

# The influence of crossbreeding and *LPL* genotype on the yield, composition and quality of goat milk

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*Lina Laučienė*<sup>1\*</sup>, *Vida Juozaitienė*<sup>2</sup>, *Birutė Šlyžienė*<sup>3</sup>, *Lina Anskienė*<sup>3</sup>,  
*Renata Bižienė*<sup>4</sup>, *Evaldas Šlyžius*<sup>3</sup>

<sup>1</sup>Lithuanian University of Health Sciences, Faculty of Veterinary Medicine, Department of Food Safety and Quality, Tilžės g. 18, Kaunas, LT 47181, Lithuania

<sup>2</sup>Vytautas Magnus University, Faculty of Natural Sciences, Department of Biology, K. Donelaičio g. 58, Kaunas, LT 44245, Lithuania

<sup>3</sup>Lithuanian University of Health Sciences, Faculty of Animal Science, Department of Animal Breeding, Tilžės g. 18, Kaunas, LT 4718, Lithuania

<sup>4</sup>Lithuanian University of Health Sciences, Faculty of Animal Science, Institute of Biology Systems and Genetic Research, Tilžės g. 18, Kaunas, LT 4718, Lithuania

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\*Corresponding author: lina.lauciene@lsmuni.lt

## Abstract

The aim of this study was to investigate the influence of crossbreeding and the *LPL* genotype on goat milk yield, composition and quality indicators. This research was carried out in a herd of pure-breed Saanen, Anglo-Nubian, and crossbred Saanen and Anglo-Nubian goats (n=137) in Lithuania. Saanen x Anglo-Nubian crossbred goats and Saanen had a significantly (P<0.05) higher (34.91% and 16.03 %, respectively) milk yield compared to Anglo-Nubian goats. The highest (P<0.05) fat and protein and the lowest (P<0.05) lactose percentages and somatic cell count were found in the milk of Anglo-Nubian goats, compared to Saanen x Anglo-Nubian crossbreds and Saanen goats. The highest (P<0.05) milk yield was determined in the CC genotype of the *LPL* gene (on average 20.08 % higher than in the CG and GG genotypes) of goats. However, the milk yield of the CC genotype was characterised (P<0.05) by the lowest fat, protein and milk urea levels, and the highest amount of lactose compared to the milk of the GG genotype. The study showed that breed and *LPL* genotype affected goat milk yield and composition and appear to be the valuable biomarkers of the goat selection process.

**Key words:** goat milk composition; crossbreeding; *LPL* genotype

## Introduction

The growing consumer interest in goat milk and dairy products is related to nutritive values and positive health benefits attached to these products (Turkmen, 2017). Nutritional and beneficial aspects of goat milk are associated with higher unsaturated fatty acids (UFA), short-chain fatty acids (SCFA), and medium-chain fatty acids (MCFA) in comparison to cow milk (Kompan and Komprej, 2012). Small fat globules and high SCFA and MCFA such as C6:0, C8:0, C10:0 content provide a typical “goat” flavour and better digestibility of goat milk products (Turkmen, 2017; Martin et al., 2017). Lower occurrence of milk protein allergies is one of the most important effects of goat milk. The  $\beta$ -casein/ $\alpha$ s1-casein ratio of goat milk proteins is close to human milk, resulting in higher digestibility compared with cow milk (Turkmen, 2017). Besides, goats have better feed uptake, and a higher proportion of body weight is in the mammary gland tissue; hence, they can produce more milk compared to live weight than other dairy ruminants (Taiwo Idowu and Olufunke Adewumi, 2017).

The goat milk yield and milk composition depend on genetic and non-genetic factors (Taiwo Idowu and Olufunke Adewumi, 2017). Different goat breeds have different milking potentials (Curro et al., 2019; Tatar et al., 2019; Taiwo Idowu and Olufunke Adewumi, 2017). This is possible because their genomes are different. Specific genes, such as *DGAT1*, *STAT5*, *PITX2*, *LIPE*, *LPL*, etc., have been identified to affect milk yields and composition traits (Martin et al., 2017; Amills, 2014). The hydrolysis of milk fat globule triglycerides into free fatty acids is carried out by lipoprotein lipase (*LPL*). It is a 56-kDa enzyme that also plays a key role in regulating the levels of plasma lipoproteins in the adipose and muscular tissues as well as in other body parts such as liver, heart, nervous system, and mammary gland (Badaoui et al., 2007). The *LPL* gene consists of nine exons and eight introns, for a total of 3555 nucleotides (Brzáková et al., 2021). There is very little information on the influence of the goat *LPL* gene on the quantity and quality of production; therefore, it is important to study the polymorphisms of this gene and their influence on production as much as possible.

In order to increase goat productivity, goats with high milk production as Saanen, Toggenburg, Alpine, and Anglo Nubian have been used for crossbreeding of local goats (Serradilla, 2001; Kume et al., 2012; Momani et al., 2012; Hadi-Tavatori et al., 2020; Çak et al., 2021). Saanen goats are valued for their high milk yields, while milk of Anglo-Nubian goats is rich in milk fat (Goetsch et al., 2011; Shuvarikov et al., 2021).

