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GENOME-WIDE ANALYSIS IN THE SEARCH FOR CANDIDATE GENES ASSOCIATED WITH MEAT PRODUCTIVITY TRAITS IN MEAT-AND-DAIRY GOATS

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Abstract
The development of the tourism cluster in the North Caucasus causes the expansion of product range with high consumer characteristics, in particular, a sustainable offer of dairy and meat products labeled as environmentally friendly. In the range of such products with high dietary properties, a special role may be played by goat meat obtained from Karachay goats, which are the most common meat-and-dairy goats in the region. The aim of the work was to search for candidate genes associated with live weight and meat productivity of Karachay goats. GWAS analysis using Goat 50K BeadChip high-density DNA microarray determined a genome-wide level of significance for six SNPs located on chromosomes 5, 6, 10 and 16 associated with the live weight of young animals (4 and 8 months old). Three of the six SNPs within the ± 200 kb region were localized to HMGA2, CRADD, and MAX genes. These genes were selected to study the meat productivity traits of young goats with different genotypes. It was found that in the locus linked with HMGA2 gene, young goats with GG genotype were characterized by the best indicators of meat productivity. Compared to AA genotype animals, they had superiority in pre-slaughter weight, slaughter carcass weight, slaughter yield, boneless meat weight and loin eye area by 8.9%, 13.6%, 4.3% (P <0.05), 10.5% (P <0.01), and 5.2% (P <0.05) respectively. Young goat meat of this genotype was characterized by the high protein content of 22.56% and low fat content of 9.12%. For the CRADD gene, animals with GG genotype had a higher pre-slaughter weight, slaughter weight, slaughter carcass yield, boneless meat weight and loin eye area. Animals with AG genotype were characterized by the lowest indicators. According to the above characteristics, the difference between the compared genotypes was 15.8%, 25.7% (P <0.01), 8.4% (P <0.05), 18.3%, and 15.7% (P <0.01) respectively. There were no significant differences in the chemical composition of muscle tissue between animals of different genotypes. HMGA2 and CRADD genes are promising for further research of Karachay goats breeding to increase meat productivity and meat quality.

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Introduction

Goats are one of the earliest domesticated ruminants. They are traditional sources of meat, milk, wool, raw leather and other animal products. The unique abilities of goats, such as unpretentiousness in maintenance and nutrition, the ability to adapt to almost any environmental conditions, made their distribution ubiquitous. More than 250 breeds of goats exist in 197 countries all over the world with total number about 1 billion 200 million animals. The number of goats in Russia is about 2 million [1,2]. It should be noted that in the last two decades, there has been an increase in the number of dairy and meat-and-dairy goats and an increase in the production of goat milk and meat. Meat-and-dairy goats are mainly represented by local breeds, which are bred mainly in the foothills and mountainous regions of Altai, Tyva, Khakassia and North Caucasus [3].

In the North Caucasus, Karachay goats are ones of the most common. They are bred in alpine and subalpine pastures, which are characterized by an exceptional rich flora often not accessible to other types of domestic animals due to steep slopes and rocky ledges [4]. This fact makes it possible to obtain environmentally friendly products from Karachay goats. Moreover, the development of tourism in the North Caucasus stimulates their intensive breeding. At the same time, along with excellent biological and productive indicators, Karachay goats (of different populations) are characterized by high variability in live weight and meat productivity, which makes it relevant to improve them by breeding.

Along with traditional methods of goat breeding, marker-assisted breeding based on the use of molecular genetic methods has become increasingly important in recent years [5,6]. Progress in genotyping technologies has made

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it possible to conduct genome-wide association studies (GWAS) to identify new single nucleotide polymorphisms (SNP) associated with indicators of body size that may affect the meat productivity of goats.

Genotyping of seven goat breeds in Pakistan using Goat 50K BeadChip DNA microarray and GWAS showed that *DKK2, TBCK, FGF, ANK2* genes were associated with body size. Functional annotation of the identified genes showed that *DKK2* (dickkopf WNT signaling pathway inhibitor 2) plays a role in embryonic development, while *TBCK* (TBC1 domain containing kinase), *FGF* (epidermal growth factor), and *ANK2* (ankyrin 2) are involved in the regulation of cell proliferation and growth [7].

