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Correlation and regression analysis of *FA2H* and *ELOVL3* functional genes for cashmere fineness with production performance in Liaoning cashmere goat

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ABSTRACT

Liaoning cashmere goat (LCG) is characterized by the highest individual cashmere yield, but its cashmere fineness tends to be coarse. Therefore, our research primarily focuses on reducing cashmere fineness. Through lipidomics screening and identification, we identified the crucial functional genes *FA2H* and *ELOVL3* associated with cashmere fineness. Subsequently, using PCR-seq, we conducted gene typing and SNP analysis on the experimental population DNA, In the *FA2H* gene, a SNP locus T42443G was detected in LCG buck, with the TT genotype showing advantageous traits in cashmere fineness, meat quality, and body size, while the TG genotype demonstrated advantages in slaughter performance,In LCG doe, the TG genotype shows advantageous traits in cashmere fineness, milk production, and meat quality, while the TT genotype exhibits advantages in slaughter performance, lambing, and body size. In the *ELOVL3* gene, a SNP locus C2133A was identified in LCG buck, where the CC genotype was advantageous for cashmere fineness, Only CA genotype was found in slaughter and meat quality. Additionally, and the CA genotype showed superiority in body size. On LCG doe, The CC genotype was the advantageous genotype in terms of cashmere fineness, milk production, slaughter performance, and meat quality. The CA genotype was the advantageous genotype in terms of lambing and body size. The dominant genotypes identified to influence both doe cashmere fineness and slaughter performance were TT and CC. The identified dominant haplotype combination for cashmere production performance in LCG was CCTG. The dominant haplotype combination for doe slaughter performance was the CCTT haplotype combination. The dominant haplotype combination for buck slaughter performance was the CATG haplotype combination. Therefore, the TT genotype of the *FA2H* gene and the CC genotype of the *ELOVL3* gene in LCG buck, and the TG genotype of the *FA2H* gene and the CC genotype of the *ELOVL3* gene in doe can be used as molecular markers for assisted selection of cashmere fineness. CCTG haplotype combination was the superior haplotype combinations for cashmere production performance. To provide a theoretical basis for the breeding and expansion of fine-fiber type new strains of LCG.

1. Introduction

The cashmere goat is a valuable biological resource that plays a crucial role in Chinese animal husbandry,[1,2,3,4] Thus, combined trials with emphasis on administration and genetic progress to improve animal outputs are of decisive significance,[5,6,7,8] Economical and biological efficiency of small ruminant production enterprises generally improves by increasing productivity and reproductive performance of these animals.[9,10,11,12,13] The cashmere goat is a valuable biological resource that plays a crucial role in Chinese animal husbandry.[14] China has over 20 native breeds of cashmere goats, which account for 75 % of the world's cashmere production. Among these breeds, LCG is renowned for its excellent cashmere yield.[15] However, the growth of cashmere is influenced by many factors such as climate, breed, gender, age, body region, genetics, and nutrient absorption.[16] In recent years, there has been increasing attention to the quality of cashmere products, with

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cashmere fineness being one of the key factors affecting cashmere quality.[17] The LCG has a high cashmere yield, but the cashmere is moderately fine, with the Ministry of Agriculture requiring a fineness of 16 μm or less, and there is still room for decline.Therefore, methods need to be found to reduce its fiber diameter. Single nucleotide polymorphisms (SNPs) are widely used in animal genetic breeding research due to their numerous, widespread distribution, strong genetic stability, and ease of large-scale rapid detection.[18] A number of genes related to cashmere fineness have been identified in the current study. The *KIF-1* gene has been found to be associated with cashmere fineness in Xinjiang goats,[19] Fu et al.,[20] identified through high-throughput RNA sequencing that *KR*T26 and other genes are involved in hair follicle morphogenesis and skin development, potentially regulating cashmere fineness. On the basis of using expression profiling microarrays to detect candidate genes related to fine wool fibre diameter, Tian [21] established a real-time fluorescence quantitative PCR method and found that genes such as *TXNIP* and *TFDP1* were related to cashmere fineness. Based on previous studies, this article found that during the growth and development of cashmere, in addition to the role played by the dermis of the skin, from September to December, the hair follicles extend into the subcutaneous adipose tissue to absorb nutrients. Therefore, through phenotypic omics screening of cashmere fineness differences, two genes, *ELOVL3* and *FA2H*, were identified as significantly differentially expressed and potentially involved in regulating cashmere fineness.

The *ELOVL3* gene is a member of the fatty acid elongase family.[22] Anders Jacobson's team first discovered the very long-chain fatty acid elongase 3 (*ELOVL3*) in brown adipose tissue (BAT) exposed to cold temperatures.[23] *ELOVL3* is primarily expressed in the liver, brown adipose tissue, white adipose tissue, skin, and triglyceride-rich glands.[24] Rolf Westerberg discovered that *ELOVL3* is involved in the formation of specific neutral lipids essential for skin function. Mice lacking *ELOVL3* exhibit hair loss, sebaceous gland hyperplasia, disrupted hair lipid content, and notably high levels of eicosenoic acid.[25] Studies in some mammals have found that the *ELOVL3* gene appears to play a role in the physiological processes of hair formation, follicle growth and development.[26] Yu [27] conducted transcriptome sequencing on the shoulder blades of LCG and identified the *FA2H* gene as potentially influencing the fineness of cashmere. Zhou [28] used transcriptome sequencing to discover differential expression of the *ELOVL3* gene in the skin tissues of Shanbei White Cashmere goats during their growth, quiescent, and regression periods. Wu [29] research on Nan jiang cashmere goats found that overexpression of the *ELOVL3* gene can promote the growth of secondary hair follicle cells, further demonstrating the regulatory role of the *ELOVL3* gene in cashmere goat traits.

FA2H is one of the metabolic enzymes for fatty acids. Research on this gene primarily focuses on human diseases such as cancer,[30] hereditary spastic paraplegia,[31] and others. Researchers have also found that this gene plays a crucial role in hair follicle growth. Wang et al. conducted weighted gene co-expression network analysis (WGCNA) on Inner mongolia cashmere goats and identified 12 candidate genes, including *FA2H*.[32] Wu et al.,[33] utilized transcriptome sequencing technology to study Nan jiang cashmere goats, identifying 7 candidate genes including *FA2H*. They found that overexpression of *FA2H* promotes proliferation of secondary hair follicle cells in cashmere goats.

This study was first carried out on LCG. The aim of this study is to investigate the effects of SNPs in the *ELOVL3* and *FA2H* genes of LCG on their cashmere production performance, body size performance, milk production performance, lambing, slaughter performance, and meat quality performance. Through genetic diversity analysis and correlation analysis of six traits, we aim to identify the genotypes and haplotype combinations that affect these six traits.This will facilitate the breeding and improvement of LCG varieties, advance genetic breeding efforts for cashmere goats, and provide theoretical support for cultivating superior cashmere goats. Compared to other relevant studies, our study is more comprehensive, And for the first time, we investigated the effects of *FA2H* and *ELOVL3* genes on the cashmere production performance of LCG.

2. Materials and methods

2.1. Experimental animals

At the Liaoning cashmere goat breeding center in Liaoning Province, China, 1,181 healthy LCG were selected, all of which were fed under consistent conditions. All animal handling procedures and protocols used in this study were approved in accordance with the guidelines of the Laboratory Animal Management Committee. (Animal Welfare Ethics Certificate Number: 2024.05.13), Blood samples for DNA extraction were collected under the guidance of a qualified veterinarian, obtaining 1 mL of blood from the jugular vein of each goat. After collection, the samples were placed into blood collection tubes containing EDTA and stored at −20°C.

