B-1257
[1-6]

RESEARCH ARTICLE Indian Journal of Animal Research, Volume Issue : ()

Gene *LPL*, *STAT5* and *AGPAT6* Polymorphisms Relationship with Goat Milk Traits

B. Šlyžienė[1], L. Anskienė[1], E. Šlyžius[1], R. Bižienė[2], V. Juozaitienė[1]

10.18805/ijar.B-1257

ABSTRACT

Background: Several single nucleotide polymorphisms had been detected in goats and for the researchers it is important to reveal candidate genes with substantial effects on the traits of economic importance. The aim of this study was to investigate the association between *LPL, STAT5* and *AGPAT6* gene polymorphisms and milk traits of goats.

Methods: We investigated about 204 goats, four different breeds (Czech White Shorthaired, Saanen, Anglo Nubian, Alpine) and two crossbreeds (Saanen and Alpine, Saanen and Anglo Nubian). The milk samples were analysed using spectrophotometers LactoScope 550 and LactoScope FTIR (Delta Instruments, the Netherlands). The somatic cell count (SCC) in milk was determined by flow cytometry method using the Somascope CA-3A4 (Delta Instruments, the Netherlands). Variations of the goat *AGPAT6, STAT5, LPL* genes were detected by PCR-RFLP method.

Result: Analysis of *AGPAT6* gene revealed that goats with GC genotype had higher milk yield, fat content and lactose content; goats with CG genotype had higher protein content. *STAT5* gene analysis showed that goats with CT genotype had higher milk yield; goats with CC genotype had higher fat content and lactose content; goats with TT genotype had higher protein and urea content and also SCC. According to *LPL* gene analysis, goats with CC genotype had higher milk yield while goats with GG genotype had higher fat and protein content. The highest milk yield was estimated in Saanen and Alpine crossbreed goats while the highest milk fat and protein content was estimated in Anglo Nubian goats.

Key words: AGPAT6, Goat, LPL, Milk, STAT5.

INTRODUCTION

Goat breeding has become an important branch of livestock production spreading all over the world (Darcan *et al*. 2018; Gautam *et al*. 2019). Selection of the most productive individuals allows achieving the best performance from dairy goats. Goat breeds commonly selected for milk production receive more research considerations regarding milk yield and quality. Genetic differences are seen as breed differences (Goetsch *et al*. 2011). Some studies have found that the level of milk production depends on the breed (Zazharska *et al*. 2018) and there is variation in milk yield among different breeds and within the goat breed (Kendalla *et al*. 2006; Sandrucci *et al*. 2018).

Molecular genetics leads to the revealing candidate genes with substantial effects on the traits of economic importance. Several single nucleotide polymorphisms (SNPs) had been detected in goats (Maitra *et al*. 2016) and some of them were associated with milk production (Badaoui *et al.* 2007; Merkel *et al.* 2002).

AGPAT6 plays a fundamental role in the milk fat synthesis. Triglyceride synthesis occurs through the stepwise addition of fatty acyl groups to glycerol-3-phosphate, with *DGAT* catalysing the last step in this chain and 1-acylglycerol-3- phosphate acyltransferases (*AGPAT*) an intermediary step (Coleman 2004). Sequence variation nearby *AGPAT6* primarily controls fat content in early lactation which is also consistent with the expression of *AGPAT6* at different stages of lactation (Bionaz *et al.* 2008). *STAT5A* is one of the members of *STAT* (signal transducer and activator of transcription) family (Zhang *et al.* 2012), which is very important in cell activity, immune system, cancer regulation mechanism (Vafaizadeh *et al.* 2010; Peck *et al.* 2011) and is discovered as a MGF (mammary gland factor) which regulates the milk protein synthesis (Xie *et al*. 2015).