Several studies performed on large populations of white cashmere goats (n=1038; 1953; 1405; 1759) genotyped with Goat 50K BeadChip DNA microarray and GWAS established a highly significant relationship between 16-bp indel mutations in prolactin (*PRLR*) and lysine-specific demethylase 6A (*KDM6A*) genes, 13-bp indel mutations in A-kinase anchor protein (*AKAP12*) gene, 17-bp and 21-bp indel mutations in sorting nexin 29 (*SNX29*) gene and height, body length, chest width and depth and live weight. The data obtained allowed the authors to recommend the selection of animal with desirable genotypes in the *PRLR, KDM6A, AKAP12, and SNX29* genes to increase goat meat production [8,9,10,11]. At the same time, it was noted that the most promising candidate gene for the live weight trait is the *SNX29* gene, the functional role of which is well known and consists in the regulation of the differentiation and proliferation of muscle tissue cells, myocytes [11].

GWAS for traits associated with body weight and meat productivity was performed for meat goats, in particular Chinese Dazu black goat. In this study, genotypes were determined by sequencing the entire genome of 30 individuals. It was found that *PSTPIP2* (proline-serine-threonine phosphatase-interacting protein 1), *CCL19 C–C* (motif ligand 2), *FGF9* (fibroblast growth factor) and *SIPA1L* (signal-induced proliferation-associated 1-like protein 1) genes were associated with body size and weight. Functional annotation of the identified genes showed that they are involved in the regulation of skeletal muscle development. The authors believe that these genes may be used as candidate genes for the meat productivity of Dazu black goats [12].

Another study performed on goats (n=1044) of the same breed, but genotyped using Goat 50K BeadChip DNA microarray revealed that 12-bp deletion in PR domain zinc finger protein (*PRDM6*) gene is associated with the height and length of the body, chest width and depth, hips width, and the live weight of young animals. Thus, selection for this gene is profitable for increasing the meat productivity of goats [13].

Given the relevance of genome-wide association analysis and the lack of such studies for goats in national selection, the aim of the work was to search for candidate genes associated with the live weight of Karachay goats, as well as to study meat productivity traits for different genotypes, taking into account the identified significant SNPs and functional annotation.

Objects and methods

The material for the study was genome-wide SNP genotypes of 281 young Karachay goats obtained using Goat 50K BeadChip high-density DNA microarray (Illumina, San Diego, CA, USA), as well as live weight indicators of genotyped animals at the age of 4 and 8 months old. Quality control and filtering of genotyping data for each SNP and each sample were performed using PLINK 1.9 software package [14].

Genome-wide association studies were performed using multiple linear regression analysis in Plink 1.90 software with preliminarily population adjustment according to its structure (–-genome, —covar). To confirm the significant influence of SNPs and identify significant regions in the goat genome, Bonferroni test was used to test null hypothesis: threshold value $P < 1.53\times10^{-6}$; 0.05/32629 SNP. Data visualization was carried out in the qqman software package using the R programming language [15].

Identified genome-wide SNPs associated with body weight at both 4 and 8 months old were selected for the list of total SNPs. This list was used for structural annotation of genes located within ± 0.2-Mb region from the identified SNP. Genes were identified using the 11.1 ARS1.2 genome assembly and Ensembl Genes release 103 database [16]. For functional annotation, DAVID software was used [17]. To simultaneously test several independent hypotheses aimed at controlling the level of false rejections defined as the expected ratio of false rejections to the total number of rejections, Benjamini-Hochberg procedures were used [18].

Three young goats of different genotypes were selected based on the results of GWAS, identified genome-wide SNPs, and functional annotation of genes, within which SNP localization was determined. Their live weight corresponded to the average value of all young goats of the same genotype from the entire sample. Meat productivity for young goats of different genotypes was studied based on the results of slaughter at the age of 8 months old.