2.2. Production performance phenotype data

The performance data of cashmere is measured by a portable all-weather cashmere fineness and length rapid testing machine. The cashmere is placed into the plate that comes with the analyser, the plate is placed into the analyser, after which the cashmere data is able to be obtained by clicking on Start Test.

The body size data is obtained from the intelligent body measurement system. The goat is driven into the instrument and its body measurements are automatically detected as it passes forward.

The lambing data is obtained through counting method. Counts were taken at lambing for each doe and summarised in the table.

The milk production data is obtained using a milk component analyzer. Prepare two sample bottles and fill them with the same goat's milk. Place one bottle with goat's milk under the test port of the milk analyzer, place the PH sensor in the other bottle with goat's milk, click on the test and wait for the test result.

Slaughter data is obtained according to the Operation Regulations for Slaughtering Poultry and Livestock (GB/T 43562–2023). All the data are obtained by weighing and calculating.

The quality of meat products is determined according to the Technical Specification for Meat Quality Determination (T/CAAA 102–2023).

2.3. DNA extraction

Take 200 μL of blood from the anticoagulant tube and transfer it to a centrifuge tube. Add 20 μL of Proteinase K and mix well. Then add Buffer DL, shake vigorously, and incubate at 56 °C in a water bath for 10 min. Next, add 200 μL of anhydrous ethanol to the centrifuge tube and mix well. Transfer the liquid to a DNA adsorption column and let it stand for two minutes. Centrifuge at 10,000 rpm at room temperature for 1 min and discard the waste liquid in the collection tube. Add 500 μL of GW Solution to the adsorption column, centrifuge at 10, 000 rpm for 30 s, and discard the waste liquid. Add 700 μL of Wash Solution to the adsorption column, centrifuge at 10, 000 rpm for 30 s, and discard the waste liquid. Repeat this step twice. Then centrifuge at 12,000 rpm at room temperature for 2 min to remove any remaining liquid. Remove the adsorption column and place it in a new centrifuge tube. Add 50 μL of CE Buffer, let it stand for 3 min, and centrifuge at 12,000 rpm at room temperature for 2 min. Collect the DNA solution and measure the sample's OD value using UV spectrophotometry. Store the qualified samples at −20 °C.

2.4. Primer design

The sequences of the *FA2H* gene (Reference number: NC_030825.1) and the *ELOVL3* gene (Reference number: NC_030833.1) were obtained from the NCBI database. Specific primers were designed using Primer

Premier 5 software [34] (Table 1).

2.5. PCR amplification

The PCR reaction system has a total volume of 50 μL, which includes 25 μL of 2x SanTaq PCR Mix solution, 1 μL of DNA template, 2 μL each of upstream and downstream primers, and 20 μL of ddH_2O. Add these reagents to the PCR tube, mix thoroughly, and centrifuge. Perform the amplification in the PCR machine according to the PCR reaction conditions.The reaction conditions were pre-denaturation at 94℃ for 5 min, denaturation at 94℃ for 30 s, adjusting the temperature to 49.8℃-52.1℃ for annealing for 30 s, extension at 72℃ for 30 s, and finally keeping the extension at 72℃ for 10 min.Then electrophoresis was conducted at 130 V and 180 W for 20 min.After electrophoresis, observe whether the band of the electrophoresis result contains the target fragment (Fig. 1). If it is present, send the sample to Shanghai Biotechnology Co., Ltd. for sequencing.

2.6. Statistical analyses

Calculate genotype and allele frequencies, polymorphic information content (PIC), effective number of alleles (Ne), and heterozygosity (He). Perform single-factor analysis using SPSS software for the *FA2H* and *ELOVL3* genes in relation to six traits of LCG. The integrity of the animal model was analyzed using Yijkl = μ + hi + pj + sk + ml + eijkl, Yijkl = observe value; μ = overall mean; hi = the effect of genotype or combined haplotype; pj = effect of season and farm; sk = effect of year; ml = effect of sire descent and eijkl = random error. Use Duncan's method for multiple comparisons. A $P > 0.05$ indicates no significant difference, <0.05 indicates a significant difference (marked with lowercase letters), and < 0.01 indicates a highly significant difference (marked with uppercase letters). Results should be presented as 'mean ± standard error.

3. Results

3.1. SNP locus sequencing map

We compared the results and gene sequences of the *FA2H* and *ELOVL3* genes. Using Chromas 2 and DNAMAN software, comparative analysis revealed one SNP (T42443G) was detected in the *FA2H* gene (Fig. 2) and one SNP (C2133A) was detected in the *ELOVL3* gene (Fig. 3).

3.2. Genetic diversity of the FA2H and ELOVL3 genes

The genotype and allele frequencies of SNP loci in the *FA2H* and *ELOVL3* genes in LCG are presented in Table 2**.** Genes with frequencies greater than 0.5 are considered dominant. The polymorphism information content (PIC) values for the two loci range from 0.25 to 0.5, indicating moderate polymorphism. This suggests a significant genetic variation in these two genes in LCG, which could lead to substantial genetic progress.

3.3. Gene substitution effect analysis

The negative additive effect value at the T42443G locus of *FA2H* gene on LCG indicates that the substitution of the T42443G locus by T into G can improve the production performance, the positive additive effect value at the C2133A locus of *ELOVL3* gene on LCG indicates that the substitution of the C2133A locus by C into A can reduce the production performance (Table 3).

3.4. Analysis of the relationship between SNPs and cashmere production performance

At the T42443G locus in buck the TT genotypes was highly significantly better than the TG genotypes in number of curls, significantly better than the TG genotypes in net cashmere rate, and the TT genotypes was also better in cashmere fineness. The CC genotypes was highly significantly better than the CA genotypes at the C2133A locus in terms of net cashmere rate, and the CA genotypes was highly significantly better than the CC genotypes in terms of cashmere yield. CC genotype was better in cashmere fineness.

At the T42443G locus in doe the TT genotypes was highly significantly superior to the TG genotypes in cashmere yield and significantly superior to the TG genotypes in cashmere length, and the TG genotypes was highly significantly superior to the TT genotypes in number of curls and net cashmere rate. The TT genotypes was significantly better than the TG genotypes in terms of cashmere fineness. At the C2133A locus, the CC genotype shows highly significantly superior net cashmere rate compared to the CA genotype, while individuals with the CA genotype exhibit significantly better cashmere fineness and number of curls than those with the CC genotype (Table 4).

3.5. Analysis of the relationship between SNPs and milk production performance

The TG genotype at locus T42443G in LCG doe was highly significantly superior to the TT genotype at Fat, N, Cond. and Cru.Prot.The CC genotype was highly significantly superior to the CA genotype at the C2133A locus of the *ELOVL3* gene in terms of Fat, Urea, and N (Table 5).

3.6. Analysis of the relationship between SNPs and slaughtering performance

At the T42443G locus in LCG buck, the TG genotype shows highly significantly superior traits in live weight before slaughter, carcass weight, net meat weight, slaughter rate, net meat rate, and GR compared to the TT genotype. At the C2133A locus, only the CA genotype was found.

At the T42443G locus in LCG doe, the TT genotype showshighly significantly superior traits in net meat weight and slaughter rate compared to the TG genotype. It was highly significantly superior to TG genotype in terms of net meat rate, carcass net meat rate. At the C2133A locus the CC genotype was significantly superior to the CA genotype in terms of carcass weight, net meat weight, slaughter rate, and net meat rate, It shows highly significant in eye muscle area (EMA) compared to the CA genotype (Table 6).

