milk from the semi-extensive (B) farm, whereas *Staphylococcus haemolyticus* was the most common isolate (25 %) in goat milk from the extensive (A) farm (Table 3). Total bacteria (TB) was 4.587 ± 1.604 (A) and 1.093 ± 0.401 (B) ($P<0.05$) (Table 3). However, the total milk somatic cell counts (SCC) were similar for both groups (362 ± 61.036 (A) and 304 ± 71.914 (B)). *Mycoplasma* and *Brucella spp.* we're not detected at either farm. Bagnicka, et al. [21] isolated minor pathogens, such as coagulase negative *Staphylococci, alpha haemolytic Streptococci, Enterococcus spp., Corynebacterium spp.* (25.3 %), and major pathogens, such as *Streptococcus agalactia, Staphylococcus intermedius, S. aureus* (9.8 %), in goat milk samples. In most samples, the presence of bacterial pathogens in goat milk led to an increase in the total SCC ($1x10^6$/ml of SCC). However, Kyozaire, et al. [22] compared the microbiological quality of milk produced under 3 different types of dairy goat production systems (intensive, semi-intensive and extensive); the lowest contamination rates were found among goats under the extensive system (13.3 %) compared with infection rates of 43.3 % and 36.7 % under the intensive and semi-intensive productions systems, respectively. *Staphylococcus intermedius, Staphylococcus epidermidis*, and *Staphylococcus simulans* were the most common bacteria (85.7 %) in milk samples, but there was no significant relation between the SCC and the presence of bacterial contamination in goat milk. Foschino, et al. [23] detected *coliforms* as a constant component of the microflora from goat milk samples. The overall mean SCC was 9.9 x 10^5 cells/ml with 47 % of samples having counts greater than 1 x 10^6 cells/ml. According to Foschino, et al. [23] SCC did not show a positive correlation with any microbial group. In addition, Pertinez, et al. [24] observed no correlation between the number of bacteria and SCC. The ability of SCC to predict intramammary infection in goat milk is lower than in cow's milk. In our study, we found no relation between total bacteria counts or bacterial composition and SCC. Instead, milking hygiene was the primary factor affecting the bacterial composition of raw goat milk. Bacteria were found in a high percentage of isolates, and their incidence was probably related to unsanitary farming practices. Based on the results in Table 2, we can say that serum values of goats from farm B

were superior to those from farm A. The serum creatinine values were significantly higher ($P<0.05$) at farm A than at farm B (1.11 and 0.56 mg dl^{-1}, respectively). This could be due to increased degradation of phosphocreatine in muscle tissues due to a lack of available energy sources to meet the vital functions of animals during feed restriction [25]. In the current study, serum glucose (mg dl-^{1}) was significantly reduced under the extensive feeding system ($P<0.05$; 24.23 - 61.43 mg dl^{-1}) (Table 2). The reduction in glucose was 37.2 % at the farm A compared with the farm B. Imasuen [26] reported that serum glucose values of African dwarf goats were lower for extensive and semi-intensive systems (47.75 and 51.66 mg dl^{-1}, respectively) and higher (61.16 mg dl^{-1}) for the intensive system. The glucose level for the extensive system studied here was observed to be lower than the value reported by Imasuen [26]. The observed decrease in glucose levels correlates with the increase in maintenance energy requirements due to grazing in a mountainous region and having low energy of acetic acid in the rumen because of roughage (acetic acid, CH_3-COOH - propionic acid, C_2H_5-COOH) [27]. The serum glucose values of goats from farm B were increased by semi-intensive feeding ($P<0.05$; 61.43 - 24.23 mg dl^{-1}) (Table 2). This result is consistent with research suggesting that high energy diets in dairy goats increase serum glucose [26, 28]. The semi-intensive feeding system had no significant effect on serum cholesterol, GGT or urea.

4. CONCLUSION

Dairy goat farms located in mountainous and hilly areas of the Karacabey district of Bursa City showed a reduction in milk yield, not only for economic reasons, but also because of the structure of the region, which results in the extensive feeding system used for goats. However, at goat farms that used semi-intensive feeding, there was a positive effect on milk yield. Goat milk production has currently been increasing in some areas in Turkey. The best ice-cream and butter products in our country are made with goat milk. Therefore, the quality of goat raw milk is important for the quality of final products. The bacterial status of milk is more likely related to maintenance of sanitary conditions and preventive measures rather than the feeding system of the farms. Improvement of sanitary conditions during milking is the principal control point for bacteriological hazards.