Preslaughter live weight was determined by weighing after 24 hours of starvation with an accuracy of 0.1 kg on VET-150–20/50–1S-DBSK balance (Mekhelectron-M LLC, Russia). Carcass yield was calculated by the ratio of carcass weight with kidneys and suet to preslaughter live weight. Slaughter weight was calculated by summing the weight of exsanguinated carcass without a head, skin, tail, internal organs, limbs cut to the hock and carpal joints and internal fat. Internal fat weight was determined by the total amount of pelvic, renal, intestinal, gastric, and diaphragmatic fat. Slaughter yield was calculated as the ratio of slaughter weight to preslaughter weight. Meatiness was determined by the ratio of boneless meat weight to bones weight. Boneless meat weight was determined with an accuracy of

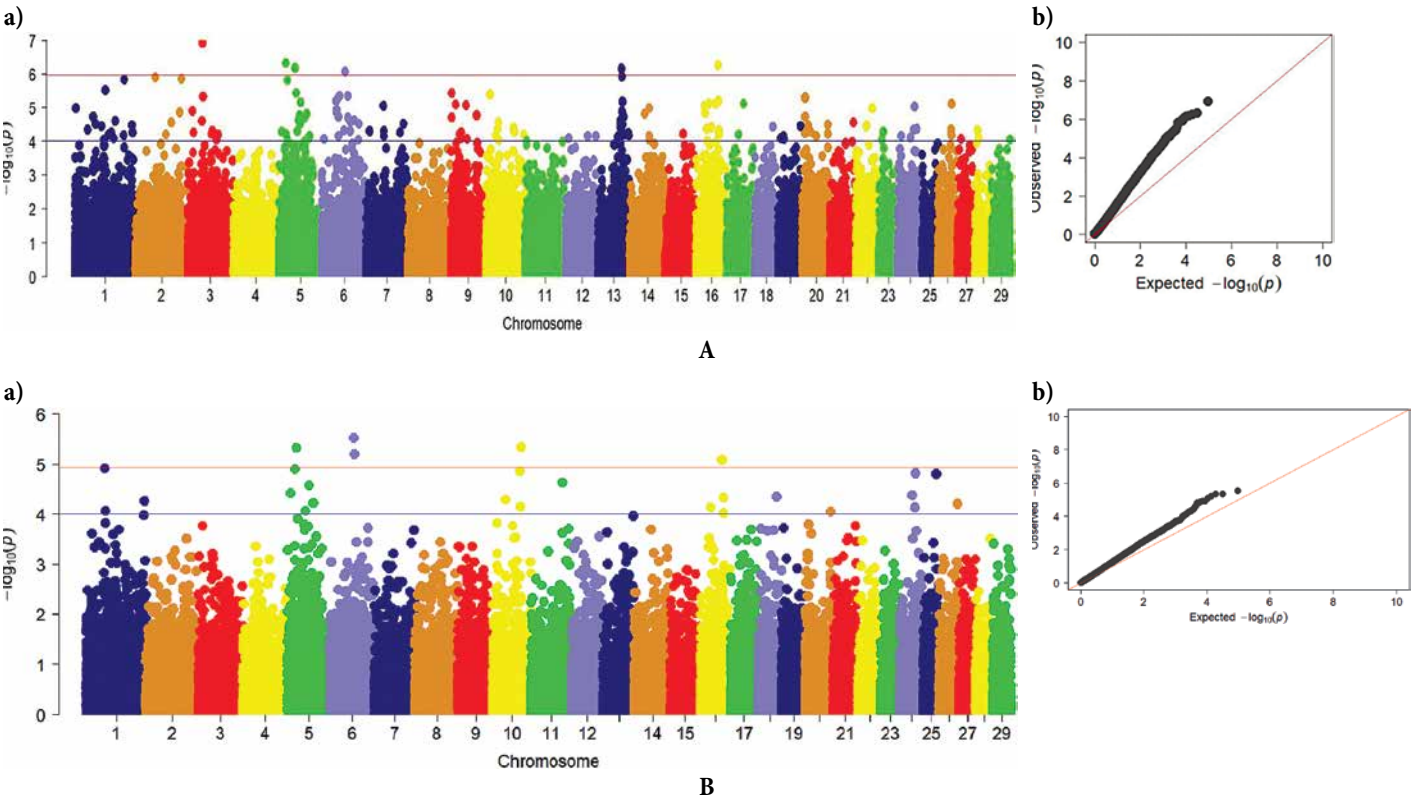

Figure 1. a) location of statistically significant SNPs in 29 autosomes of Karachay goats for the live weight trait: **A** — at the age of 4 months old; **B** — at the age of 8 months old; the negative logarithm of q value (Y-axis) is plotted for each chromosome (X-axis); on the Y-axis — the lower line corresponds to the significance level $p \leq 0.00001$, the upper line corresponds to the significance level $p \leq 0.000001$; **b)** quartile of the probability distribution of the expected and observed deviations from the normal distribution for the significance values

0.05 kg by deboning the carcass on SW-10 balance (CAS, South Korea).