3.7. Analysis of the relationship between SNPs and meat quality performance

TT genotype was extremely significant to TG genotype in meat color b, dry matter and cooked meat rate at T42443G locus of *FA2H* gene of LCG buck. TG genotype was extremely significant to TT genotype in fat content. Only CA genotype was found at *ELOVL3* gene.

TT genotype was significantly superior to TG genotype in meat color L and dry matter at T42443G locus of *FA2H* gene in LCG doe. TG genotype was extremely significant to TT genotype in meat color A, PH,

Table 1
Primer design of *FA2H* and *ELOVL3* genes.

Gene	Sense primer (Forward)	Anti-sense primer (Reverse)	TM(℃)F/R	Fragment size	Regions
FA2H	5′GTTGGGATGAAGGGTTAG3′	5′CAGGAGGAGGAAAGAAGA3′	49.8	722 bp	42249–42971
ELOVL3	5′ACCCCTATCCTGCCACCTGT3′	5′GTGTTGGGACCACCCTCTGA3′	52.1	664 bp	1681–2325

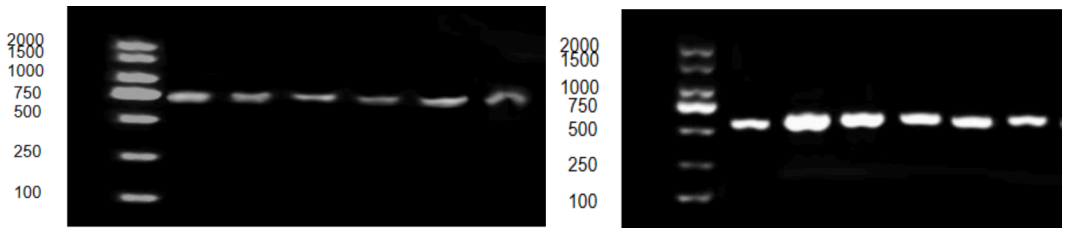

Fig. 1. Electrophoretic image FA2H (left), ELOVL3 (right).

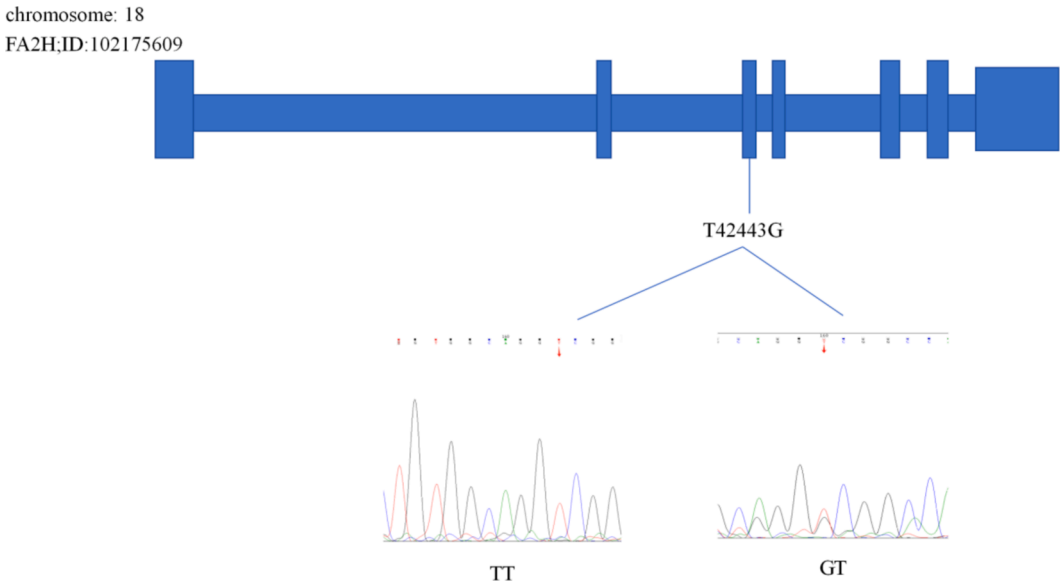

Fig. 2. The T42443G locus of the *FA2H* gene.

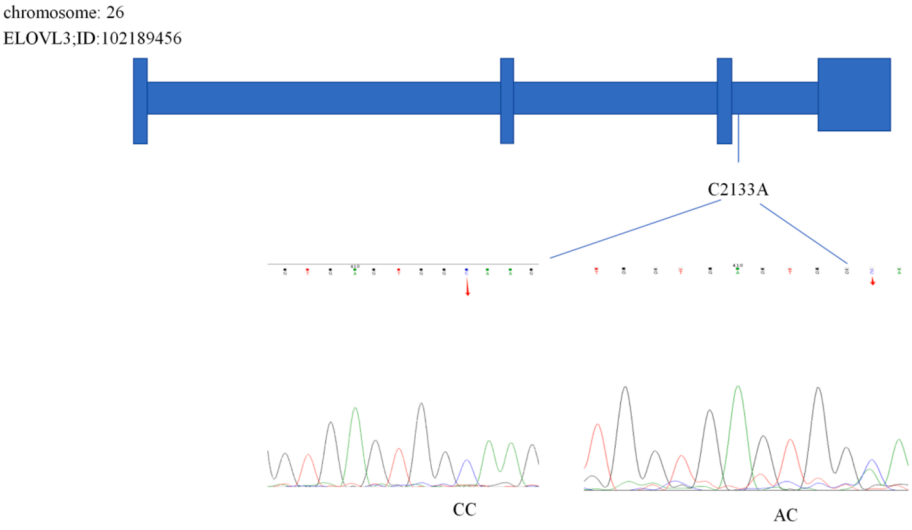

Fig. 3. The C2133A locus of the *ELOVL3* gene.

protein content and fat content. CC genotype was extremely significant to CA genotype in meat color a, meat color b, fat content, cooked meat rate and shear force at C2133A locus of *ELOVL3* gene (Table 7).

3.8. Analysis of the relationship between SNPs and lambing performance

At the T42443G locus in LCG doe, the TT genotype shows superiority in lambing compared to the TG genotype. At the C2133A locus, the CA genotype shows superiority in lambing compared to the CC genotype (Table 8).

3.9. Analysis of the relationship between SNPs and body size performance

At the T42443G locus in LCG buck, the TG genotype shows extremely significantly superior traits in sacral height compared to the TT genotype, The TT genotype shows significantly superior traits in body length

Table 2
Genetic diversity analysish of the *FA2H* and *ELOVL3* genes in LCG.

Name	loci	Genotype Frequency			Allelic Frequencies		PIC	He	Ne	χ^2	P
		MM	Mm	mm	M	m					
buck	T42443G	0.43	0.57	0	0.72	0.28	0.32	0.41	1.68	3.57	0.06
doe	T42443G	0.37	0.63	0	0.69	0.31	0.34	0.43	1.76	16.36	5.24458E-05
buck	C2133A	0.08	0.92	0	0.54	0.46	0.37	0.50	1.99	18.14	2.05105E-05
doe	C2133A	0.24	0.76	0	0.62	0.38	0.36	0.47	1.89	30.30	3.70735E-08

Table 3
Gene substitution effect analysis.