Lipoprotein lipase (LPL) is a glycoprotein that plays a central role in plasma triglyceride metabolism by hydrolysing triglyceride-rich chylomicrons (Badaoui *et al.* 2007) and regulating energy balance, fat deposition and growth traits (Ling *et al.* 2015). Milk *LPL* activity in goats is influenced by the stage of lactation, milking frequency, lipid supplementation (Chilliard *et al.* 2003) and has been shown to differ among several goat breeds (Badaoui *et al.* 2007).

Understanding of genetic information, particularly for those

[1]Department of Animal Breeding, Lithuanian University of Health Sciences, 47181 Kaunas, Lithuania.
[2]Institute of Biology Systems and Genetic Research, Lithuanian University of Health Sciences, 47181 Kaunas, Lithuania.

Corresponding Author: B. Šlyžienė, Department of Animal Breeding, Lithuanian University of Health Sciences, 47181 Kaunas, Lithuania. Email: birute.slyziene@gmail.com

How to cite this article: Šlyžienė, B., Anskienė, L., Šlyžius, E., Bižienė, R. and Juozaitienė, V., Gene *LPL*, *STAT5* and *AGPAT6* Polymorphisms Relationship with Goat Milk Traits. Indian Journal of Animal Research. doi: 10.18805/ijar.B-1270.

Submitted: 16-02-2020 **Accepted**: 16-07-2020 **Published**: 28-09-2020

loci which affect the performance traits, is an important tool in the breeding programmes (Selvaggi *et al.* 2009). Therefore, the aim of this study was to investigate the association between *LPL*, *STAT5* and *AGPAT6* gene polymorphisms and milk traits of goats.

MATERIALS AND METHODS

Animals and milk sample collection

The research (period during 2018-2019 year) was carried out in the herd of goats (n=204) and in Lithuanian University of Health Sciences, Department of Animal Breeding. All investigated goats were raised at the same feeding and housing conditions. The goats were milked twice a day and milk yields were recorded using monthly control milking data during 2018-2019 year. The milk samples were analysed for milk fat, milk protein, lactose and urea concentrations. The analysis was carried out together with Pieno Tyrimai SE (Lithuania), using spectrophotometers LactoScope 550 and LactoScope FTIR (Delta Instruments, the Netherlands). SCC in milk was determined by flow cytometry method using the Somascope CA-3A4 (Delta Instruments, the Netherlands).

DNA Extraction and SNP Genotyping

Analyses were done in Lithuanian University of Health Sciences, Institute of Biology Systems and Genetic Research, Dr. K. Janušauskas Laboratory of Genetic.

Genomic DNA was extracted from the hair roots using DTT (1M), Chelex 100, Proteinase K (20mg/ml) chemicals (Thermo Fisher Scientific, Waltham, MA, USA). The samples with lysis mixture were incubated for 45 min at 56°C. After incubation, the samples were heated at 94°C for 10 min.

The method of polymerase chain reaction and restriction length polymorphism were used to genotype *Lipoprotein Lipase (LPL) AGPAT 6(1-acylglycerol-3- phosphate acyltransferase)* and *STAT5 (signal transducer and activator of transcription*) gene polymorphisms., Using Primer3 and CLC Sequence Viewer 7 programs, the oligonucleotide primers and restriction enzyme were designed according to the goat *LPL, STAT5* and *AGPAT6* gene sequences. The PCR-RFLP reactions were carried out using *LPL* F: 5'-AGACCGCTGCTCCAGCCT-3', *LPL* R: 5'-CAGCCCTCCGT GGGAGAC-3' oligonucleotide primers (10pmol) and *SchI* restriction enzyme, *STAT5* F: 5'- CTGCAGGGCTGTTCTGA GA-3', *STAT5* R: 5'- TGGTACCAGGACTGTAGCACAT-3' oligonucleotide primers (10pmol) and *AvaI* restriction enzyme and *AGPAT6* F: 5'-ATCTGGCATTTTCACACATT-3', *AGPAT6* R: 5'- CTGACTCCATCTAAGAGCCT-3' oligo-nucleotide primers (10pmol) and *NcoI* restriction enzyme. The reaction conditions were as follows: an initial denaturation step at 95°C for 2 min; 35 cycles of denaturation at 94°C for 30 s, annealing for 45 s at temperature presented in Table 1 and elongation at 72°C for 45 s; and a final elongation step at 72°C for 7 min. After amplification, 10 µl of PCR product were digested with selected restriction enzyme (Table 1) according to producer recommendations (Thermo Fisher Scientific, Waltham, MA, USA).