During the control slaughter, meat samples were taken from the main areas of the carcass for the preparation of an average sample and chemical analysis. Moisture content in the average sample of minced meat was determined according to GOST 9793–2016[1]. Fat content was determined according to GOST 23042–2015[2], protein content was determined according to GOST 25011–2017[3] (by the Kjeldahl method; calorie content was determined by calculation using the equation of V. M. Aleksandrov: K = [D — (F + A)] x4.1 + (F × 9.3), where K is calorie content, kcal; D, A, F are dry matter, ash, and fat contents respectively.

Slaughter of experimental animals was carried out in accordance with the requirements of GOST 33215–2014[4] by cutting the jugular vein and exsanguination. During slaughter, the recommendations of the Directive 2010/63/EU of the European Parliament and the Council of the European Union [19], the European Convention for the Protection of Vertebrate Animals used for Experimental and other Scientific Purposes (ETS No. 123) [20] were strictly followed.

The resulting raw data were subjected to biometric processing using Microsoft Office and BIOSTAT software. Based on the mean values and standard errors, the significance of the difference in the mean values were calculated using Student's t-test.

Results and discussion

For GWAS, a sample of 281 young animals was used. Average values and phenotypic variability in the live weight at the age of 4 and 8 months old were 24.8 kg and 14.5%, 36.3 kg and 11.1% respectively.

The results of GWAS analysis are presented in Figure 1.

Visualization of the genome-wide analysis results allows to state that GWAS patterns for live weight at the age of 4 and 8 months old are generally similar. A match was found for 18 SNPs located on chromosomes 5, 6, 10, 16, 18, 20, and 24 (Figure 1a). At the same time, genome-wide level of significance was established for 6 SNPs located on chromosomes 5, 6, 10, and 16, the localization and description of polymorphism for which are presented in Table 1. It should be noted that the distribution of deviations from the normal distribution for the significance values of the live weight both at the age of 4 and 8 months old were close to expected (Figure 1b).

[1] GOST 9793–2016. "Meat and meat products. Method for determination of moisture content". Moscow: Standartinform, 2018. Retrieved from https://docs.cntd.ru/document/1200144231 Accessed September 16, 2022 (In Russian)

[2] GOST 23042–2015 "Meat and meat products. Methods of fat determination". Moscow: Standartinform, 2019. Retrieved from https://docs.cntd.ru/document/1200133107 Accessed September 16, 2022 (In Russian)

[3] GOST 25011–2017 "Meat and meat products. Protein determination methods". Moscow: Standartinform, 2018. Retrieved from https://docs.cntd.ru/document/1200146783 Accessed September 16, 2022 (In Russian)

[4] GOST 33215–2014 "Guidelines for accommodation and care of animals. Environment, housing and management" Moscow: Standartinform, 2019. Retrieved from https://docs.cntd.ru/document/1200127789 Accessed September 16, 2022 (In Russian)

Analysis of six selected SNPs showed the presence of genes localized within the ± 200-kb region for two SNPs: T47480416C (rs268269710 A/G) on chromosome 5 and A25854668G (rs268234545 A/G) on chromosome 10, and directly within the gene for one SNP, A23345368G (rs268270492 G/A) on chromosome 5 (Table 2). These genes were selected as candidate genes associated with the live weight trait in young Karachay goats.

Analysis of scientific information sources for the previously described functions of the genes presented in Table 2 showed that they were associated with growth and development rates in animals of other species (mice and pigs).

Thus, it was found that *CRADD* gene, along with *SOCS2* and *PLXNC1* genes, is localized within the so-called "high-growing region" on chromosome 10 in mice. These genes are associated not only with the phenotype of high growth in mice, but also with no obesity [21]. Another study demonstrated a significant relationship between the "high-growing region" mouse genes, *CRADD*, *SOCS2* and *PLXNC1*, as well as two closely located genes, *ATP2B1* and *DUSP6*, with the growth rate in pigs, as well as the quality of meat and fat [22].