Name	Loci	Dominant effect	Additive effect	Average effect of u gene	Average effect of U gene	The average effect of u instead of U
		d	a	a1	a2	a
buck	T42443G	8	−5	−1.09	0.43	−1.52
doe	T42443G	34.5	−14.5	−1.15	0.53	−1.67
buck	C2133A	22	−1	0.41	−0.35	0.76
doe	C2133A	52	−10	1.67	−1.01	2.68

Table 4
The cashmere production performance related to the *FA2H* and *ELOVL3* genes in LCG.

Name	Loci	Genotype	Quantities	Cashmere yield (g)	Cashmere fineness (μm)	Cashmere length (cm)	number of curls	Short cashmere rate (%)	Net cashmere rate (%)
buck	T42443G	TT	18	2000.00 ± 94.11	16.55 ± 0.26	9.73 ± 0.31	8.83 ± 0.19^{aA}	19.91 ± 3.15	78.20 ± 2.30^{a}
buck	T42443G	TG	26	1984.62 ± 60.56	16.80 ± 0.22	9.16 ± 0.52	5.29 ± 0.84^{bB}	16.92 ± 3.67	70.30 ± 2.72^{b}
buck	C2133A	CC	4	2025.00 ± 101.04	16.44±0.32	8.31 ± 1.40	4.10 ± 2.37^{ab}	26.97 ± 1.32^{a}	76.76 ± 0.22
buck	C2133A	CA	46	1904.35 ± 52.24	16.48 ± 0.16	9.44 ± 0.36	7.08 ± 0.57^{a}	17.35 ± 2.60^{ab}	76.32 ± 1.86
doe	T42443G	TT	261	1700.00 ± 20.57^{b}	16.95 ± 0.07^{a}	10.39 ± 0.17	5.71 ± 0.23^{b}	16.66 ± 0.79^{b}	70.57 ± 0.83^{bB}
doe	T42443G	TG	441	1836.73 ± 15.02^{a}	16.41 ± 0.06^{b}	9.55 ± 0.15	7.16 ± 0.19^{a}	18.01 ± 0.73^{a}	78.00 ± 0.69^{aA}
doe	C2133A	CC	180	1807.50 ± 26.98	16.32 ± 0.11^{b}	9.44 ± 0.236	8.69 ± 0.19^{aA}	15.32 ± 1.11	78.58 ± 1.13^{a}
doe	C2133A	CA	558	1770.97 ± 12.86	16.82 ± 0.05^{a}	9.96 ± 0.132	6.13 ± 0.17^{bB}	16.89 ± 0.59	72.44 ± 0.64^{b}

Table 5
Analysis of the milk production performance of genes polymorphic loci.

Name	Loci	Genotype	Quantities	Fat	Cru.Prot	Lactose	Urea	N	SnF	TS	Cond.	H.Index
doe	T42443G	TT	128	7.22 ± 0.22	4.51 ± 0.03^{bB}	5.29 ± 0.02^{aA}	37.50 ± 0.26^{bB}	17.49 ± 0.12^{bB}	10.30 ± 0.04^{b}	17.88 ± 0.24	738.70 ± 5.84^{bB}	0.48 ± 0.01
doe	T42443G	TG	184	7.57 ± 0.23	5.29 ± 0.14^{aA}	5.02 ± 0.04^{bB}	41.34 ± 0.44^{aA}	19.29 ± 0.20^{aA}	10.92 ± 0.13^{a}	18.88 ± 0.25	784.57 ± 4.96^{aA}	0.49 ± 0.01
doe	C2133A	CC	84	7.96 ± 0.27^{aA}	5.31 ± 0.17	4.95 ± 0.06	42.51 ± 0.59^{aA}	19.84 ± 0.28^{aA}	10.85 ± 0.14	19.19 ± 0.33	789.90 ± 7.33	0.50 ± 0.01
doe	C2133A	CA	234	7.07 ± 0.18^{bB}	5.32 ± 0.18	5.09 ± 0.05	39.83 ± 0.57^{bB}	18.58 ± 0.26^{bB}	11.02 ± 0.18	18.48 ± 0.24	775.14 ± 7.50	0.47 ± 0.01

and chest depth compared to the TG genotype. At the C2133A locus, the CA genotype shows significantly superior traits in chest width and chest circumference compared to the CC genotype.

At the T42443G locus in LCG doe, the TT genotype shows significantly superior traits in sacral height and body length compared to the TG genotype. At the C2133A locus, the CA genotype shows extremely significantly superior traits in body length and chest depth compared to the CC genotype **(**Table 9**)**.

3.10. Analysis of the correlation between cashmere fineness and cashmere production performance in LCG

From Table 10, The length and net cashmere rate of doe was highly significantly correlated with cashmere fineness, cashmere yield, number of curls and short cashmere rate were significantly correlated with cashmere fineness, cashmere yield and net cashmere rate of buck was highly significantly correlated with cashmere fineness **(**Table 10**)**.

3.11. Path analysis results of fineness of LCG cashmere and cashmere production performance

From Table 11, it can be seen that the Net cashmere rate of LCG doe has the greatest direct effect on cashmere fineness (−0.905) followed by cashmere length (0.06), cashmere yield (0.036), number of curls (−0.028) and short cashmere rate (0.011), The maximum indirect effect of cashmere length on cashmere fineness is 0.262, followed by short cashmere rate (−0.248), cashmere yield (0.241),number of curls (−0.219) and net cashmere rate (−0.031). The direct effect of net

Table 6
Analysis of the Slaughtering performance of genes polymorphic loci.

Name	Loci	Genotype	Quantities	Live weight before slaughter (kg)	Carcass weight (kg)	Net meat weight (kg)	Slaughter rate (%)	Net meat rate (%)	Carcass net meat rate(%)	EMA (cm^2)	GR(mm)	BFT (mm)
buck	T42443G	TT	15	45.02 ± 0.67^{bB}	22.48 ± 0.53^{bB}	17.52 ± 0.49^{bB}	49.95 ± 0.99^{bB}	38.90 ± 0.91^{bB}	77.82 ± 0.57	23.40 ± 1.53	4.73 ± 0.44^{bB}	1.62 ± 0.12
buck	T42443G	TG	12	49.75 ± 2.13^{aA}	26.20 ± 1.16^{aA}	20.63 ± 1.07^{aA}	52.65 ± 0.35^{aA}	41.30 ± 0.51^{aA}	78.42 ± 0.68	21.24 ± 0.51	7.73 ± 0.33^{aA}	1.92 ± 0.27
buck	C2133A	CA	26	46.30 ± 0.94	23.82 ± 0.64	18.60 ± 0.62	51.37 ± 0.66	40.01 ± 0.70	77.80 ± 0.59	22.41 ± 0.87	6.13 ± 0.38	2.09 ± 0.19
doe	T42443G	TT	42	48.94 ± 1.03	25.86 ± 0.67	21.59 ± 0.58^{a}	52.68 ± 0.43^{a}	43.94 ± 0.37^{aA}	83.40 ± 0.24^{aA}	20.45 ± 0.46	7.73 ± 0.27	2.89 ± 0.14
doe	T42443G	TG	18	43.30 ± 1.04	21.37 ± 0.46	17.07 ± 0.39^{b}	49.40 ± 0.17^{b}	39.46 ± 0.32^{bB}	79.86 ± 0.45^{bB}	19.07 ± 1.08	8.86 ± 0.46	2.98 ± 0.16
doe	C2133A	CC	5	55.00 ± 1.23	30.10 ± 0.78^{a}	25.40 ± 0.53^{a}	54.73 ± 0.76^{a}	46.18 ± 0.46^{a}	84.39 ± 0.31	26.95 ± 0.33^{aA}	9.37 ± 0.00	2.53 ± 0.00
doe	C2133A	CA	55	47.66 ± 0.83	24.11 ± 0.49^{b}	19.79 ± 0.44^{b}	50.58 ± 0.41^{b}	41.48 ± 0.41^{b}	81.97 ± 0.29	19.86 ± 0.29^{bB}	8.09 ± 0.25	2.81 ± 0.13

Table 7
Analysis of the meat quality performance of genes polymorphic loci.