There are sufficient data on improving the productivity of local goat breeds. However, analysis of scientific literature has shown that there is still a lack of data on the crossbreeding of high-producing goat breeds and how this affects milk composition, quality, and milk yield. Therefore, the aim of this study was to investigate the influence of crossbreeding and the *LPL* genotype on goat milk yield, composition and quality indicators.

## Materials and methods

### Animals and management

This study was conducted in 2020 at a Lithuanian dairy goat farm, from May to July. It involved two purebred goat breeds, Saanen (n=57) and Anglo-Nubian (n = 35), as well as their crossbreds (Saanen (♀) x Anglo-Nubian (♂), n=45). All 137 selected dairy goats had no swollen udders, did not exhibit any visible clinical signs, were on average 3.4±0.11 parity (1<sup>st</sup> parity = 15, 2<sup>nd</sup> parity = 19, 3<sup>rd</sup> parity = 40 goats, 4<sup>th</sup> and more parity = 63 goats) and on average 35±2.00 days of lactation at the start of the experiment. All investigated goats were raised in the same housing and feeding conditions and received a total mixed ration (TMR) from pasture grass and hay (ad libitum) and concentrates (600 g) (Table 1). Drinking water was given ad libitum.

The animals were milked twice a day (7:00 a.m. and 6:00 p.m.). The milking parlour had a low-line design, self-locking gates, and 2 platforms with 8 milking units and milking posts per platform. The research was conducted following the provisions of the Republic of Lithuania on Animal Welfare and Protection, No XI-2271 (2012), and the Requirements of keeping, maintenance, and use for animals used for scientific and educational purposes, No XI-2271 (n.d.).

### Milk yield, composition and quality investigations

Milk samples of individual goats were collected from May 1, 2020, to July 31, 2020, three times per experiment (on the 15<sup>th</sup> day of each month). Analysis

**Table 1.** Chemical composition of TMR ingredients

Indicators	Pasture grass	Hay	Concentrate
Dry matter, g/kg	269	840	844
Ash, g/kg	77	60	19
Crude protein, g/kg	119	110	100
Crude fibre, g/kg	241	252	50
Crude fat, g/kg	31	20	19
Total sugar, g/kg	109	127	50
Acid detergent fibre (ADF), g/kg	287	355	-
Acid detergent lignin, g/kg	47	44	-
Neutral detergent fibre (NDF), g/kg	453	476	178
Net energy for lactation (NEL), MJ	6.1	8.3	8.2
Digestibility of organic matter (% OM)	70.7	59	83.8

of goat milk composition (fat, protein, lactose, and urea) was made by Lithuanian accredited central milk testing laboratory CJSC Pieno Tyrimai, using spectrophotometers LactoScope 550 and LactoScope FTIR (Delta Instruments, the Netherlands). The somatic cell count (SCC) in milk was determined by the flow cytometry method using the Somascope CA-3A4 (Delta Instruments, the Netherlands). Goat milk yield was analysed during control milking and evaluated according to the information made available by the Agricultural Information and Rural Business Centre.

Analysis of the fatty acids (FA) composition of goat milk was carried out at the Chemical Laboratory of the Livestock Farming Institute of the Lithuanian University of Health Sciences. The cream of goat milk was separated by centrifugation (4000 rpm). The fat was extracted with a mixture of chloroform and methanol (3:1) and methylated with 2 % sodium methylate solution (Christopherson and Glass, 1969). The mixture of the FA methyl esters was injected in the CG-2010 SHIMADZU gas chromatographer equipped with the hydrogen flame detector. The FA were identified according to output times of a known FA standard composition (Supelco 37 FAME mix, Linoleic acid methyl ester isomer mix, Supelco Trans FAME mix K110) and were calculated by using the CG Solution data processing programme. Individual FA were expressed as the percentage of the total FA identified. Depending on the number of carbon atoms, FA were summed into short-chain fatty acids (SCFA; C2-C4), medium-chain fatty acids (MCFA; C8-C15), and long-chain fatty acids (LCFA; C16 and more) (Yilmaz-Ersan, 2013). According to the presence and the number of single and double bonds, FA were grouped into saturated fatty acids (SFA), unsaturated fatty acids (UFA), monounsaturated fatty acids (MUFA), and polyunsaturated fatty acids (PUFA).

### Goat gene variation investigations

Goat gene analyses were performed at the Lithuanian University of Health Sciences, Institute of Biology Systems and Genetic Research, Dr. K. Janušauskas Laboratory of Genetics. Goat hair samples were collected for the DNA extraction and SNP genotyping. Genome DNA was extracted from the hair follicle using lysis buffer containing DTT (1M), Chelex 100, Proteinase K (20 mg/mL) (Thermo Fisher Scientific, Waltham, MA, USA). The samples were incubated together with the lysis buffer at 56 °C for 45 min. After the incubation, the samples were heated at 94 °C for 10 min. The polymerase chain reaction method and the restriction length polymorphism methods were used for the determination of lipoprotein lipase (*LPL*) gene polymorphism. In regard to the goat *LPL* gene sequence (GenBank accession number:DQ370053), Primer3 and CLC Sequence Viewer 7 programmes were used to select the oligonucleotide primers and restriction enzyme. PCR-RFLP reactions were conducted using *LPL* F: 5'-AGACCGTGCTCCAGCCT-3', *LPL* R: 5'CAGCCCTCGTGGGAGAC-3' oligonucleotide primers (10

pmol) and *SchI* restriction enzyme. Reaction conditions were as follows: initial denaturation at 95 °C for 2 min; 35 cycles of denaturation at 94 °C for 30 s, primer joining temperature 58 °C for 40 s and chain synthesis at 72 °C for 45 s; and final synthesis at 72 °C for 7 min. After amplification, 10 µL of the PCR product was digested with the selected restriction enzyme according to the recommendations of the manufacturer (Thermo Fisher Scientific, Waltham, MA, USA).