HMGA2 gene has also been identified as a candidate gene associated with the growth and development of pigs [23]. *HMGA2* gene is activated only during early postnatal development and controls the total number of cells in the animal. Its expression level was determined to be proportional to the body weight in pigs [24,25].

The protein encoded by the *MAX* gene is a member of *bHLHZ* family of transcription factors. *MAX* as a partner of *MYC* is involved in the control of cell proliferation [26].

Our own data and the results of studies by other authors substantiated the feasibility for conducting studies on meat productivity traits and chemical analysis of muscle tissue

Table 1. Candidate SNPs that were associated with body weight at the age of 4 and 8 months old

SNP name	SNP	Address A_ID	AlleleA_ProbeSeq	Chr	MapInfo	Source Strand	SourceSeq
snp14251-scaffold157-188734	[T/C]	60796360	CCAAAACACCAAGTCTGC TGGCTCCAGGTAATCTG AAGACTCAATATGCT	5	19 934 148 (Manifest) / 19 499 085 (GWAS)	TOP	CCCACAGAGGGTGGGAGAGACAGG AGGTGGGCGTTGCGGTTAGGAGGGC ACATTAGCAGC[A/G]AGCATATTGA GTCT
snp38426-scaffold486-2412676	[A/G]	15705507	AGCTGTTTTAAATCAGATTGT GTCTTTCAGCTTAAGCTATGT TCTGAGAC	5	23 345 368 (Manifest) / 22 879 856 (GWAS)	BOT	CCCTGCAATTACACACTATGGATTTT CAATAACACCTATCAGATTTTTTGTC CATTTATG[T/C]GTCTCAGAACATAG CTTAAGCTGAAAGACACAATCTGAT TTAAAACAGCTAGGGGCTGAA
snp37630-scaffold463-64670	[T/C]	25802440	CCTTGTTTAACGGATAGAGTA AGTCACATTTCCTGTTTTCCTC TTAGTCA	5	47 480 416 (Manifest) / 46 630 429 (GWAS)	TOP	TTAGCATTTGTCTTGAGGGTTTGAG GCCTTAGAAAATATTGTTTTTATCCT ACAGAGTAC[A/G]TGACTAAGAGGA AAACAGGAAATGTGACTTACTCTAT CCGTTAAACAAGGAATTTTTTTT
snp40083-scaffold511-2344051	[A/G]	18716406	ATCTGTTCAAACTTTGTTCAT GACATACAAAAGGACTGGGA GTGGGAGGT	6	62 949 329 (Manifest) / 60 553 915 (GWAS)	BOT	CTAATACCTATTTTGAGACTGGAGC TAAACTGAATACAGAGGATGACCTA AATCAGAATG[T/C]ACCTCCCACTCC CAGTCCTTTTGTATGTCATGAACAA AGTTTGAACAGATAAAAAACAAA
snp1448-scaffold104-1147808	[T/C]	43609359	CTAGATGTCAGGTGTTGGGAC AGGGGTGTAGAAGGGAGATT TGAGAGCCA	10	25 854 668 (Manifest) / 73 347 268 (GWAS)	TOP	GCTTGAGCTACCCAGGTGTGATCCT CGCTCCACGGCATGAGCTCAGAGGT GCTGCAAACC[A/G]TGGCTCTCAAAT CTCCCTTCTACACCCCTGTCCCAACA CCTGACATCTAGACCAAGAAGG
snp8624-scaffold131-2001386	[A/C]	52698321	GTGATCCTTCGGAGGTTGTTC TTAAAATTCACATTTCCACTC GAAGTTAT	16	57 408 452 (Manifest) / 56 416 291 (GWAS)	BOT	GAACTAACAGTACGTCTTTTAACAT ACTTGTACATGTGTAAGTCAGAACC ATTAAAATGC[T/G]ATAACTTCGAGT GGAAATGTGAATTTTAAGAACAACC TCCGAAGGATCACGGGAAGATGG

Table 2. Characteristics of candidate SNPs associated with live weight of Karachay goats