Name	Loci	Genotype	Quantities	Meat color			pH	Dry matter (%)	Protein content (%)	Fat content (%)	Drip loss (%)	Cooked meat rate (%)	Shear force(N)
				L	a	b							
buck	T42443G	TT	15	29.36 ± 0.23	14.86 ± 0.50	1.69 ± 0.03^{aA}	6.01 ± 0.02	26.72 ± 0.44^{aA}	21.66 ± 0.15	1.77 ± 0.16^{bB}	1.58 ± 0.07	67.06 ± 0.78^{aA}	73.80 ± 1.86
buck	T42443G	TG	12	29.60 ± 0.66	15.03 ± 0.59	1.56 ± 0.02^{bB}	6.05 ± 0.03	25.10 ± 0.21^{bB}	21.35 ± 0.25	2.39 ± 0.23^{aA}	1.65 ± 0.03	65.26 ± 0.20^{bB}	76.21 ± 2.25
buck	C2133A	CA	26	29.24 ± 0.32	14.94 ± 0.35	1.71 ± 0.07	6.06 ± 0.03	25.88 ± 0.30	21.39 ± 0.20	1.91 ± 0.14	1.65 ± 0.04	66.15 ± 0.75	75.61 ± 1.36
doe	T42443G	TT	42	30.69 ± 0.35^{a}	13.95 ± 0.18^{bB}	1.89 ± 0.11	5.95 ± 0.01bB	28.37 ± 0.66^{a}	20.30 ± 0.20bB	2.07 ± 0.13^{bB}	1.81 ± 0.04	67.99 ± 0.96	69.26 ± 1.87
doe	T42443G	TG	18	29.51 ± 0.25^{b}	15.03 ± 0.44^{aA}	2.00 ± 0.13	6.03 ± 0.02aA	26.29 ± 0.24^{b}	21.44 ± 0.08aA	2.79 ± 0.22^{aA}	1.85 ± 0.07	69.92 ± 0.24	69.83 ± 2.04
doe	C2133A	CC	5	31.17 ± 0.31	16.39 ± 0.00^{aA}	3.03 ± 0.02^{aA}	5.92 ± 0.01	24.43 ± 0.20^{bB}	20.71 ± 0.12	3.29 ± 0.11^{aA}	1.84 ± 0.03	77.99 ± 0.68^{aA}	86.87 ± 1.63^{aA}
doe	C2133A	CA	55	29.74 ± 0.30	14.13 ± 0.18^{bB}	1.80 ± 0.06^{bB}	5.96 ± 0.02	28.07 ± 0.47^{aA}	20.89 ± 0.18	2.28 ± 0.14^{bB}	1.78 ± 0.05	68.37 ± 0.60^{bB}	69.58 ± 1.43^{bB}

Table 8
Analysis of the lambing performance of genes polymorphic loci.

Name	Loci	Genotype	Quantities	Number of kids
doe	T42443G	TT	108	1.41 ± 0.5
doe	T42443G	TG	180	1.29 ± 0.04
doe	C2133A	CC	72	1.17 ± 0.04
doe	C2133A	CA	220	1.40 ± 0.03

cashmere rate on cashmere fineness is highest for LCG buck (−0.770), followed by cashmere yield (0.321). The largest indirect effect is cashmere yield (0.293), followed by net cashmere rate (−0.122) (Table 11).

3.12. Results of stepwise multiple regression analysis of cashmere fineness and cashmere production performance in LCG

Table 12 shows that the optimal regression equation for doe is

Table 9
Analysis of the body size traits of genes polymorphic loci.

Name	Loci	Genotype	Quantities	Body height (cm)	sacral height (cm)	Body oblique (cm)	Chest depth (cm)	Chest width (cm)	Waist width (cm)	Chest circumference (cm)	tube circumference	Waist height (cm)
buck	T42443G	TT	28	74.66 ± 0.69	71.71 ± 0.72^{bB}	87.75 ± 0.92^{a}	36.14 ± 0.54^{a}	26.79 ± 0.92	21.43 ± 0.87	105.26 ± 1.00	12.57 ± 0.24	69.71 ± 0.73
buck	T42443G	TG	22	75.41 ± 0.78	74.05 ± 0.79^{aA}	81.41 ± 3.97^{b}	33.47 ± 1.72^{b}	26.98 ± 1.09	20.55 ± 0.63	105.71 ± 0.85	12.41 ± 0.20	69.18 ± 0.89
buck	C2133A	CC	20	74.90 ± 0.85	72.30 ± 1.04	87.10 ± 1.18	35.77 ± 0.52	25.70 ± 0.76^{b}	21.78 ± 0.75	103.27 ± 1.02^{b}	12.80 ± 0.31	68.00 ± 1.15
buck	C2133A	CA	30	75.82 ± 0.63	73.13 ± 0.53	88.33 ± 0.98	33.77 ± 1.42	28.53 ± 1.13^{a}	20.57 ± 0.59	105.96 ± 0.85^{a}	12.73 ± 0.18	70.43 ± 0.62
doe	T42443G	TT	282	64.05 ± 0.19	64.86 ± 0.19^{a}	79.99 ± 0.41^{a}	32.53 ± 0.13	23.54 ± 0.23	22.58 ± 0.27	99.29 ± 0.52	9.56 ± 0.06	63.79 ± 0.27
doe	T42443G	TG	444	63.87 ± 0.17	66.05 ± 0.15^{b}	77.67 ± 0.29^{b}	32.30 ± 0.14	23.47 ± 0.20	22.40 ± 0.23	99.51 ± 0.42	9.54 ± 0.05	63.80 ± 0.23
doe	C2133A	CC	210	63.50 ± 0.25	66.22 ± 0.25	76.07 ± 0.46^{bB}	31.82 ± 0.19^{bB}	23.67 ± 0.28	22.56 ± 0.34	100.95 ± 0.68	9.40 ± 0.06	64.64 ± 0.34
doe	C2133A	CA	594	64.27 ± 0.15	65.72 ± 0.14	78.86 ± 0.25^{aA}	32.90 ± 0.11^{aA}	23.79 ± 0.16	23.18 ± 0.19	99.64 ± 0.38	9.55 ± 0.04	64.03 ± 0.20

Table 10
Correlation coefficients between fineness of LCG and cashmere production performance.

buck doe	Cashmere fineness (μm)	Cashmere yield (g)	Cashmere length (cm)	number of curls	Short cashmere rate (%)	Net cashmere rate (%)
Cashmere fineness (μm)	–	0.278*	0.322**	−0.246*	−0.238*	−0.936**
Cashmere yield (g)	0.541**	–	0.055	−0.049	−0.054	−0.263*
Cashmere length (cm)	0.084	−0.266	–	0.078	−0.309**	−0.293**
number of curls	−0.033	0.174	0.345*	–	−0.146	0.243*
Short cashmere rate (%)	−0.257	0.035	−0.256	−0.206	–	0.256*
Net cashmere rate (%)	−0.866**	−0.38**	0.02	0.096	0.389**	–

** indicates highly significant correlation ($P < 0.01$), while.
* indicates significant correlation ($P < 0.05$).

Table 11
Path coefficients of cashmere production Performance on fineness of LCG.