PCR product restriction site locations were identified by the electrophoresis method using a 3 % agarose gel with ethidium bromide. Ethidium bromide was added to agarose up to the final concentration of 0.5 µg/mL (Thermo Fisher Scientific, Waltham, MA, USA). Identification of fragments was performed in the ultraviolet light using MiniBIS Pro Video Documenting system (DNA Bio Imaging System, Neve Yamin, Israel). Genetic tests were performed on 137 goats.

### Statistical analysis of the data

Statistical data analysis was conducted using SPSS 25.0 (SPSS, Inc., Chicago, IL, USA) software. The data were presented using descriptive statistics and normal distribution analysis methods. One-way analysis of variance was used for analysis of data. The impact of crossbreeding and the *LPL* genotype on milk yield, milk composition and quality indicators was evaluated. Multiple comparisons of group means were calculated using the Tukey test. The differences were considered as significant at  $P < 0.05$ .

## Results and discussion

### *The influence of crossbreeding on goat milk yield, composition and quality*

The analysis of the parameters showed that crossbreeding affected daily milk yield (Table 2) of crossbred goats. Saanen x Anglo-Nubian crossbred goats had from 22.49 % to 34.91 % higher ( $P < 0.001$ ) milk yield compared to purebred Saanen and Anglo-Nubian goats. Gadir and El-Zubeir (2005) found a lower milk yield of Nubian x Saanen crossbreds ( $1.24 \pm 0.34$  L/d) than that estimated in this study ( $1.69 \pm 0.08$  kg/milking). Generally, Saanen, Alpine, and Anglo-Nubian goats with excellent milk production are used for crossbreeding to local goats to improve their milk yield in many countries (Kume et al., 2012; Momani et al., 2012; Hadi-Tavatori et al., 2020; Çak et al., 2021). In the meantime, there is a lack of data regarding milk yield and composition of Saanen x Anglo-Nubian crossbreds. However, this study showed a positive effect of crossbreeding on the milk yield estimated by crosses of high-producing goat breeds.

The current study indicated that the milk yield of

purebred Saanen goats was significantly (by 16.03 %) higher compared with Anglo-Nubian goats ( $P<0.05$ ). Rojo-Rubio et al. (2016) have also indicated that Anglo-Nubian goat breed had significantly ( $P<0.05$ ) lower daily milk production compared to Saanen ( $2.07\pm 0.22$  vs.  $2.62\pm 0.17$  kg/d). Shuvarikov et al. (2021) have found a similar trend that the daily milk yield was  $2.15\pm 0.13$  kg/d for Saanen and  $1.84\pm 0.20$  kg/d for Anglo-Nubian goat breed. Lotrič et al. (2017) have estimated that the milk yield of Saanen goats was higher compared to Alpine goats in Croatia ( $585.09\pm 18.03$  vs.  $499.59\pm 7.88$  kg/lactation) and Slovenia ( $511.74\pm 28.92$  vs.  $486.38\pm 18.86$  kg/lactation).

The average fat content was  $3.57\pm 0.08$  %,  $3.98\pm 0.14$  %, and  $5.01\pm 0.12$  % for Saanen, crossbreds of Saanen x Anglo-Nubian, and Anglo-Nubian, respectively; these differences between the goats were statistically significant. These data were consistent with the results reported by Clark and Sherbon (2000) and confirmed that fat content in Anglo-Nubian milk was 1.4 times higher than in Saanen milk. Shuvarikov et al. (2021) have also found a higher ( $P<0.05$ ) fat content in the milk of the Nubian breed ( $4.30\pm 0.03$  %) compared to the milk of the Saanen breed ( $4.02\pm 0.05$  %). In the current study, it was observed that the milk yield of Saanen x Anglo-Nubian crossbreds took an intermediate position according to the fat content ( $3.98\pm 0.14$  %) and statistically significantly differed from the milk yield of Anglo-Nubian ( $P<0.001$ ) and Saanen ( $P<0.01$ ) goats. Gadir and El-Zubeir (2005) estimated similar fat content ( $4.17\pm 1.40$  %) for crossbreds of Nubian x Saanen goats.