SNP	Polymorphism	Chromosome	Name of		Localization in the reference sequence of NCBI: NC_030812.1
			gene	protein	
snp37630-scaffold463–64670	T47480416C, rs268269710 A/G	5	*HMGA2* — high-mobility group AT-hook 2	high mobility group protein *HMGI-C*	47,162,168 … 47,306,445
snp38426-scaffold486-2412676	A23345368G, rs268270492 G/A	5	*CRADD* — CASP2 and RIPK1 domain containing adaptor with death domain	death domain-containing protein *CRADD*	23,232,979 … 23,425,649
snp1448-scaffold104–1147808	A25854668G, rs268234545 A/G	10	*MAX* — MYC associated factor X	*MYC*-associated factor X protein *MAX*	25,900,233 … 25,924,465

in young Karachay goats at the age of 8 months old with different genotypes according to the identified SNPs in *HMGA2*, *CRADD*, and *MAX* genes.

This age was used due to the fact that in previous studies it was found that the most intensive growth of young Karachay goats is observed before this age period. Until this age, animals are most efficient at converting the nutrients they consume into meat products. Subsequently, the synthesis of bone and muscle tissues slows down and the synthesis of adipose tissue increases, which is not effective from an economic point of view [27].

An analysis of the data obtained made it possible to establish that in *HMGA2* gene, the best meat productivity traits were observed in young goats with GG genotype. So, compared to animals with AA genotype, they had a significant advantage in preslaughter weight, slaughter carcass weight, slaughter yield, boneless meat weight and loin eye area by 8.9%, 13.6%, 4.3% ($P < 0.05$), 10.5% ($P < 0.01$), and 5.2% ($P < 0.05$) respectively. Animals with AG genotype also demonstrated superiority over young goats with AA genotype. However, the difference between the studied meat productivity traits was not significant (Table 3).

Comparison of *CRADD* gene for meat productivity traits in young goats with different genotypes revealed that animals with GG genotype had a higher preslaughter weight, slaughter weight, carcass yield, boneless meat weight and loin eye area. Animals with AG genotype were characterized by the lowest indicators. The difference between the compared genotypes according to the above characteristics was 15.8%, 25.7% ($P < 0.01$), 8.4% ($P < 0.05$), 18.3%, and 15.7% ($P < 0.01$) respectively.

Comparison of animals with different genotypes in *MAX* gene did not reveal a significant advantage in meat productivity traits of any of the established genotypes. Animals with AA genotype had a tendency to superiority in most indicators.

It should be noted that the difference in the studied meat productivity traits between the compared genotypes in *CRADD* gene was more significant than between the genotypes in *HMGA2* gene. It is also necessary to emphasize animals with GG genotypes in *HMGA2* and *CRADD* genes according to the content of boneless meat, which is the most valuable part of the carcass. It makes carriers of these genotypes the most preferable for breeding in terms of obtaining more meat products.

Comparison of chemical composition indicators in young goat meat did not reveal a significant superiority between the compared genotypes in *HMGA2, CRADD*, and *MAX* genes. At the same time, it should be noted that the meat of young goats with all genotypes at the age of 8 months old had high nutritional properties due to its rather high protein content of 20.9 to 22.56% and low fat content of 7.65 to 9.62%. At the same time, animals with GG genotype in HMGA2 gene had not only the best slaughter properties, but also the best ratio of protein to fat in meat from the functional nutrition point of view. So, in the average sample of minced meat from animals with this genotype, 1.0 gram of fat accounted for 2.47 grams of protein, while in samples of meat from AA and AG genotypes, 1.0 gram of fat accounted for 2.38 and 2.29 grams of protein respectively. No such dependence was found for other genes. A greater amount of protein in meat in relation to fat was in animals with AG genotype in *CRADD* gene, and with GG genotype in *MAX* gene, i. e. 2.65 and 2.71 grams, while in animals with other genotypes this value was 2.33 to 2.46 grams. At the same time, the carriers of these genotypes had no best slaughter properties (Table 3).

The generalization of the results obtained allows to conclude that the identified SNPs and candidate genes, *HMGA2*, *CRADD* and *MAX*, associated with the live weight of young Karachay goats are to some extent involved in their meat productivity. The most promising for further research and use in Karachay goat breeding to increase meat productivity, in our opinion, is the SNP in *HMGA2* gene. GG genotype in rs268269710 position is associated not only with a higher live weight, carcass yield, and boneless meat content, but also with the ratio of protein to fat in meat that is preferable for functional nutrition. At the same time, it should be noted that in order to confirm the revealed patterns, it is necessary to test the results obtained on a larger sample of animals with additional researches to study the meat properties from animals of different genotypes.