Sex	Independent variable	Correlation coefficient	Direct action	Indirect effect				
				Cashmere yield	Cashmere length	number of curls	Short cashmere rate	Net cashmere rate
doe	Cashmere yield	0.278	0.036		0.003	0.001	−0.001	0.238
	Cashmere length	0.322	0.06	0.002		−0.002	−0.003	0.265
	Number of curls	−0.246	−0.028	−0.002	0.005		−0.002	−0.220
	Short cashmere rate	−0.238	0.011	−0.002	−0.019	0.004		−0.231
	Net cashmere rate	−0.936	−0.905	−0.009	−0.018	−0.007	0.003	
buck	Cashmere yield	0.541	0.321					0.293
	Net cashmere rate	−0.866	−0.770	−0.122				

Table 12
Results of stepwise multiple regression analysis of cashmere production performance on cashmere fineness in LCG.

Sex	Model	R^2	Adjusted R-squared	Standard error of estimate	F	P
doe	cashmere fineness = -0.08net cashmere rate + 22.586	0.876	0.876	0.459	5199.056	0.000
	cashmere fineness = -0.078net cashmere rate + 0.021cashmere length + 22.280	0.878	0.878	0.454	2655.831	0.000
	cashmere fineness = -0.078net cashmere rate + 0.022cashmere length + 0.0001cashmere yield + 21.959	0.880	0.879	0.453	1787.580	0.000
	cashmere fineness = -0.077net cashmere rate + 0.024cashmere length + 0.0001cashmere yield-0.01number of curls + 21.946	0.880	0.880	0.451	1349.376	0.000
buck	cashmere fineness = -0.077net cashmere rate + 22.374	0.750	0.745	0.543	144.052	0.000[b]
	cashmere fineness = -0.069net cashmere rate + 0.001cashmere yield + 20.256	0.803	0.794	0.488	95.494	0.000[c]
	cashmere fineness = -0.067net cashmere rate + 0.001cashmere yield + 0.016 cashmere length + 19.073	0.832	0.821	0.455	76.117	0.000[d]

cashmere fineness = -0.077 net cashmere rate + 0.024 cashmere length + 0.0001 cashmere yield − 0.01 number of curls + 21.946.The optimal regression equation for buck is: fineness = -0.067 net cashmere rate + 0.001 cashmere yield + 0.016 cashmere length + 19.073. The multiple regression equations have final determination coefficients (R2) of 0.880 and 0.832, respectively. It means that the cashmere length, net cashmere rate, cashmere yield, number of curls, and short cashmere rate together can explain 88.0 % of the variation in cashmere fineness for doe. net cashmere rate, cashmere yield, and cashmere length explain 83.2 % of the variation, indicating a well-constructed model (Table 12).

3.13. Correlation analysis between cashmere fineness and slaughter performance of LCG

From Table 13, it is clear that carcass net meat rate and EMA of buck was highly significantly correlated with cashmere fineness and net meat

Table 13
Correlation coefficients between cashmere fineness and slaughter performance of LCG.

doe buck	Cashmere fineness	Live weight before slaughter	Carcass weight	Net meat weight	Slaughter rate	Net meat rate	Carcass net meat rate	EMA	GR	BFT
Cashmere fineness	–	−0.117	−0.196	−0.237	−0.285	−0.409*	−0.506**	−0.542**	0.002	0.044
Live weight before slaughter	0.196	–	0.915**	0.921**	0.165	0.398*	0.702**	−0.254**	0.282**	0.812**
Carcass weight	0.277**	0.96**	–	0.995**	0.548**	0.716**	0.723**	0.05	0.421*	0.781**
Net meat weight	0.227	0.953**	0.992**	–	0.527**	0.723**	0.788**	0.051	0.417*	0.78**
Slaughter rate	0.313*	0.449**	0.68**	0.677**	–	0.939**	0.347	0.656**	0.474*	0.203*
Net meat rate	0.174	0.54**	0.73**	0.769**	0.93**	–	0.647**	0.567**	0.509**	0.368
Carcass net meat rate	−0.173	0.465**	0.49**	0.593**	0.374**	0.688**	–	0.098	0.361	0.521**
EMA	0.367**	0.474**	0.432**	0.393**	0.137	0.086	−0.071	–	−0.167	−0.082
GR	0.025	0.71**	0.583**	0.532**	−0.001	−0.018	−0.061	0.28**	–	0.089
BFT	−0.418**	0.462**	0.356**	0.377**	−0.067	0.063	0.261**	−0.12	0.538**	–

** indicates highly significant correlation ($P < 0.01$), while.
* indicates significant correlation ($P < 0.05$).

rate was significantly correlated with cashmere fineness. Carcass weight, EMA, and BFT of doe was highly significantly correlated with cashmere fineness, and slaughter rate was significantly correlated with cashmere fineness (Table 13).

3.14. Results of through-traffic analysis of cashmere fineness and slaughter performance in LCG

From Table 14, it can be seen that the direct maximum of net meat rate and cashmere fineness of LCG buck is 5.718. Next is carcass net meat rate (−2.532) and EMA (−0.954). The maximum indirect path coefficient between carcass net meat rate and cashmere fineness is 3.577, followed by EMA (2.992) and net meat rate (−2.179). The direct throughput coefficient of BFT and cashmere fineness in doe is −0.711, Next is EMA (−0.159). The indirect flux coefficient of EMA versus cashmere fineness was 0.085, followed by BFT (0.019) (Table 14).

3.15. Results of stepwise multiple regression analysis of slaughter performance and cashmere fineness in LCG

From Table 15, the optimal regression equation for doe is cashmere fineness = -0.833 BFT + 0.19 Carcass weight − 0.187 carcass net meat rate + 29.921. For buck it is cashmere fineness = -0.183 EMA − 0.379 carcass net meat rate + 0.188 net meat rate + 42.595. The coefficients of determination (R-squared) for the multiple regression equation are 0.471 and 0.589, respectively (Table 15).

3.16. The haplotype combinations of the FA2H gene T42443G and the ELOVL3 gene C2133A

Using SHEsis software, analysis of SNP loci in the *FA2H* and *ELOVL3* genes revealed four haplotype combinations.(See Table 16)

3.17. Correlation analysis of haplotype combinations of FA2H gene T42443G and ELOVL3 gene C2133A with cashmere production performance

A total of four haplotype combinations were found on LCG buck.The CCTT haplotype combination was highly significantly superior to the other haplotype combinations in terms of cashmere length, number of curls, and net cashmere rate.The CCTG haplotype combination was highly significantly superior to the other haplotype combinations in terms of cashmere yield, The CATG haplotype combination superior to other haplotype combinations in cashmere fineness.

A total of four haplotype combinations were found in LCG doe, The CCTG genotype was highly significantly superior to other haplotype combinations in terms of cashmere yield, number of curls, net cashmere rate and short cashmere rate. And CCTG haplotype combination of cashmere fineness was also the best (Table 17).

3.18. Correlation analysis of haplotype combinations of FA2H gene T42443G and ELOVL3 gene C2133A with slaughter performance

In the haplotype combinations of LCG doe, The CCTT haplotype combination shows highly significantly superior over other haplotype combinations in terms of live weight before slaughter, carcass weight, net meat weight, net meat rate, and EMA. The combination of CCTT and CATT haplotypes was highly significantly superior to the combination of CATG haplotypes in slaughtering rate, carcass net meat rate and GR. Therefore, CCTT was the dominant haplotype combination.

