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GH and DGAT1gene polymorphism effect on beef production traits of Hereford and Limousine bull calves

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ABSTRACT

The purpose of the given study was to identify interrelation between GH and DGAT1 gene polymorphism and beef production traits of Hereford and Limousine bull calves in conditions of the Cis-Ural steppe zone. The study deals with one-month-old Hereford bull calves, offspring of animals brought to private company Sava-Argo-Usen from southeast states of Australia and Tasmania Island and Limousine bull calves, offspring of cross-bred animals of Simmental cows and French servicing bulls bred in private farm SAVA-agro-Yapryk. Life-animal beef production estimate of bull calves of different genotypes in the studied gene polymorphism was carried out on liveweight gain indexes, after slaughter chemical composition of the rib eye was investigated according to hot carcass, raw visceral fat and slaughter weight and output. It is proved that the studied SNP in GH gene of Limousine bull calves is for certain associated with intramuscular fat content in the rib eye. When K232A polymorphism in DGAT1 gene was studied no AA genotypes were found in both populations that perhaps is due to the low number of animals. We find it necessary to continue the investigation by increasing the amount of the livestock as well as studying other beef cattle bred in the region. The received results are recommended to be used to improve genetic potential of the beef cattle kept in the Cis-Ural steppe zone.

Keywords: polymorphism, GH, DGAT1, SNP, Hereford cattle, Limousine cattle.

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INTRODUCTION

In many regions of Russia cattle breeds are presented by local and adapted foreign animal populations being different in their morphology as well as gene complex developed as the result of selection. When a breed is kept as a potential material for further selection information on its genofond is very vital since genes and their combinations determine effective properties of the breed. The genetic structure of any population being a part of the breed is changed under current selection processes at the account of gene migration, their elimination as well as genetic recombination. Using genetic markers it becomes possible to make mass estimate of genetic material on existence of preferred allelic gene combinations related to productivity traits and inherited diseases [41,6].

Achievements of current molecular genetics enable to find genes responsible for economic traits. Discovering variants of such genes makes possible selection on the DNA level additionally to the traditional one as well as early diagnosis of productive traits to understand future perspectives and commercial price of animals [41,12,30]

Currently many studies are being conducted aimed to find interrelation between beef production traits of animals and single nucleotide polymorphisms (SNP) of candidate genes.

Growth hormone gene (GH) is located in chromosome 19 of cattle *(National Center for Biotechnology Information)*. Growth hormone is synthesized in the pituitary and encoded by a gene consisting of five exons separated by introns. Six sites of variable nucleotide are found in the 5'-flanking region of the gene and one site in intron I, later 14 different GH haplotypes were detected and sequenced by SSCP-gene technologies [18]. Moreover, *Rodrigues et al. [27]* identified AAG deletion in the promoter region of the GH gene. *Lee et al*. [19] found ten *SNP* within 2856 bp of the *GH* gene including four (*253 C>T, 303 C>T, 502 C>T, 559 G>A*) in the promoter, one (679 *C>T*) in exon 1, one (1,692 T>C) in intron 3 and four (*2141 C>G, 2258 C>T, 2277 C>T u 2291 A>C*) in exon 5, the studies showed that only 4 *SNP* ($p<0,05$) are closely associated with liveweight of six-months-aged bull calves (303 *C>T*, in the promoter region), rib eye area (559 *G>A*), average daily liveweight gain (2141 *C>G,* in exon 5), average daily carcass weight and its gain (2258 *C>T*). In terms of association with beef production traits the most investigated is mutation representing *C→G* transversion in the nucleotide sequence 2141 in exon 5 [21,36,23,2], where the result is substitution of leucine aminoacid *(L)* for valine *(V)* in 127 polypeptide site. Thus this separate nucleotide polymorphism develops two alleles: *L-GH* and *V-GH*. Studies of gene polymorphism is of interest to examine genetic potential of cattle on quantitative and qualitative production traits [2,6,8,12,13,17,23,25,29,30,36].