The digested products were detected by electrophoresis in 2% and 3% (*LPL*) agarose gel stained with ethidium bromide. The ethidium bromide was added to agarose to a final concentration of 0.5 µg/ml (Thermo Fisher Scientific, Waltham, MA, USA). Fragment identification was performed in ultraviolet light, using MiniBIS Pro Video Documentation System (DNR Bio Imaging System, Neve Yamin, Israel).

The observed heterozygosity (H_O) per animal, within breed, was calculated, based on the markers which passed the quality control and compared to the expected heterozygosity under Hardy Weinberg Equilibrium (H_E). H_O was calculated as the number of heterozygotes divided by the total number of genotypes.

Statistical analysis

Genotypic and allelic frequencies of polymorphism sites on the *AGPAT6*, *STAT5*, *LPL* genes were analysed by the Chi-square test; statistical characteristics in the sample (n) – arithmetic mean (M) and standard error of the mean (SE) – were calculated using the SPSS software (version 20.0). Values of SCC (×1000 cells/mL) were transformed into base 10 logarithm to normalize their distributions. Student T-test was calculated for comparison between quantitative variables. The results were considered statistically significant as $P \leq 0.05$.

RESULTS AND DISCUSSION

Variations of the goat *AGPAT6, STAT5, LPL* genes were detected by PCR-RFLP method (Table 2). In the investigated group, the genotype CG of *AGPAT6* gene was present in 44.0 % of goats, the genotype CC of *STAT5* gene was found in 69.0 % of goats and, with the highest frequency, GG genotype (51.0 %) was found in the *LPL* gene. Allele C of the gene *AGPAT6* had higher frequency than G allele. Allele C of the gene *STAT5* had higher frequency than T allele, while allele G of *LPL* gene had higher frequency than G allele.

The results of our study on the *AGPAT6* gene were different from those obtained by other researchers. For instance, He with other researchers (2011) found the following genotype frequencies: GG (0.922 in Xinong Sannen, 0.890 in Guanzhong), GC (0.067 in Xinong Sannen, 0.093 in Guanzhong), CC (0.011 in Xinong Sannen, 0.018 in Guanzhong goats).

The frequencies of *STAT5* alleles C and T of 0.863 and 0.137 respectively reported by Selvaggi *et al.* (2015) were close to our results. The results of our study on the *STAT5* allele frequencies differed from those obtained by Wu *et al.* (2014), they found the frequencies of *STAT5* alleles C – 0.638 and T – 0.362 in Xinong Saanen goats.

Crepaldi *et al.* (2013) estimated lower genotype frequencies of *LPL* gene in Alpine goats: (CC – 0.02, CG – 0.26) compared to our results, while frequency of GG genotype was similar (0.764).

Table 1: LPL, STAT5 and AGPAT6 genes polymorphisms and reaction conditions.

Gene	Polymorphism	Restriction enzyme	Annealing temperature, °C	Product length, bp
LPL	G50C	*SchI*	58°C	156 bp; 24 bp146 bp; 34 bp
STAT5	C6853T	*AvaI*	60°C	215 bp181 bp; 34 bp
AGPAT6	C9263G	*NcoI*	57°C	241 bp130 bp; 130 bp

Table 2: Genotype and allele frequencies of AGPAT6, STAT5 and LPL.