In the haplotype combinations of LCG buck, The CATG haplotype combination was significantly better than the CATT haplotype combination in GR, Therefore, CATG was the dominant haplotype combination (Table 18).

Table 15
Path coefficients between slaughter performance and cashmere fineness in LCG.

Sex	Model	R^2	Adjusted R-squared	Standard error of estimate	F	P
doe	Cashmere fineness = -0.625BFT + 18.549	0.175	0.161	1.16209	12.315	0.001[b]
	Cashmere fineness = -0.884BFT + 0.144carcass weight + 15.773	0.383	0.361	1.01424	17.654	0.000[c]
	Cashmere fineness = -0.833BFT + 0.19carcass weight-0.187carcass net meat rate + 29.921	0.471	0.442	0.94750	16.590	0.000[d]
buck	Cashmere fineness = -0.19EMA + 19.305	0.294	0.265	0.953	10.398	0.003[b]
	Cashmere fineness = -0.12EMA-0.226carcass net meat rate + 36.728	0.501	0.460	0.818	12.064	0.000[c]
	Cashmere fineness = -0.183EMA-0.379carcass net meat rate + 0.188net meat rate + 42.595	0.589	0.535	0.758	10.988	0.000[d]

Table 16
The haplotype combinations of the *FA2H* gene T42443G and the *ELOVL3* gene C2133A.

Haplotype	H1:TT	H2:TG
H1:CC	CCTT	CCTG
H2:CA	CATT	CATG

Table 14
Path coefficients between slaughter performance and cashmere fineness in LCG.

Sex	Independent variable	Correlation coefficient	Direct effect	Indirect effect			
				Net meat rate	Carcass net meat rate	EMA	BFT
buck	Net meat rate	−0.409*	5.718		−1.638	−0.541	
	Carcass net meat rate	−0.506**	−2.532	3.670		−0.093	
	EMA	−0.542**	−0.954	3.24	−0.248		
doe	EMA	0.367**	−0.159				0.085
	BFT	−0.418**	−0.711			0.019	

Table 17
Haplotype combinations of two genes related to cashmere production performance in LCG.

Name	Haplotype	Quantities	Cashmere yield(g)	Cashmere Fineness(μm)	Cashmere length(cm)	number of curls	Short cashmere rate (%)	Net cashmere Rate(%)
buck	CCTT	2	1850.00 ± 34.72	16.99 ± 0.12	10.74 ± 0.08^{a}	8.20 ± 0.16^{aA}	19.68 ± 2.37	77.14 ± 2.54
	CCTG	2	2200.00 ± 18.57	15.89 ± 0.16	8.58 ± 0.10^{b}	4.32 ± 0.17^{bB}	19.26 ± 1.37	76.37 ± 2.17
	CATT	14	1950.00 ± 108.18	16.39 ± 0.32	9.345 ± 0.17^{a}	9.10 ± 0.19^{aA}	19.67 ± 4.05	80.02 ± 2.68
	CATG	20	1900.00 ± 64.69	16.82 ± 0.21	9.60 ± 0.31^{a}	5.04 ± 0.95^{aAB}	17.37 ± 4.61	70.39 ± 2.36
doe	CCTT	10	1700.00 ± 15.48^{cB}	18.10 ± 0.26^{aA}	9.12 ± 0.17	4.12 ± 0.20^{bC}	11.06 ± 1.26	56.94 ± 4.76^{bB}
	CCTG	180	1866.67 ± 21.76^{aA}	16.20 ± 0.11^{cB}	9.54 ± 0.12	9.18 ± 0.13^{aA}	15.82 ± 1.17	79.72 ± 1.13^{aA}
	CATT	270	1722.22 ± 17.71^{bA}	16.86 ± 0.06^{bB}	10.33 ± 0.09	5.86 ± 0.23^{bA}	16.68 ± 0.80	71.82 ± 0.79^{bA}
	CATG	260	1788.46 ± 20.01^{bA}	16.49 ± 0.07^{bcB}	9.32 ± 0.10	6.14 ± 0.28^{bA}	18.55 ± 0.99	77.23 ± 0.83^{abA}

Table 18
Haplotype combinations related to slaughter performance in LCG.

Name	Haplotype	Quantities	Live weight before slaughter(kg)	Carcass weight (kg)	Net meat weight (kg)	Slaughter rate (%)	Net meat rate (%)	Carcass net meat rate(%)	EMA (cm^2)	GR(mm)	BFT(mm)
odoe	CCTT	6	55.00 ± 0.76^{aA}	30.10 ± 0.54^{aA}	25.40 ± 0.56^{aA}	54.73 ± 0.32^{aA}	46.18 ± 0.63^{aA}	84.39 ± 0.23^{aA}	26.95 ± 0.48^{aA}	9.37 ± 0.39^{aA}	2.53 ± 0.15^{b}
	CATT	36	47.93 ± 1.12^{bB}	25.15 ± 0.71^{bB}	20.95 ± 0.62^{bB}	52.34 ± 0.48^{bA}	43.56 ± 0.40^{bB}	83.24 ± 0.27^{aA}	19.37 ± 0.23^{cB}	7.46 ± 0.29^{bB}	2.95 ± 0.16^{ab}
	CATG	12	45.90 ± 0.81^{bB}	22.45 ± 0.41^{bB}	17.80 ± 0.45^{cB}	48.91 ± 0.02^{cB}	38.72 ± 0.30^{cC}	79.17 ± 0.58^{bB}	21.32 ± 1.15^{bB}	9.81 ± 0.49^{aA}	3.32 ± 0.16^{a}
buck	CATT	15	45.02 ± 0.67	22.48 ± 0.53	17.52 ± 0.49	49.95 ± 0.99	38.90 ± 0.91	77.82 ± 0.57	23.40 ± 1.53	4.73 ± 0.44b	1.62 ± 0.12
	CATG	9	48.67 ± 2.79	25.93 ± 1.56	20.37 ± 1.44	53.22 ± 0.26	41.60 ± 0.66	78.14 ± 0.90	21.78 ± 0.58	7.41 ± 0.38a	1.99 ± 0.36

4. Discussion

LCG is the world's highest yielding white cashmere goat breed, known for its long fiber length, high clean cashmere yield, moderate fineness of fiber, pure white coat, robust physique, strong adaptability, stable genetic performance, and effective improvement of medium to low yielding cashmere goats. It is hailed as a "Chinese national treasure". Using LCG as the paternal line, five new local varieties have been cultivated, making outstanding contributions to the improvement and cultivation of Chinese cashmere goat breeds. Therefore, it is honored with the title "Father of Cashmere Goats". This study primarily analyzed the effects of genotypes at different loci of the *FA2H* and *ELOVL3* genes on six traits of LCG, as well as the influence of haplotype combinations of these two genes on cashmere production performance and slaughter performance. The SNP loci on the *FA2H* gene is T42443G, and on the *ELOVL3* gene it is C2133A. The PIC values of the *FA2H* gene T42443G locus and the *ELOVL3* gene C2133A locus in LCG range between 0.25 and 0.5, indicating moderate polymorphism. A higher HE value at these two loci indicates higher genetic variation, reflecting rich genetic resources and diversity. The Ne value at these two loci indicates a poor ability of the population to maintain allele stability during selection, mutation, or genetic variation. According to the X^2 values, the T42443G and C2133A loci were not in Hardy-Weinberg equilibrium, likely due to high artificial selection intensity in the breeding farms, which might affect allele and genotype frequencies.