In discussing the results obtained in this study, it should be noted that of the three genes that were associated with body weight of goats at both 4 and 8 months old, two, *HMGA2* and *CRADD*, were significantly associated with postmortem meat parameters. Functional annotation of these genes showed that they control cell proliferation at early stages of embryogenesis and also regulate the growth of muscle tissue cells, myocytes [17].

In a number of studies, it was also found that *SNX29* and *FGF* genes associated with the live weight of goats had a pronounced function of regulating the differentiation and proliferation of muscle and connective tissue cells, myocytes and fibroblasts [11].

When studying 11 signs of growth and meat productivity (birth weight, weight at the age of 4 and 6 months old, body weight gain before and after 4 months, daily weight gain for the entire growing period, loin eye area, fat thickness, height at the withers, chest circumference and shank circumference) in sheep, the influence of *MEF2B, RFXANK, CAMKMT, TRHDE, RIPK2, GRM1, POL, MBD5, UBR2, RPL7* and *SMC2* genes on the formation of these traits was established. Gene annotation showed that these identified genes are transcription factors that regulate myocyte proliferation and fatty acid metabolism [28].

In another study, GWAS analysis revealed that *AADACL3, VGF, NPC1* and *SERPINA12* genes were also significantly associated with the live weight and meat productivity of sheep. Ontology analysis and signaling pathways study showed that these genes are involved in the development of skeletal muscles and lipid metabolism [29].

Table 3. Meat productivity traits of young goats with different genotypes for SNPs in *HMGA2*, *CRADD* and *MAX* genes (8 months)

Indicator	Gene/Polymorphism/Genotype								
	HMGA2 / rs268269710 A/G			*CRADD* / rs268270492 G/A			*MAX* / rs268234545 A/G		
	AA	AG	GG	AA	AG	GG	AA	AG	GG
Slaughter indicators, morphological composition of carcasses									
Preslaughter weight, kg	32.81 ± 0.59	34.16 ± 0.37	35.73 ± 0.42*	34.64 ± 0.33	31.22 ± 0.54	36.15 ± 0.48**	34.92 ± 0.37	34.83 ± 0.21	33.82 ± 0.46
Hot carcass weight, kg	14.24 ± 0.38	15.12 ± 0.24	16.07 ± 0.29	15.88 ± 0.21	12.65 ± 0.32	15.86 ± 0.29	15.85 ± 0.22	15.02 ± 0.14	14.42 ± 0.27
Internal fat weight, kg	0.96 ± 0.06	1.12 ± 0.12	1.20 ± 0.17	1.00 ± 0.04	0.89 ± 0.06	1.17 ± 0.09	1.15 ± 0.10	1.10 ± 0.04	1.00 ± 0.07
Slaughter weight, kg	15.20 ± 0.32	16.24 ± 0.19	17.27 ± 0.24*	16.88 ± 0.12	13.54 ± 0.24	17.03 ± 0.12**	17.00 ± 0.20	16.12 ± 0.10	15.42 ± 0.18
Slaughter yield, %	46.32 ± 0.44	47.54 ± 0.22	48.33 ± 0.32*	48.73 ± 0.28	43.37 ± 0.32	47.11 ± 0.44*	48.86 ± 0.25	46.28 ± 0.12	45.59 ± 0.21
Boneless meat weight, kg	10.38 ± 0.13	11.28 ± 0.06	12.46 ± 0.10**	12.22 ± 0.05	10.32 ± 0.10	12.21 ± 0.08**	12.04 ± 0.06	11.96 ± 0.03	11.42 ± 0.09
Bone and tendon weight, kg	3.32 ± 0.16	3.64 ± 0.07	3.70 ± 0.09	3.61 ± 0.08	3.35 ± 0.05	3.59 ± 0.04	3.45 ± 0.06	3.49 ± 0.04	3.37 ± 0.04
Ratio of boneless meat to bones and tendons	3.13 ± 0.12	3.10 ± 0.07	3.37 ± 0.10	3.38 ± 0.06	3.08 ± 0.09	3.40 ± 0.11	3.49 ± 0.11	3.42 ± 0.08	3.39 ± 0.09
Loin eye area, cm^2	12.44 ± 0.17	12.46 ± 0.09	13.09 ± 0.14*	13.01 ± 0.04	11.47 ± 0.10	13.21 ± 0.12**	12.26 ± 0.12	12.08 ± 0.06	11.95 ± 0.10
The content in the average sample of minced meat, %									
Moisture	69.40 ± 0.68	68.55 ± 0.72	67.20 ± 0.67	69.14 ± 0.59	69.21 ± 0.72	66.90 ± 0.41	68.72 ± 0.68	68.25 ± 0.72	69.05 ± 0.67
Fat	8.75 ± 0.21	9.23 ± 0.26	9.12 ± 0.18	8.65 ± 0.19	8.41 ± 0.26	9.62 ± 0.18	9.10 ± 0.17	8.88 ± 0.26	8.06 ± 0.18
Ash	1.0 ± 0.04	1.0 ± 0.05	1.1 ± 0.07	1.0 ± 0.05	1.0 ± 0.05	1.1 ± 0.06	1.0 ± 0.05	1.0 ± 0.06	1.0 ± 0.05
Protein	20.90 ± 0.21	21.20 ± 0.34	22.56 ± 0.17	21.21 ± 0.27	22.34 ± 0.43	22.48 ± 0.52	21.16 ± 0.23	21.87 ± 0.43	21.87 ± 0.27
Calorie content, kcal/100 g	167.06 ± 0.39	172.94 ± 0.47	177.38 ± 0.55	167.40 ± 0.40	170.01 ± 0.34	181.63 ± 0.63	171.47 ± 0.39	172.24 ± 0.47	164.71 ± 0.32