Gene	Genotype	N	Frequency	Allele	N	Frequency
AGPAT6	CC	30	0.384	C	47	0.603
	CG	34	0.435	G	31	0.397
	GG	14	0.179			
STAT5	CC	70	0.686	C	84	0.824
	CT	28	0.274	T	18	0.176
	TT	4	0.039			
LPL	CC	48	0.255	C	70	0.372
	GC	44	0.234	G	118	0.628
	GG	96	0.511			

Comparison of CC, CG, GG genotypes of goat *AGPAT6* gene shows (Table 3) that goats with CG genotype have higher milk yield (27.31 % higher compared to CC, P<0.05; 21.01% – to GG genotype, P<0.05). The comparison of CC, CG, GG genotypes of goat *AGPAT6* gene shows that the average of fat and lactose did not differ significantly. Meanwhile, goats with CG genotype have higher protein content (0.4% higher compared to CC and 0.36% - to GG genotype, P<0.05). In the examined group, the goats with the genotype GG have higher content of urea and SCC (P<0.01). In comparison with our results, He with other researchers (2011) found that *AGPAT6* genotype GG and CG goats showed significantly higher milk fat, protein content and milk yield than those with the CC genotype (P<0.05).

Study in goat *STAT5* gene shows that goats with CT genotype had higher, but non-significant, milk yield compared to CC and TT genotype. The *STAT5* CC genotype had higher fat and lactose content and the lowest urea and SCC compared to genotypes CT and TT. An *et al.* (2013) studied the association among genotypes at *STAT5* locus and milk performance traits of animals: the goats with CT genotype had greater milk yield than those with CC genotype (P<0.05). Researcher Bao *et al.* (2010) found that cows of genotype CT showed higher protein content than cows of the CC genotype (P<0.05).

The results showed that the goat *LPL* gene with CC genotype has higher milk yield (37.39% higher compared to CG, P<0.001 and 8.05% higher compared to GG genotype, P<0.05). The goats with GG genotype produce milk with higher fat content (0.12% higher compared to CC, 0.22% higher compared to GC genotype, P<0.05) and protein content (0.08% higher compared to CC; 0.01% higher compared to CG genotype, P<0.05). In comparison with our results, Svitáková *et al*. (2014), in the research with Czech dairy goats, found a significant effect of LPL gene on fat percentage and protein percentage. Crepaldi *et al*. (2013) in the research with Alpine goats reported that the *LPL* was highly associated with goat's milk yield of CC genotype compared to GG genotype goats and fat percentage showed a rather consistent difference among genotypes during lactation, whereas differences for protein content were relevant mainly until about 120 days in milk.

The mean values of milk yield and content of different goat breeds are demonstrated in Table 4, where Saanen and Alpine crossbreed goats showed significant highest milk yield compared to Czech White, Shorthaired, Saanen, Anglo Nubian, Alpine, Saanen and Anglo Nubian crossbreeds (25.35%, 25.07%, 0.14 %, 3.82% and 2.24%, respectively). Mioč *et al.* (2008) reported similar results with Saanen goat breed (2.63 kg/day), while milk yield of Alpine breed was lower (2.08 kg/day). In the present study, the daily milk yield ranged from 1.148 in Anglo Nubian goats to 1.686 in Saanen and Alpine crossbreds. The milk yield of Czech White, Saanen and Anglo Nubian was lower than that reported by Bolacali and Kucuk (2012) but higher than estimated by Rojo-Rubio *et al.* (2015), where milk yield of Alpine goats was – 1.41/day kg, Saanen – 1.28 kg/day and Anglo Nubian – 1.18 kg/day.

Anglo Nubian goats showed significantly higher milk fat (0.50 %-0.74 % higher in Saanen and Anglo Nubian and Saanen and Alpine crossbreed) and protein (0.14 %-0.35 % higher in Saanen and Anglo Nubian and Saanen and Alpine crossbreeds) content compared to other breeds. The breed influence on milk lactose was significant and ranged from 3.81 % (Anglo Nubian breed) to 4.30 % (Saanen breed).