Curro et al.'s (2019) study with 6 purebred goat breeds has not revealed a breed effect on the total fat percentage but the authors have found some on a few FA. C4:0, C14:0, iC15:0, aC15:0, C16:0, C16:1, iC17:0, aC17:0, and C18:0 differ between Saanen and 5 local Italian breeds. In this study, crossbreeding did not affect SCFA significantly but showed some differences on a few MCFA (Table 3). The Saanen goat milk had less ( $P<0.05$ ) C13:0 than Saanen x Anglo-Nubian crossbred and less ( $P<0.05$ ) C15:0 than Saanen x Anglo-Nubian crossbred and Anglo-Nubian goat milk. Differences in LCFA were more pronounced. The lowest amount of C16:0 and the highest amount of C18:1n9t, C18:2n6t, C18:2n6ct (compared with Saanen and Saanen x Anglo-Nubian crossbred), C18:1n9, and C20:1n9 (compared with Saanen) were found in the milk of Anglo-Nubian goats. The milk of Saanen goats had more iC17:0, C17:1n9, and less C21:0 and C20:1n9 than the milk of Saanen x Anglo-Nubian crossbreds. In

general, the most abundant FA in the milk of all goat breeds was C10:0, C12:0, C14:0, C16:0, and C18:1n9, which is consistent with the findings of other researchers (Ripoll et al., 2020; Lopez et al., 2019).

Overall, FA differences were more pronounced between purebred goat breeds in this study. Anglo-Nubian milk had a higher ( $P<0.05$ ) amount of PUFA, MUFA, and a lower ( $P<0.05$ ) amount of SFA compared to the milk of Saanen goats, and was more favourable to human nutrition (Djordjevic et al., 2019). Meanwhile, the FA content of Saanen x Anglo-Nubian crossbreds took an intermediate position and did not differ significantly from pure breed goat milk.

Protein content (Table 2) in the goat milk ranged from  $2.96\pm 0.04$  % to  $3.51\pm 0.09$  %, which was consistent with data of other authors' (Lotrič et al., 2017; Clark and Mora García, 2017). A 10.25 % to 15.66 % higher ( $P<0.001$ ) protein content was found in the milk of Anglo-Nubian goats compared to Saanen x Anglo-Nubian crossbred and Saanen breed. This was in agreement with the study of Clark and Sherbon (2000) who found that the milk of the Nubian breed had the highest percentage of total solids, fat, and protein among six goat breeds (LaMancha, Saanen, Alpine, Oberhasli, Toggenburg) and two crossbreed combinations (Nubian x Alpine and Saanen x Alpine). Opposite results have been established for Saanen goat milk, showing the significantly lowest protein percentage compared with the rest of the goats, which is in line with other studies (Vulić et al., 2021; Curro et al., 2019). Çak et al. (2021) have determined a significant influence of crossbreeding on milk composition: protein, lactose, and total solids percentages were higher ( $3.59\pm 0.02$  vs.  $3.48\pm 0.02$ ,  $5.24\pm 0.03$  vs.  $5.08\pm 0.03$ , and  $13.51\pm 0.08$  vs.  $13.04\pm 0.10$ , respectively) in pure Hair goat milk than those of crossbred (Saanen x Hair goat) goats within 5 months of the study.

In contrast to results of protein and fat, lactose content ( $3.79\pm 0.12$  %) of Anglo-Nubian goat milk was significantly lower than that of Saanen ( $4.24\pm 0.03$  %,  $P<0.01$ ) and crossbred ( $4.14\pm 0.02$  %,  $P<0.001$ ) goat milk. Shuvarikov et al. (2021) revealed that lactose percentage did not differ in samples of Saanen and Nubian goat milk. The average lactose content ( $4.06\pm 0.06$  %) in Lithuanian goat milk was lower than that estimated by Cak et al. (2021), Curro et al.'s (2019) and Gadir and El-Zubeir's (2005). However, it was consistent with the average lactose content of Saanen goats kept in Serbia (Čobanović et al., 2019).

**Table 2.** The influence of crossbreeding on milk yield, composition and quality indicators

Breed	Milk yield, kg/milking	Fat, %	Protein, %	Lactose, %	Urea, mg/dL	SCC, $\times 10^3$ cells/mL
Anglo-Nubian <sup>a</sup>	$1.10\pm 0.07^{***b; *c}$	$5.01\pm 0.12^{***b; c}$	$3.51\pm 0.09^{***b; c}$	$3.79\pm 0.12^{**b; ***c}$	$41.97\pm 2.36$	$575.00\pm 106^{**b; ***c}$
Saanen x Anglo-Nubian crossbreed <sup>b</sup>	$1.69\pm 0.08^{***a; c}$	$3.98\pm 0.14^{***a; **c}$	$3.15\pm 0.06^{***a; *c}$	$4.14\pm 0.02^{**a}$	$41.82\pm 2.03$	$1494.00\pm 293^{**a}$
Saanen <sup>c</sup>	$1.31\pm 0.05^{**a; ***b}$	$3.57\pm 0.08^{***a; **b}$	$2.96\pm 0.04^{***a; *b}$	$4.24\pm 0.03^{***a}$	$36.64\pm 1.67$	$1424.00\pm 206^{***a}$

\* $P<0.05$ ; \*\* $P<0.01$ ; \*\*\* $P<0.001$

The crossbreeding influence on milk urea was not determined, since the average urea amount was  $40.14 \pm 2.02$  mg/dL for all goats. In this study, milk urea value was lower than in the Saanen goat milk (46.27 mg/dL) examined by Superchi et al. (2007), but higher than the values obtained by analysing the Saanen goat milk (29.94 mg/dL) in the study of Čobanović et al. (2019).