Based on the gene replacement effect, the T42443G locus showed a gene mutation with a negative additive effect, which has a positive impact. Conversely, the C2133A locus showed a gene mutation with a positive additive effect, which has a negative impact. In this study, it was found that in LCG buck, the TT genotype at the *FA2H* gene T42443G locus was the dominant genotype for cashmere production performance, while the TG genotype was dominant for slaughter performance, The CC genotype at locus C2133A of the *ELOVL3* gene was the dominant genotype for cashmere producing performance, and only the CA genotype was found for slaughter performance. In LCG doe, the TG genotype at the *FA2H* gene T42443G locus was the dominant genotype for cashmere production performance, while the TT genotype was dominant for slaughter performance, The CC genotype at the C2133A locus of the *ELOVL3* gene was the dominant genotype for cashmere production performance and slaughter performance. Haplotype combinations of the two genes revealed that the dominant haplotype combination for cashmeret production performance was CCTG. The dominant haplotype combination for buck in slaughter performance was CATG, and the dominant haplotype combination for doe in slaughter performance was CCTT. Reducing the fineness of LCG fibers has always been a concern for people, In previous studies, SNP analyses of the *KRT26*, *TCHH*,[35] *COL6A5*, and *LOC102181374*[36] genes were found to be associated with cashmere fineness. It has been suggested that the *FA2H* gene may be involved in the formation of myelin 2-hydroxygalactose cebuckide and sulpholipids.[37] Deletion of the *ELOVL3* gene leads to anti-obesity effects in mice, and the effect of the *ELOVL3* gene in the liver on metabolic homeostasis and diet-induced metabolic diseases is dispensable.[24] In medicine autosomal recessive mutations in the *FA2H* gene cause *FAHN* degeneration, which results in neurodegeneration.[38] Wu et al.,[33] conducted transcriptome sequencing of Jiang Nan cashmere goat skin tissues and speculated that the *FA2H* gene may be associated with cashmere fineness. The Xinjiang Academy of Animal Science, Institute of Animal Husbandry, has applied for a patent titled "Application, Regulation Methods, and Products of *FA2H* Gene in Preparation Controlling Cashmere Fineness," indicating the correlation between the *FA2H* gene and cashmere fineness.

Ge et al.,[39] conducted correlation regression analysis on body size and cashmere production performance in Yan Mountain cashmere goats, revealing that traits such as height, body length, and chest circumference are significantly positively correlated with cashmere yield. Gao et al.,[40] conducted a correlation regression analysis on body measurements and body weight in Shaanbei White Cashmere goats, revealing significant or highly significant correlations between body length and body weight, Based on the literature above, we speculate whether there is a correlation between cashmere fineness and cashmere production performance as well as slaughter performance. Through correlation analysis, it is evident that in LCG, cashmere yield, cashmere length, net cashmere rate, were significantly or highly significantly correlated with cashmere fineness. Correlation analysis between cashmere fineness and

slaughter performance showed that net meat rate and EMA were significantly or highly significantly correlated with fineness. Shi et al.,[41] found a highly significant correlation between cashmere fineness and cashmere length in doe of northern Shaanxi white cashmere goats. Zhang et al.,[42] found a highly significant correlation between cashmere fineness and cashmere yield in Yanshan cashmere goats. This is the same as the results analysed in this paper, suggesting that the analysis of correlations in this paper is of value.

LCG are important local breeds, and enhancing their production performance while reducing fineness has become a crucial research direction. In this study, we analysed the production performance of the SNP loci of *FA2H* and *ELOVL3* genes from the genetic point of view to provide some help for the development of LCG breeding.

5. Conclusion

The Chinese Ministry of Agriculture and Rural Affairs has set forth core targets in the National goat Genetic Improvement Plan (2021–2035), requiring a 10 % increase in cashmere yield and cashmere fineness below 16 μm for Liaoning cashmere goat (LCG). LCG is characterized by the highest individual cashmere yield, but its cashmere fineness tends to be coarse. The findings of this study, In the *FA2H* gene, a SNP locus T42443G was detected in LCG buck, with the TT genotype showing advantageous traits in cashmere fineness, meat quality, and body size, while the TG genotype demonstrated advantages in slaughter performance,In LCG doe, the TG genotype shows advantageous traits in cashmere fineness, milk production, and meat quality, while the TT genotype exhibits advantages in slaughter performance, lambing, and body size. In the *ELOVL3* gene, a SNP locus C2133A was identified in LCG buck, where the CC genotype was advantageous for cashmere fineness, Only CA genotype was found in slaughter and meat quality. Additionally, and the CA genotype showed superiority in body size. On LCG doe, The CC genotype was the advantageous genotype in terms of cashmere fineness, milk production, slaughter performance, and meat quality. The CA genotype was the advantageous genotype in terms of lambing and body size. Phenotypic correlation analysis of cashmere fineness with cashmere production performance and slaughter performance, Through multiple linear regression analysis, it was found that the trait positively correlated with cashmere fineness in buck' cashmere production performance was cashmere yield, the correlation coefficient was 0.541. The trait negatively correlated was net cashmere rate, the correlation coefficient was −0.866. The dominant genotypes identified to affect both cashmere fineness and cashmere production performance in buck was TT and CC. The traits positively correlated with the production performance of cashmere in doe was cashmere yield and cashmere length. The correlation coefficients were 0.278 and 0.322, The traits negatively correlated were number of curls, Short cashmere rate, and net cashmere rate, The correlation coefficients were −0.246, −0.238, and −0.936. The dominant genotypes identified to affect both the fineness of doe cashmere and cashmere production performance were TG and CC. Through multiple linear regression analysis, it was found that the traits negatively correlated with buck slaughter performance and cashmere fineness were net meat rate, carcass net meat rate, and EMA, The correlations were −0.409, −0.506, and −0.542. The dominant genotypes identified to affect both buck cashmere fineness and slaughter performance were TG and CA. The trait positively correlated with doe slaughter performance and cashmere fineness was EMA. The correlation coefficient was 0.367. The trait negatively correlated was backfat thickness, with a correlation coefficient of −0.418. The dominant genotypes identified to influence both doe cashmere fineness and slaughter performance were TT and CC. The identified dominant haplotype combination for cashmere production performance in LCG was CCTG. The dominant haplotype combination for doe slaughter performance was the CCTT haplotype combination. The dominant haplotype combination for buck slaughter performance was the CATG haplotype combination. Therefore, the TT genotype of the *FA2H* gene and the CC genotype of the *ELOVL3* gene in LCG buck, and the TG genotype of the *FA2H* gene and the CC genotype of the *ELOVL3* gene in doe can be used as molecular markers for assisted selection of cashmere fineness. It is hoped that this experiment can provide reference for future research.

Ethical approval

The goats all followed the guidelines of the journal Genetic Engineering and Biotechnology.

To ensure the ethical treatment of animals, all procedures and handling involving goat are carried out in accordance with the guidelines established by the Experimental Animal Management Committee of Shenyang Agricultural University.

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CRediT authorship contribution statement

Shuaitong Li: Writing – original draft, Software. **Lingchao Kong:** Writing – review & editing. **Siyi Li:** Investigation. **Yining Liu:** Data curation. **Yuan Pan:** Methodology. **Qingkun Liu:** Data curation. **Weihang Hong:** Conceptualization. **Hua Ma:** Data curation. **Qingyu Yuan:** Formal analysis. **Ran Duan:** Formal analysis. **Qiying Zhan:** Formal analysis. **Zeying Wang:** Supervision, Funding acquisition.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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