The mean values of fat, protein and lactose contents in the present study in a milk of investigated breeds were within the range of the estimates recorded for dairy goats by Mioč *et al.* (2008), where Alpine goats' fat content was 3.47%, Saanen – 3.25%; protein content of Alpine goats was 3.08%, Saanen – 3.25%; lactose content of Alpine goats was 4.54 %, Saanen – 4.46%. In the research conducted by Ferro *et al.* (2017), the milk fat, protein and lactose content was lower compared to the present study results.

Table 3: Investigated traits between genotypes of examined genes.

Gene	Genotype	Milk yield, kg	Fat, %	Protein, %	Lactose, %	Urea, mg/dl	SCC_log10
AGPAT6	CC[a]	1.267±0.101*[b]	3.444±0.176	2.923±0.099*[b]	4.121±0.104	37.864± 2.867***[c]	5.825±0.111*[b]
	CG[b]	1.613±0.149*[a;c]	3.313±0.120*[c]	3.322±0.062*[a]	4.426±0.039***[c]	30.107±2.620***[c]	5.876±0.112*[a;c]
	GG[c]	1.333±0.142*[b]	3.439±0.137*[b]	2.958±0.028*[b]	4.095±0.064***b	52.500± 3.293***[a;b]	5.990±0.142*[b]
STAT5	CC[a]	1.404±0.072	3.853±0.156	3.053±0.052	4.165±0.044	35.810±1.797	5.659±0.072*[b]
	CT[b]	1.484±0.166	3.514±0.232	2.857±0.138*[c]	4.031±0.021	36.667±3.973	5.968±0.196*[a]
	TT[c]	1.432±0.166	3.500±0.289	3.500±0.289*[b]	4.051±0.031	45.000±8.660	5.973±0.088*[b]
LPL	CC[a]	1.624±0.097***[b]; *[c]	3.751±0.168*[c]	2.986±.0760*[c]	4.066±0.037*[c]	38.947±2.398	5.540±0.087*[b];**[c]
	GC[b]	1.182±.0967***[a];*[c]	3.648±0.136*[c]	3.055±0.064*[c]	4.180±0.063*[c]	33.533±2.814	5.829±0.084*[a]
	GG[c]	1.503±0.059**b*[a]	3.867±0.109*[ab]	3.065±0.059*[ab]	4.023±0.048*[ab]	40.643±1.674	5.908±0.055***[a]

Differences of means between genotypes is significant at level: *P<0.05; **P<0.01; ***P<0.001

Table 4: Milk production and composition of different goat breeds.

Breed	Milk yield, kg	Fat, %	Protein, %	Lactose, %	Urea, mg/dl	SCC_log10
Czech White Shorthaired [a]	1.345±0.076***[d]; *[f]	3.553±0.094***[c;f]	2.968±0.048***[c]	4.203±0.038 *[c;e]	38.57±2.06 **[f]	5.895±0.085**[c]
Saanen [b]	1.348±0.048 ***[d;f]	3.501±0.091***[c;f]	3.020±0.057***[c]	4.303±0.036 **c	37.46±2.07 **[f]	5.940±0.060**[c];*[e]
Anglo Nubian [c]	1.148±0.106***[d];**[f]	5.208±0.210***[a;b;c;d]	3.467±0.122***[a;b;d;e; *f]	3.809±0.164 *[a;d]; **[b]; ***e	41.00±3.34	5.553±0.050**[a;d]; **b
Alpine [d]	1.624±0.109***[a;b;c];	3.811±0.204***[c;f]	3.088±0.059***[c]	4.149±0.027 *[c]	36.68±3.06 *[f]	5.937±0.091*[c; e]
Saanen and Alpine crossbreeds [e]	1.686±0.146*[a;b;c;d;f]	3.471±0.166***[c;f]	2.917±0.116***[c]	4.234±0.062 *[a;f; ***c]	35.07±4.36 *[f]	5.612±0.149 *[b;d]
Saanen and Anglo-Nubian crossbreeds [f]	1.649±0.131*[a];**[b;c]	4.705±0.199***[a;b;d;e]	3.228±0.092*[c]	4.086±0.028 *e	46.30±2.16 **[a;b];*[d;e]	5.733±0.115

Differences of means between breeds is significant at level: *P<0.05; **P<0.01; ***P<0.001

Table 5: Genetic equilibrium evaluation in goats according to individual gene polymorphism.