The SCC of goat milk is higher than that of cow milk, but goats suffer from mastitis less often (Csanádi et al., 2015). According to Paape et al. (2001), the SCC in goat milk can range from  $270 \times 10^3$  to  $2000 \times 10^3$  cells/mL in the absence of mastitis. In 2008, an examination of 110 goat flocks showed an average of  $1344 \times 10^3$  cells/mL in bulk milk (Vasiu et al., 2008). In this study, an average SCC in Anglo-Nubian milk was  $575 \times 10^3$  cells/mL and significantly differed from Saanen x Anglo-Nubian crossbred ( $P < 0.01$ ) and Saanen ( $P < 0.001$ ) milk, in which the SCC value was around 3-fold higher and exceeded the 1 million threshold ( $1494 \times 10^3$  cells/mL and  $1424 \times 10^3$  cells/mL, respectively). The study of Csanádi et al. (2015) has revealed an average of  $906 \times 10^3$  cells/mL SCC in Hungarian white goat milk,  $604 \times 10^3$  cells/mL in Saanen goat milk, and  $793 \times 10^3$  cells/mL in crossbreed (Alpine x Saanen) goat milk.

### The LPL genotype influence on goat milk yield, composition and quality

The distribution of genotypes in the *LPL* gene was as follows: the CC genotype was found in 26.00 % of goats, the CG genotype was found in 23.00 %, and the highest frequency was estimated for the GG genotype (51.00 %).

Analysis of the *LPL* gene (Table 4) showed that the milk yield of goats with the CC genotype was on average 20.08 % higher ( $P < 0.05$ ,  $1.61 \pm 0.13$  kg/d) compared to the CG and GG genotypes ( $1.21 \pm 0.09$  kg/d and  $1.34 \pm 0.04$  kg/d, respectively). Crepaldi et al. (2013) have confirmed the influence of genotype CC on milk yield. Alpine goats with the CC genotype yielded 0.5 L more milk than goats with the GG genotype (Crepaldi et al., 2013). A study by Mathivathani et al. (2020) has shown a significant ( $P < 0.05$ ) association of genotype CC, CT, and TT with an average daily milk yield in Malabari and Attappady Black goats.

Despite a high milk yield of goats with the CC genotype, the milk of goats with the CC genotype contained 8.04 % less fat, 5.73 % less protein, 16.26 % less milk urea, and 6.94 % more lactose than the milk of goats with the GG genotype. These data agree with those obtained in Svitáková et al.'s (2014) study, where a significant effect of the *LPL* gene on fat and protein percentage was found. Czech dairy goats with the GG genotype produced milk with the highest fat and protein content. Badaoui et al. (2007) did not find any association between *LPL* single nucleotide polymorphism C2094T and goat milk components. However, *LPL* single nucleotide polymorphism G50C affected milk fat ( $P < 0.05$ ): a difference of -0.55 kg of