One more candidate gene for metabolism is diacylglycerol acyltransferase gene *(DGAT1*). *DGAT* is a microsomal enzyme catalyzing the last stage of the triglyceride synthesis. The given stage can run in two ways [16]. Reaction of acyl-CoA addition to diacylglycerol can be presented either by phosphatidic acid hydrolysis into a glycerolphosphate path or acetyling monoacylglycerol into a monoacylglycerol path. The enzyme takes part in transformation of carbohydrates into fats and their storage in the fat depo. *DGAT1* is localized in cattle chromosome centromere 14. Zhengrong *et al.* [40] found 17 *SN*P in *DGAT1* gene with the help of Bioinformation Science and experimental methods, among three studied it was seen that *c.572A>G* and *c.1416T>G* are associated with subcutaneous fat thickness, intramuscular fat content of the rib eye, meat marbling , color and cutting force. Currently the most studied are *QTL* changes in *DGAT1* gene resulted from dinucleotide substitution *ApA→GpC* at the beginning of exon VIII (6829 site of base pair) [4]. This mutation brings in nonconservative substitution of lysine (K) for alanine (A) [37]. Earlier studies showed interrelation between *K232A* polymorphism in *DGAT1* gene and carcass fatness and meat quality traits [1,3,5,20,35,38]. Some researches didn't prove this association, namely for Bos Taurus cattle [22,24] *u Bos Indicus[9,32]* or they found polymorphism absence in *DGAT1* with low frequency of K allele (lysine) [15,24]. *A* allele is found only in *Bos Taurus* cattle but doesn't exist (or presented in low frequency) in *Bos indicus, Bos grunniens, Bos bubalus* cattle [33].

Accordingly our research deals with studies of association of *GH* and *DGAT1* gene polymorphism with beef production traits of Hereford and Limousine bull calves kept in conditions of the Cis-Ural steppe zone.

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MATERIAL AND METHODS

Animals:

The study deals with one-month-old Hereford bull calves (38 heads), offspring of animals (second Russian generation) brought to private company Sava-Argo-Usen from southeast states of Australia and Tasmania island (in 2009) and Limousine bull calves (26 heads), offspring of cross-bred animals of Simmental cows and French servicing bulls (fourth Russian generation) bred in private farm SAVA-agro-Yapryk. Both farms are located in Tuymazy district of Bashkortostan Republic (The Cis-Ural steppe zone) and use a resource-saving stable and pasture technology for keeping beef cattle [11,28].

Depending on the established bull calf genotypes of each breed we distinguished groups of different allele combinations of the studied GH and DGAT1genes using an analog method of liveweight and growth traits: according to allele 1 homozygote ones – 11 – group 1; heterozygote ones – 12 – group 2; homozygote ones according to allele 2 – 22 – group 3. Calves were grown for about 20 months. Investigation on beef production development of bull calves was carried out according to changes in liveweight of new-born calves and at the age of 8, 12, 16 and 20 months using common absolute and average daily weight gain, relative growth rate, yielding and pre-slaughter liveweight methods.

During the colostrums calves were kept with their mothers in separate stables, then in groups of 10-12 heads using timely suckling until they were moved to natural pasture feeding. Calves were weaned at the age of 6-8 months that is before moving to stable housing. Later on bull calves were kept outdoors until their slaughter according to the procedure of the scientific and economic experiment. During the stable housing calves were fed with feed mix of 58 % of succulent feed, 12 % of rough feed and 30 % of grain forage. When calves were fattened they were given 58-60 %, 6-8 % and 32-34 % of feed respectively. During summer winter rations were mainly fed. Feed was prepared and distributed by feed distributor ISRK “Khozyain” twice a day.

Sample collection and phenotyping:

Post-slaughter estimation was conducted in meat processing plant “SAVA” according to the following indicators: hot carcass, raw visceral fat and slaughter weight and output. Carcass was treated by cold in accordance with running standards. Samples to determine chemical composition of the rib eye were selected between 11 and 13 ribs. The samples were frozen and taken to the department of biochemical and chemical-analytical studies of the All-Russian Research Institute of Animal Husbandry named after L.K. Ernst. Studies of physical and chemical indicators included examining chemical composition of muscle tissue according to Russian state standard GOST 23042-86: Meat and meat products. Fat defining methods; Russian state standard GOST P 53642-2009: Meat and meat products. Total ash weight fraction measuring method; Russian state standard GOST 25011-81: Meat and meat products. Protein measuring methods. Russian state standard GOST P 51479-99: Meat and meat products. Mass moisture rate measuring method.

DNA extraction and genotyping:

Studies were conducted at the premises of the Shared knowledge centre “Bioresources and bioengineering of farm animals” of the All-Russian Research Institute of Animal Husbandry named after L.K. Ernst. Data for studies were ear notches of bull calves. DNA extraction was performed with a set of reagents DNA-Ekstran-2 produced by private company “Syntol”. In the course of investigation GH and DGAT1 genes were studied by a polymerase chain reaction (PCR) method and restriction fragment length polymorphism (RFLP) of DNA. To amplify a DGAT1 gene fragment with 10433/104346 mutation 5' – gtt-ctt-cct-tgg-tgg-ctc-ag-3', R: 5' – ctg-tag-ggg-agc-aga-acc-ag-3' F-primers were used. Reactions were conducted on «Eppendorf» thermal cycler. PCR (30 cycles) was done at annealing temperature of 57 є C for GH and 58,5 є C for DGAT1. The received GH and DGAT1 gene amplificants were dissolved by AluI and CfrI endonucleases respectively. The number and length of the received restriction fragments were determined electrophoretically with 3 % agarose gel in TAE buffer at voltage of 120 V. The results were recorded in ultraviolet using «UVT-1» documentation system (Biometra, Germany).