Gene	Observed heterozygosity Ho	Expected heterozygosity He	*P*-value
AGPAT6	0.436	0.479	< 0.05
STAT5	0.288	0.291	< 0.05
LPL	0.234	0.467	< 0.05

P-value was presented as a result of Pearson Chi-Square test.

The mean values of milk urea of different breeds of goats ranged from 35.07 mg/dl in Saanen and Alpine crossbreeds to 46.30 mg/dl Saanen and Anglo Nubian crossbreeds and were consistent with the results reported by Giaccone *et al.* (2007).

In the present research, SCC of Saanen goats was the highest and significant differences of SCC variations between breeds were estimated between Saanen and Anglo Nubian 6.97 %, P<0.01 and between Saanen and Alpine crossbreeds 5.85 %, P<0.05. Significant variation in SCC among breeds was noted by Csanadi *et al.* (2015) in the research with Saanen and Alpine x Saanen crossbred goats and in the research announced by Pleguezuelos *et al.* (2015) SCC was equal to 5.780.

Evaluating the Hardy-Weinberg equilibrium principle, the calculation of the observed and expected heterozygosity in the studied group of goat genes *AGPAT6* (P<0.05) and *LPL* (P<0.05) was found to be lower than expected, indicating a lack of heterozygosity; *STAT5* was near expected heterozygosity, but still lower than P<0.05 (Table 5).

He *et al.* (2011) reported *AGPAT6* significant differences with an observed heterozygosity higher than expected and it was in disagreement with the results of our research. Coizet *et al.* (2017) in the research with Bubalus Bubalis estimated that *STAT5* was not in HW equilibrium, with significantly different values for the observed and expected heterozygosity (P<0.05), where the observed heterozygosity was higher than expected, but no bibliographic references were found about goats. Crepaldi *et al.* (2013) reported LPL deviated significantly from the Hardy-Weinberg equilibrium, with an observed heterozygosity lower than expected and it was in agreement with the present study.

CONCLUSION

Examined *AGPAT6*, *STAT5* and *LPL* genes polymorphisms appear to be the valuable biomarkers of the goat selection process. Also, further research on larger samples of goats is needed to properly assess the effect of these genes, especially for those markers that show rare genotypes, which may offer useful indications for the development of gene assisted programs.

REFERENCES

Badaoui, B., Serradilla, J.M., Toma's, A., Urrutia, B., Ares, J.L., Carrizosa, J., Sa'nchez, A., Jordana, J., Amills, M. (2007). Goat acetyl-coenzyme A carboxylase α: Molecular characterization, polymorphism and association with milk traits. Journal of Dairy Science. 90: 1039-1043.

Bao, B., Zhang, C., Fan, X., Zhang, R., Gu, C., Lei, C., Chen, H. (2010). Association between polymorphism in STAT5A gene and milk production traits in Chinese Holstein cattle. Animal Science Papers and Reports. 28: 5-11.

Bionaz, M., Loor, J.J. (2008). ACSL1, AGPAT6, FABP3, LPIN1 and SLC27A6 are the most abundant isoforms in bovine mammary tissue and their expression is affected by stage of lactation. Journal of Nutrition. 138: 1019-24.

Bolacali, M. and Küçük, M. (2012). Fertility and milk production characteristics of Saanen goats raised in Muş region. Journal of the Faculty of Veterinary Medicine, Kafkas University. 18(3): 351-358.