In a study performed on the Rendena cattle bred in the Italian Alps important for beef production, it was found that *SLC12A1, CGNL1, PRTG* genes were associated with average daily body weight gain, *LOC513941* gene was associated with carcass yield, *CDC155* gene was associated with the content of boneless meat in the carcass, *NLRP2* gene was associated with both indicators of carcass quality. Metabolic pathways analysis showed that some of the genes were associated with neurogenesis and synaptic signaling in cells, and some were associated with actin synthesis and transmembrane transport [30].

Thus, the results of our research and researches by other authors show that GWAS is the most commonly used and informative method of searching for candidate genes associated with body size indicators and affecting the meat productivity of animals. Despite the fact that different studies have identified different genes, in most cases they were transcription factors that control the differentiation and proliferation of muscle and connective tissue cells, and regulate signaling transmembrane cell pathways.

Conclusion

GWAS analysis using Goat 50K BeadChip high-density DNA microarray determined a genome-wide level of significance for six SNPs located on chromosomes 5, 6, 10, and 16 associated with the body weight of young Karachay goats at the age of 4 and 8 months old.

Of the six SNPs, one was determined to be localized within *CRADD* gene, and other two were localized within the ± 200-kb region in *HMGA2* and *MAX* genes. These SNPs were selected to study the meat productivity traits of young Karachay goats.

It was found that the best meat productivity traits were in young goats with GG genotype in *HMGA2* gene. Compared to animals with AA genotype, they had superiority in preslaughter weight, slaughter carcass weight, slaughter yield, boneless meat weight and loin eye area by 8.9%, 13.6%, 4.3% ($P < 0.05$), 10.5% ($P < 0.01$), and 5.2% ($P < 0.05$) respectively. The meat of young goats with this genotype was characterized by a high protein content of 22.56% and low fat content of 9.12%.

Animals with GG genotype in *CRADD* gene had a higher preslaughter weight, slaughter weight, carcass slaughter yield, boneless meat weight, and loin eye area. Animals with AG genotype were characterized by the lowest indicators. The difference between the compared genotypes in the above characteristics was 15.8%, 25.7% ($P < 0.01$), 8.4% ($P < 0.05$), 18.3%, and 15.7% ($P < 0.01$) respectively. There were no significant differences in the chemical composition of muscle tissue between animals of different genotypes.

HMGA2 and *CRADD* genes are promising for further research, accumulation of more experimental data, approbation of the results obtained with the aim of subsequent use in breeding the Karachay goats to increase meat productivity and meat quality.

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