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Statistical analysis:

Analyzing the data of calves genotype based on DNA markers the number of effective alleles was calculated according to the formula: $N_e=1/(1-H_e)$, where *Ne* stands for the number of effective alleles in population, H_e – expected heterozygosity rate. Expected heterozygosity rate (H_e) was computed by the formula: $H_e=1-\Sigma p_i^2$ **(**where p_i is incidence of i allele**)**. Observed heterozygosity (H_o) was calculated as ratio of heterozygote number to the total number of the studied animals: $H_o=n/N$ (where n stands for the number of animal units heterozygous according to the given allele, *N* – sampling size). To assess correspondence of real and expected genotype distribution in the studied animal sampling χ^2 was used that was computed by the formula $\chi^2 = \sum^{k}(O-E)^2/E$ (where O and E stand for observed and theoretically expected genotype numbers of specific types, k – genotype class number). Statistical data processing was done with STATISTICA 5.0 software.

RESULTS

An important beef production trait is liveweight, its change during growth and development proves intensive metabolic processes in the animal body. Growth hormone (*GH*) is directly involved in regulating areal growth of the body thus influences development of production traits of cattle. *GH* gene polymorphism in Hereford and Limousine bull calves is shown in Table 1.

Table 1. 1 *GH* gene polymorphism in Hereford and Limousine bull calves.

Breed	n	Genotypes						Allele frequency	
		LL		LV		VV			
		heads	%	heads	%	heads	%	L	V
Hereford	38	18	47,37	16	42,10	4	10,52	0,684	0,316
Limousine	26	15	57,70	8	30,76	3	11,54	0,731	0,269

The data presented in the table indicate that Hereford bull calves have more *LL* genotype (47,37%) being at 5,27 % more than heterozygous *LV* genotype while the first genotype prevails greater in Limousine cattle (57,7%) with incidence frequency difference between the given genotypes being 26,94 %. Allele L is more evident for Limousine bull calves (0,731).

The most important requirement for fresh meat is its high-quality traits and biological full value. Diacylglycerol acyltransferase (DGAT) enzyme strength is considered to have positive correlation with fat deposition in animal carcass and muscles and this enzyme strength is much higher in KK genotype cattle.

DGAT1 gene polymorphism in Hereford and Limousine bull calves is presented in Table 2.

Table 2 DGAT1 gene polymorphism in Hereford and Limousine bull calves.

Breed	n	Genotypes						Allele frequency	
		KK		AK		AA			
		heads	%	heads	%	heads	%	K	A
Hereford	38	31	81,58	7	18,42	0	0	0,908	0,092
Limousine	26	18	69,23	8	30,77	0	0	0,846	0,154

The data of Table 2 shows higher KK genotype frequency for bull calves of both breeds and total absence of AA genotype among the studied animals. For Hereford bull calves KK genotype frequency is higher compared to heterozygous genotype at 63,16 %. Among Limousine bull calves there are more AK heterozygous genotype animals (30,77%). K allele frequency is higher for Hereford bull calves.

Real and expected heterozygosity in *GH* and *DGAT1* genes are presented in Table 3.

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Table 3 Real and expected heterozygosity rate in bGH and DGAT1 genes.

Bredd	H_o	H_e	F	N_e	χ^2
GH					
Hereford	0,421	0,433	-0,012	1,764	0,03
Limousine	0,308	0,394	-0,086	1,650	1,87
DGAT1					
Hereford	0,184	0,168	0,016	1,202	0,15
Limousine	0,307	0,260	0,047	1,049	0,85

H_o – observed heterozygosity; H_e – expected heterozygosity; N_e – number of effective alleles; F - Ho-He diffeerence, «+/-» - heterozygote surplus/shortage, χ^2 – correspondence criteria of observed and expected genotype distribution.

The Table data give evidence that expected rate of heterozygosity in GH gene is higher than of the observed indicators in the studied populations of Hereford and Limousine bull calves.

There is higher observed heterozygosity in DGAT1 gene. The number of effective alleles in the studied genes is higher for Hereford bull calves. In total according to the correspondence criteria of observed and expected genotype distribution in GH and DGAT1 genes both studied populations are equal.