Chilliard, Y.A., Ferlay, J., Rouel, J., Lamberet, G. (2003). A review of nutritional and physiological factors affecting goat milk lipid synthesis and lipolysis. Journal of Dairy Science. 86: 1751-1770.

Coizet, B., Frattini, S., Nicoloso, L., Iannuzzi, L., Coletta, A., Talenti, A., Minozzi, G., Pagnacco, G., Crepaldi, P. (2018). Poly--morphism of the STAT5A, MTNR1A and TNF-α genes and their effect on dairy production in Bubalus bubalis. Italian Journal of Animal Science. 17: 31-37. DOI: 10.1080/1828051X.2017.1335181.

Coleman, R. (2004). Enzymes of triacylglycerol synthesis and their regulation. Progress in Lipid Research. 43: 134-176.

Crepaldi, P., Nicoloso, L., Coizet, B., Milanesi, E. G., Pagnacco, P., Fresi, C., Dimauro, N., Macciotta, P.P. (2013). Associations of acetyl-coenzyme A carboxylase α, stearoyl -coenzyme A desaturase and lipoprotein lipase genes with dairy traits in Alpine goats. Journal of Dairy Science. 96: 1856-1864.

Csanadi, J., Fenyvessy, J., Bohata S. (2015). Somatic cell count of milk from different goat breeds. An International Scientific Journal of Sapientia Hungarian University of Transylvania, 8: 45-54.

Darcan, N.K. and Silanikove, N. (2018). The advantages of goats for future adaptation to climate change: a conceptual overvie. Small Ruminant Research. 163: 34-38.

Ferro, M.M., Tedeschi, L.O., Atzori, A.S. (2017). The comparison of the lactation and milk yield and composition of selected breeds of sheep and goats. Translational Animal Science. 1: 498-506.

Gautam, L., Waiz, H.A., Nagda, R.K. (2019). Significance of Environmental Influences on Average Daily Milk Traits of Sirohi Goats in Their Native Tract. Indian Journal of Animal Research. Online. DOI: 10.18805/ijar.B-3834.

Giaccone, P., Todaro, M., Scatassa, M.L. (2007). Factors associated with milk urea concentrations in Girgentana goats. Italian Journal of Animal Science. 6: 622-624.

Goetsch, A.L., Zeng, S.S., Gipson, T.A. (2011). Factors affecting goat milk production and quality. Small Ruminant Research. 101: 55-63.

He, C., Wang, C., Chang, Z.H., Guo, B.L., Li, R., Yue, X.P., Lan, X.Y., Chen. H., Lei, C.Z. (2011). AGPAT6 polymorphism and its association with milk traits of dairy goats. Genetics and Molecular Research. 10(4): 2747-2756.

Kendalla, P.E., Nielsena, P.P., Webstera, J.R., Verkerkb, G.A., Littlejohnc, R.P., Matthewsa, L.R. (2006). The effects of providing shade to lactating dairy cows in a temperate

climate. Livestock Science. 103(1-2): 148-157.

Ling, Y., Wang, K., Yin, J., Zhu, L., Zhang, X., Han, C., Ding, J. (2015). Molecular analyses for genetic polymorphisms of the LPL gene and their associations with intramuscular fat content in goats. Journal of Animal and Plant Sciences. 25(5): 1238-12442.

Maitra, A., Sharma, R., Ahlawat, S., Boranal, K., Tantia, M.S. (2016). Fecundity gene *SNPs* as informative markers for assessment of Indian goat genetic architecture. Indian Journal of Animal Research. 50: 349–356.

Merkel, M., Eckel, R. H., Goldberg, I. J. (2002). Lipoprotein lipase: genetics, lipid uptake and regulation. Journal of Lipid Research. 43: 1997-2006.

Mioč, B., Prpić, Z., Vnučec, I., Barać, Z., Sušić, V., Samaržija, D., Pavic, V. (2008). Factors affecting goat milk yield and composition. Mljekarstvo., 58(4): 305-313.