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Table-1. Chemical composition of diets and roughages DM (g kg^{-1})

Nutrient composition	Extensive farm A	Semi-intensive farm B			
	Oat hay	Corn Silage	Alfalfa hay	Barley hay	Diet
DM	945.0	316.6	942.5	668.6	880.0
OM	894.1	263.0	857.6	599.7	790.0
CP	27.9	69.4	128.0	35.3	180.0
EE	5.7	25.9	10.3	7.6	44.0
CELL	306.5	226.3	328.0	365.2	112.0
CA	50.9	53.6	84.9	68.9	90.0
Nitrogen free ext	554.0	-	391.3	191.6	454.0
Starch	16.3	275.1	19.5	10.8	-
NDF	757.7	484.4	511.4	759.7	-
ADF	607.4	363.3	450.8	612.9	-
ADL	64.0	45.2	124.2	75.0	-
ME (Kcal kg DM^{-1})[3]	1710	731.34	1837.87	1183.42	2600

DM, dry matter; OM, organic matter; CP, crude protein; EE, ether extract; Cell, cellulose; CA, crude ash; NDF, neutral detergent fiber; ADF, acid detergent fiber; [3] obtained by calculation [11].

Table-2. DM intake, milk yield and composition and blood metabolites from two different goat farms (mean±SE).

Item	N	A	N	B	
		$\overline{X} \pm S_{\overline{X}}$		$\overline{X} \pm S_{\overline{X}}$	P-value
Body-weight	16	43.219±0.860	16	45.192±1.313	NS
Silage DM intake (kg d^{-1})	-	--	-	0.47	
Alfalfa DM intake (kg d^{-1})	-	-	-	0.94	
Barley straw DM intake	-	-	-	0.26	
Oat straw DM intake	-	1.89	-	-	
Concentrate DM intake	-	-	-	0.18	
Total DM intake[1]		1.89		1.86	
Milk yield (kg d^{-1})	16	1.38±0.08	16	1.76±0.07	*
Fat (%)	16	4.40± 0.28	16	1.89± 0.19	*
SNF (%)	16	9.12±0.07	16	8.92±0.13	NS
Protein (%)	16	3.64±0.05	16	3.39±0.13	NS
Lactose (%)	16	4.65±0.04	16	4.74±0.02	NS
SCC(x log10 mL^{-1})	16	362±61.03	16	304±71.91	NS
TB (x log10 cfu mL^{-1})	16	4.58±1.60	16	1.09±0.40	*
Blood parameters					
CRE (mg dl^{-1})	6	1.11±0.07	6	0.56±0.17	*
Cholesterol (mg dl^{-1})	6	111.33±7.85	6	101.83±3.24	NS
GGT (U L^{-1})	6	37.95±0.49	6	37.61±1.79	NS
Glucose (mg dl^{-1})	6	24.23±1.83	6	61.43±1.46	*
Urea (mg dl^{-1})	6	30.77±1.05	6	31.10±0.95	NS

[1]Total DM intake values for goats were not added to pasture consumption. SNF, non-fat solids; SCC, somatic cell count;

TB, total bacteria; CRE, creatinine; GGT, gamma glutamyl transpeptidase; SEM=standard error of the mean; NS, not significant;

*P-value<0.05. ** P-value<0.01.

Table-3. Summary of bacteriological results from the milk of farm A and farm B

Extensive farm A		
Bacteria	**Isolates Number (n)**	**Isolation Ratio (%)**
Staphylococcus haemolyticus	8	25.0
Staphylococcus chromogenes	5	15.6
Enterococcus faecium	4	12.5
E.coli	3	9.4
Staphylococcus aureus	3	9.4
Staphylococcus warneri	2	6.3
Bacillus cereus	2	6.3
Staphylococcus caprae	2	6.3
Bacillus pumilus	1	3.1
Bacillus licheniformis	1	3.1
Staphylococcus pasteuri	1	3.0
Total	32	100
Semi-intensive farm B		
Bacillus cereus	11	47.8
Enterococcus faecium	1	4.3
Bacillus licheniformis	2	8.7
Pseudomonas fluorescens	1	4.3
E.coli	1	4.3
Enterococcus hirae	1	4.3
Streptococcus bovis I (Group D	1	4.3
Pseudomonas putida	1	4.3
Staphylococcus haemolyticus	1	4.3
Enterococcus feacalis	1	4.3
Cedecea lapagei	1	4.3
Acinetobacter lwoffii /haemolyticus	1	4.4
Total	23	100

Source: Bacterial identification based on BBL Crystal identification systems [29].