**Table 3.** The influence of crossbreeding on goat milk fatty acid composition

Fatty acids, %	Breed		
	Saanen <sup>a</sup>	Saanen x Anglo-Nubian crossbreed <sup>b</sup>	Anglo-Nubian <sup>c</sup>
C4:0	1.22±0.13	1.35±0.19	1.44±0.11
C6:0	1.03±0.03	0.97±0.03	1.03±0.03
<b>Σ SCFA</b>	<b>2.25±0.14</b>	<b>2.32±0.19</b>	<b>2.47±0.12</b>
C8:0	1.87±0.06	1.80±0.06	1.85±0.07
C10:0	7.71±0.24	7.58±0.35	7.48±0.30
C11:0	0.19±0.01	0.23±0.02	0.21±0.01
C12:0	3.72±0.15	3.78±0.26	3.52±0.16
C13:0	0.14±0.01 <sup>b</sup>	0.20±0.03 <sup>a</sup>	0.17±0.02
C14:0	9.68±0.18	9.33±0.38	9.08±0.28
iC14:0	0.54±0.03	0.54±0.04	0.56±0.03
C14:1n7	0.19±0.03	0.17±0.02	0.16±0.02
C15:0	0.91±0.05	0.99±0.04	0.88±0.03
iC15:0	0.09±0.01	0.07±0.02	0.09±0.02
aC15:0	0.25±0.02 <sup>b,c</sup>	0.32±0.03 <sup>a</sup>	0.32±0.02 <sup>a</sup>
<b>Σ MCFA</b>	<b>25.29±0.59</b>	<b>25.02±0.98</b>	<b>24.33±0.75</b>
C16:0	28.01±0.44 <sup>***c</sup>	27.12±0.56 <sup>c</sup>	25.39±0.60 <sup>***a,b</sup>
C16:1n9t	0.56±0.02	0.61±0.04	0.57±0.03
C16:1n9	0.84±0.02	0.89±0.03	0.89±0.03
C16:1n7	0.66±0.03	0.67±0.05	0.60±0.02
C17:0	0.82±0.04	0.85±0.03	0.84±0.05
iC17:0	0.16±0.015 <sup>b</sup>	0.09±0.02 <sup>a</sup>	0.15±0.02
C17:1n9	0.40±0.03 <sup>b</sup>	0.31±0.02 <sup>a</sup>	0.35±0.03
C18:0	10.42±0.30	10.43±0.73	10.92±0.34
C18:1n9t	1.61±0.09 <sup>c</sup>	1.53±0.14 <sup>c</sup>	1.97±0.16 <sup>a,b</sup>
C18:1n9	23.13±0.53 <sup>c</sup>	23.84±1.24	25.22±0.80 <sup>a</sup>
C18:1n7	0.97±0.03	0.92±0.06	0.92±0.05
C18:2n6t	0.33±0.02 <sup>c</sup>	0.30±0.03 <sup>***c</sup>	0.42±0.02 <sup>a,***b</sup>
C18:2n6c,t	0.20±0.01 <sup>c</sup>	0.18±0.01 <sup>c</sup>	0.24±0.02 <sup>a,b</sup>
C18:2n6t,c	0.20±0.01	0.17±0.02 <sup>c</sup>	0.21±0.01 <sup>b</sup>
C18:2n6	2.08±0.04	2.28±0.16	2.28±0.12
C18:3n3	0.59±0.03	0.55±0.04	0.55±0.03
C20:0	0.26±0.02	0.27±0.02	0.307±0.025
C20:1n9	0.07±0.01 <sup>***b,c</sup>	0.12±0.01 <sup>***a</sup>	0.12±0.01 <sup>***a</sup>
C20:4n6	0.15±0.01	0.17±0.01	0.17±0.01
C20:5n3	0.02±0.01	0.02±0.01	0.01±0.00
C21:0	0.56±0.03 <sup>**b</sup>	1.01±0.23 <sup>**a</sup>	0.78±0.07
C22:0	0.10±0.02	0.11±0.01	0.10±0.01
C22:4n6	0.04±0.01	n. d.	n. d.
C22:5n3	0.14±0.01	0.15±0.01	0.15±0.01
<b>Σ LCFA</b>	<b>72.33±0.64</b>	<b>72.61±0.86</b>	<b>73.17±0.79</b>
<b>Σ SFA</b>	<b>67.69±0.58<sup>c</sup></b>	<b>67.05±1.27</b>	<b>65.14±1.09<sup>a</sup></b>
<b>Σ UFA</b>	<b>32.19±0.55<sup>c</sup></b>	<b>32.90±1.27</b>	<b>34.83±1.09<sup>a</sup></b>
<b>Σ MUFA</b>	<b>28.43±0.56<sup>c</sup></b>	<b>29.06±1.24</b>	<b>30.79±0.96<sup>a</sup></b>
<b>Σ PUFA</b>	<b>3.76±0.07</b>	<b>3.84±0.21</b>	<b>4.04±0.17</b>

<sup>a,b,c</sup> - values denoted in rows by different letters indicate statistically significant differences; \* $P < 0.05$ ; \*\* $P < 0.01$ ; \*\*\* $P < 0.001$ ; Σ SCFA - all short-chain fatty acids; Σ MCFA - all medium-chain fatty acids; Σ LCFA - all long-chain fatty acids; Σ SFA - all saturated fatty acids; Σ UFA - all unsaturated fatty acids; Σ MUFA - all monounsaturated fatty acids; Σ PUFA - all polyunsaturated fatty acids; n. d. - not detected.

**Table 4.** The influence of the *LPL* genotype on goat milk yield, composition, and quality indicators

<i>LPL</i> genotype	Milk yield, kg/milking	Fat, %	Protein, %	Lactose, %	Urea, mg/dL	SCC, ×10 <sup>3</sup> cells/mL
CC <sup>a</sup>	1.61±0.13 <sup>abc</sup>	3.77±0.12 <sup>**c</sup>	2.96±0.06 <sup>abc</sup>	4.32±0.05 <sup>***c</sup>	33.36±2.56 <sup>*c</sup>	923.00±277
CG <sup>b</sup>	1.21±0.09 <sup>*a</sup>	3.82±0.18	3.16±0.06 <sup>*a</sup>	4.26±0.02 <sup>***c</sup>	36.36±2.67	902.00±112 <sup>**c</sup>
GG <sup>c</sup>	1.34±0.04 <sup>*a</sup>	4.10±0.10 <sup>**a</sup>	3.14±0.05 <sup>*a</sup>	4.02±0.05 <sup>***ab</sup>	39.84±1.52 <sup>*a</sup>	1489.00±195 <sup>**b</sup>

\**P*<0.05; \*\**P*<0.01; \*\*\**P*<0.001**Table 5.** The influence of the *LPL* genotype on goat milk fatty acid composition