Peck, A.R., Witkiewicz, A.K., Liu, C., Klimowicz, A.C., Stringer, G.A., Pequignot, E., Freydin, B., Yang, N., Tran, T.H., Rosenberg, A., Hooke, J.A., Shriver, C.D., Rimm, D.L., Magliocco, A.M, Hyslop, T., Rui, H. (2011). Nuclear localization of STAT5a predicts response to antiestrogen therapy and prognosis of clinical breast cancer outcome. Cancer Research. 71: 6-24.

Pleguezuelos, F.J., De La Fuente, L.F., Gonzalo, C. (2015). Variation in Milk Yield, Contents and Incomes According to Somatic Cell Count in a Large Dairy Goat Population. Journal Advances in dairy Research. 3:145. DOI:10.4172/2329-888X.1000145.

Rojo-Rubio, R., Kholif, A.E., Salem, A.Z.M., Mendoza, G.D., Elghandour, M.M.M.Y., Vazquez-Armijo, J. F., Lee-Rangel, H. (2016). Lactation curves and body weight changes of Alpine, Saanen and Anglo-Nubian goats as well as pre-weaning growth of their kid. Journal of Applied Animal Research. 44: 331-337. DOI: 10.1080/09712119.2015.1031790.

Sandrucci, A., Bava, L., Tamburini, A., Gislon, G., Zucali, M. (2018). Management practices and milk quality in dairy goat farms in Northern Italy. Italian Journal of Animal Science. 18(1): 1-12. DOI: 10.1080/1828051X.2018.1466664.

Selvaggi, M., Dario, C., Normanno, G., Celano, G.V., Dario, M. (2009). Genetic polymorphism of STAT5A protein: relation--ships with 2 production traits and milk composition in Italian Brown cattle. Journal of Dairy Research. 76: 1-5.

Selvaggi, M., Ioanna, F., Pinto, F., Dario, C. (2015). Analysis of A Sequence Nucleotide Polymorphism of STAT5A Gene in Garganica Goat Breed. International Journal of Advanced Science Engineering Information Technology. 5: 323-325.

Svitáková, A., Rychtárová, J., Sztankóová, Z., Schmidová, J., Luboš, V. (2014). Polymorphism of LPL gene and its effect on milk production traits in Czech dairy goat. Conference: 34th International Society for Animal Genetics Conference, Xí´an China.

Vafaizadeh, V., Klemmt, P., Brendel, C., Weber, K., Doebele, C., Britt, K., Grez, M., Fehse, B., Desriviéres, S., Groner, B. (2010). Mammary epithelial reconstitution with gene-modified stem cells assigns roles to STAT5 in luminal alveolar cell fate decisions, differentiation, involution and mammary tumor formation. Stem Cell Research. 28: 928-938.

Wu, X., Jia, W., Zhang, J., Li, X., Pan, C., Chen, H., Dang, R., Lan, X. (2014). Determination of the novel genetic variants of goat STAT5A gene and their effects on body measurement traits in two Chinese native breeds. Small Ruminant Research. 121: 232-243.

Xie, H.Q., Sun, Y.Y., Pan, D.X., Yang, Y.Q., Jiao, R.G., Gong, Y., Luo, W.X., Zhang, Y.Y., Liu, R.Y. (2015). Association analysis between polymorphism of STAT5A gene and growth traits in Chinese Guizhou black goats. Pakistan Journal of Agricultural Sciences. 52(4): 1119-1123.

Zazharska, N., Boyko, O., Brygadyrenko, V. (2018): Influence of diet on the productivity and characteristics of goat milk. Indian Journal of Animal Research. 52(5): 711-717. DOI: 10.18805/ijar.v0iOF.6826

Zhang, S.Y., Xu, Y.M., Song, Y.C., Chen, F.X. (2012). Stat5: A versatile transcription factor. Chem Life Sciences. 32: 180-184.