Fatty acids, %	<i>LPL</i> genotype		
	CC <sup>a</sup>	CG <sup>b</sup>	GG <sup>c</sup>
C4:0	1.21±0.23	1.01±0.15	0.88±0.07
C6:0	1.00±0.06	0.99±0.04	0.95±0.02
<b>Σ SCFA</b>	<b>2.21±0.61</b>	<b>2.00±0.64</b>	<b>1.83±0.46</b>
C8:0	2.00±0.22	1.89±0.07	1.84±0.04
C10:0	7.37±0.60	8.52±0.39	7.46±0.25
C11:0	0.14±0.04 <sup>c</sup>	0.19±0.01	0.20±0.01 <sup>a</sup>
C12:0	3.30±0.29 <sup>b</sup>	4.41±0.14 <sup>a,***c</sup>	3.48±0.15 <sup>ab</sup>
C13:0	0.15±0.05	0.18±0.02	0.13±0.02
C14:0	8.32±0.08 <sup>***b</sup>	10.69±0.20 <sup>***b,c</sup>	8.98±0.26 <sup>***b</sup>
iC14:0	0.28±0.10 <sup>***b,c</sup>	0.52±0.05 <sup>***a</sup>	0.49±0.03 <sup>***a</sup>
C14:1n7	0.15±0.05	0.20±0.03	0.16±0.02
C15:0	1.21±0.13 <sup>***b,c</sup>	0.85±0.03 <sup>***a</sup>	0.84±0.03 <sup>***a</sup>
iC15:0	n. d.	0.11±0.01 <sup>***c</sup>	0.04±0.01 <sup>***b</sup>
aC15:0	0.24±0.07	0.27±0.01	0.27±0.02
<b>Σ MCFA</b>	<b>23.15±3.10<sup>***b</sup></b>	<b>27.82±2.95<sup>***a,***c</sup></b>	<b>23.89±4.07<sup>***b</sup></b>
C16:0	26.44±1.61	27.88±0.42	25.95±0.56
C16:1n9t	0.77±0.06 <sup>***b,***c</sup>	0.49±0.02 <sup>***a,c</sup>	0.59±0.02 <sup>***a,b</sup>
C16:1n9	1.03±0.04 <sup>***b</sup>	0.79±0.02 <sup>***a,c</sup>	0.97±0.02 <sup>***b</sup>
C16:1n7	0.70±0.08	0.61±0.04	0.63±0.02
C17:0	1.28±0.08 <sup>***b</sup>	0.74±0.02 <sup>***a,c</sup>	1.13±0.03 <sup>***b</sup>
iC17:0	0.04±0.02 <sup>***b</sup>	0.15±0.04 <sup>***a,c</sup>	0.09±0.01 <sup>***b</sup>
C17:1n9	0.66±0.09 <sup>***b,***c</sup>	0.32±0.02 <sup>***a,c</sup>	0.50±0.03 <sup>***a,***b</sup>
C18:0	11.08±0.02	10.25±0.55	10.82±0.41
C18:1n9t	1.98±0.28	1.83±0.18	1.79±0.12
C18:1n9	23.87±1.31	21.27±1.04 <sup>***c</sup>	25.29±0.75 <sup>***b</sup>
C18:1n7	1.18±0.05 <sup>***b</sup>	0.85±0.06 <sup>***a,***c</sup>	1.04±0.03 <sup>***b</sup>
C18:2n6t	0.32±0.09	0.42±0.05	0.38±0.03
C18:2n6c,t	0.19±0.05	0.22±0.02	0.25±0.02
C18:2n6t,c	0.26±0.08	0.20±0.01 <sup>c</sup>	0.29±0.02 <sup>b</sup>
C18:2n6	2.25±0.10	1.97±0.08	2.14±0.10
C18:3n3	0.92±0.08 <sup>***b</sup>	0.63±0.06 <sup>***a,c</sup>	0.79±0.04 <sup>***b</sup>
C20:0	0.14±0.04 <sup>***b</sup>	0.29±0.02 <sup>***a,c</sup>	0.22±0.01 <sup>b</sup>
C20:1n9	0.03±0.02	0.07±0.02	0.07±0.01
C20:4n6	0.10±0.02 <sup>***c</sup>	0.14±0.01 <sup>***c</sup>	0.19±0.01 <sup>***a,b</sup>
C20:5n3	0.04±0.02	0.05±0.02	0.07±0.01
C21:0	0.46±0.11	0.63±0.06	0.66±0.06
C22:0	0.04±0.02	0.11±0.02	0.06±0.01
C22:4n6	n. d.	0.10±0.03	n. d.
C22:5n3	0.10±0.03 <sup>***b,***c</sup>	0.17±0.01 <sup>***a,c</sup>	0.22±0.01 <sup>***a,b</sup>
C22:6n3	n. d.	n. d.	0.01±0.00
<b>Σ LCFA</b>	<b>73.87±2.65<sup>***b</sup></b>	<b>70.16±2.92<sup>***a,***c</sup></b>	<b>74.16±4.08<sup>***b</sup></b>
<b>Σ SFA</b>	<b>64.40±3.79<sup>b</sup></b>	<b>69.15±4.91<sup>a,***c</sup></b>	<b>64.00±5.02<sup>***b</sup></b>
<b>Σ UFA</b>	<b>34.55±3.23<sup>b</sup></b>	<b>30.31±4.77<sup>a,***c</sup></b>	<b>35.39±4.97<sup>***b</sup></b>
<b>Σ MUFA</b>	<b>30.37±3.82</b>	<b>26.42±4.59<sup>***c</sup></b>	<b>31.05±4.96<sup>***b</sup></b>
<b>Σ PUFA</b>	<b>4.18±0.95</b>	<b>3.89±0.46<sup>c</sup></b>	<b>4.34±0.63<sup>b</sup></b>

<sup>a, b, c</sup> - values denoted in rows by different letters indicate statistically significant differences; \**P*<0.05; \*\**P*<0.01; \*\*\**P*<0.001; Σ SCFA - all short-chain fatty acids; Σ MCFA - all medium-chain fatty acids; Σ LCFA - all long-chain fatty acids; Σ SFA - all saturated fatty acids; Σ UFA - all unsaturated fatty acids; Σ MUFA - all monounsaturated fatty acids; Σ PUFA - all polyunsaturated fatty acids; n. d. - not detected.

fat/100 kg of milk was observed between the CG and GG genotypes (Badaoui et al., 2007).

The study findings showed that the milk of the CG genotype took an intermediate position between the CC and GG genotypes according to a major milk composition.

The *LPL* genotype did not affect SCFA (Table 5) of goat milk in this research. The SCFA and MCFA are *de novo* synthesised in the goat mammary gland (Zhu et al., 2014), while LCFA is derived from dietary lipids (Bionaz et al., 2020). A study with a crucial *de novo* synthesis enzyme fatty acid synthase (FASN) inhibition showed a reduction only in MCFA synthesis in goat mammary gland epithelial cells (Zhu et al., 2014). Maroteau et al. (2014) results have shown that the highest heritability among 18 FA was estimated for C6:0, C8:0, and C10:0 in Saanen and Alpine goat milk. SCFA seem to be more resistant to genetic factors and are more stable than MCFA and LCFA in milk fat composition.

Despite significant differences in milk fat quantity, the CC and GG genotype milk was similar (Table 4) for MCFA, LCFA, SFA, UFA, MUFA, and PUFA percentage. Meanwhile, the CG genotype milk had significantly more MCFA (14.13-16.79 %) and SFA (6.87-7.45 %), and less UFA (12.27-14.35 %), MUFA (13.01-14.91 %) and PUFA (6.94-10.37 %) than the CC and GG milk. In terms of the FA effect on human health (Haug et al., 2007), the milk of the CC and GG genotypes was more favourable due to lower SFA and higher UFA content than CG milk. Sztankooova et al. (2021) have found that sheep milk within *LPL* genotype CTCTAT had a significantly higher percentage of fat and a significantly lower amount of hypercholesterolemic FA (C12:0, C14:0, and C16:0). The effect of the CC and GG genotypes on hypercholesterolemic FA (except C16:0) in this study was similar to that observed in sheep milk: CC and GG milk had significantly less C12:0 and C14:0. In addition, the quantity of LCFA, consisting mainly of health-promoting UFA, was significantly higher than in the milk within the CG genotype. This study showed that *LPL* genotypes affected the FA profile of goat milk, but further and more extensive research is needed.

## Conclusions

The present study showed that crossbreeding and the *LPL* genotype affected goat milk yield and milk composition. The highest milk yield was found in Saanen x Anglo-Nubian crossbred goats, which was significantly higher compared with Anglo-Nubian and Saanen goats. The highest fat and protein and the lowest lactose

percentages were estimated in Anglo-Nubian goat milk. Although the highest milk yield was determined in the *LPL* gene CC genotype of goats, this milk had the lowest amount of fat, protein, and milk urea and the highest amount of lactose. The study showed that breed and *LPL* genotype affected goat milk yield and composition and appear to be the valuable biomarkers of the goat selection process.

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## Utjecaj križanja i *LPL* genotipa na prinos, sastav i kvalitetu kozjeg mlijeka

### Sažetak

Cilj ovog istraživanja bio je ispitati utjecaj križanja koza i genotipa *LPL* na prinos, sastav i kvalitetu kozjeg mlijeka. Istraživanje je provedeno u Litvi na stadu čistih sanskih, anglo-nubijskih i križanaca sanskih i anglo-nubijskih koza (n=37). Križanke sanske i anglo-nubijske koze te sanske koze imaju značajno ( $P<0,05$ ) više (34,91 % i 16,03 %) prinose mlijeka od anglo-nubijske pasmine koza. U usporedbi s kozama križanih pasmina i sanskim kozama, najveći ( $P<0,05$ ) udio masti i proteina, kao i najniži ( $P<0,05$ ) udio laktoze i broj somatskih stanica utvrđeni su za anglo-nubijsku pasminu koza. Najveći prinos mlijeka ( $P<0,05$ ) utvrđen je u genotipu CC gena *LPL* (u prosjeku 20,08 % veći nego u genotipu CG i GG) koza. Međutim, mlijeko genotipa CC okarakterizirano je i najnižim ( $P<0,05$ ) udjelom masti, proteina i uree te najvećim udjelom laktoze u usporedbi s mlijekom genotipa CG. Istraživanje je pokazalo da pasmina i genotip *LPL* utječu na prinos i sastav kozjeg mlijeka te se čine vrijednim biomarkerima u procesu odabira koza.

**Ključne riječi:** sastav kozjeg mlijeka; križanje; genotip *LPL*

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