In terms of collective genotype distribution in GH and DGAT1 genes there are more LL/КК genotype animals (39,48%) and LV/КК genotype animals (34,22%) among Hereford cattle, while there are mostly animals of LL/КК genotype (50%), LV/АК genotype (19,23%) and LV/КК genotype (11,54%) among Limousine cattle that signals quite good genetic potential of the studied bull calves.

Studies of live animal beef production traits and finding out association between genotypes in GH and DGAT1 genes were carried according to the weighing of bull calves under the experiment at the age of 8, 12, 16 and 20 months. Growth and development indicators of different genotype bull calves are given in Tables 4 and 5.

Table 4 Liveweight gain of different genotype bull calves according to bGH gene, ($X \pm S_x$)

Indicator	Breed/genotype					
	Hereford			Limousine		
	LL (n=18)	LV (n=16)	VV (n=4)	LL (n=15)	LV (n=8)	VV (n=3)
Liveweight, kg - new-born bull calves	33,4 ±0,93	32,9 ±0,68	33,6 ±0,61	34,3 ±0,75	33,7 ±0,66	33,8 ±0,81
- at the end of fattening	580,6 ±9,18*	569,4 ±8,34	553,7 ±8,98	608,9 ±10,05*	597,6 ±9,89	578,3 ±9,62
Absolute weight gain during the trial time, kg	547,2 ±9,05*	536,5 ±8,99	520,1 ±9,01	574,6 ±10,81*	563,9 ±9,85	544,5 ±9,13
Average daily weight gain during the trial time, g	908,8 ±15,58*	891,2 ±16,11	864,0 ±15,29	954,5 ±17,05*	936,7 ±15,08	904,5 ±16,05
Relative growth rate, %	178,2 ±1,25	178,0 ±1,95	177,1 ±1,11	181,9 ±1,53	178,6 ±1,91	177,9 ±1,65

*P<0,05

Table 4 data prove that LL genotype Hereford and Limousine animals have the highest rate of liveweight of 580,6 kg and 608,9 kg, that is certainly higher (P<0,05) than liveweight of VV genotype cattle at 4,6 % and 5,0 % correspondingly. The share of heterozygous genotype LV animals is 42-30 % of the total amount. On the whole it is expectedly that LL genotype Hereford and Limousine animals have higher absolute and average daily weight gains ((P<0,05) compared to the VV genotype cattle of the same age at 4,9 % and 5,5 %. Relative growth rate of LL and LV genotype Hereford bull calves is equal being less for VV genotype animals. LL genotype Limousine calves grow faster that is proved by the fact that this indicator is lower for LV and VV genotype animals at 3,3 % and 4,0 % correspondingly.

ISSN: 0975-8585

Table 5. Liveweight gain of different genotype bull calves according to DGAT1 gene, ($X \pm S_x$)

Indicator	Breed/genotype			
	Hereford		Limousine	
	КК (n=31)	АК(n=7)	КК (n=18)	АК (n=8)
Liveweight, kg - of new-born calves	33,0 ±0,74	32,9 ±0,81	33,9 ±0,79	34,1 ±0,90
- at the end of fattening	569,3 ±7,31	576,7 ±8,35	591,8 ±8,18	597,9 ±6,19
Absolute weight gain for the raising period,kg	536,3 ±7,11	543,8 ±7,09	557,9 ±7,89	563,8 ±6,00
Average daily weight gain for the raising period, g	890,8 ±9,02	903,3 ±9,61	926,7 ±9,11	936,5 ±8,77
Relative growth rate, %	178,1 ±1,42	181,4 ±1,53	178,3 ±1,44	178,4 ±1,58

It should be noted that at the end of the experiment there was no evident difference in liveweight of animals of different genotypes in DGAT1 gene that can be explained with high association of DGAT1 gene with beef quality traits rather than areal growth of the body. Nevertheless while there were no AA genotype animals, AK genotype cattle gained some liveweight at 1,3 % for Hereford bull calves and 1 % for Limousine ones. In a similar way indicators of absolute and average daily weight gain are different. Relative growth rate of the studied genotype animals was about 178 %, except AK genotype Hereford bull calves (181,4 %).

Indicators of post-slaughter estimate of beef production traits for different genotype bull calves in GH gene are given in Table 6.

Table 6 Slaughter results of different genotype bull calves in GH gene, ($X \pm S_x$)

Indicator	Breed/genotype					
	Hereford			Limousine		
	LL (n=5)	LV (n=5)	VV (n=3)	LL (n=5)	LV (n=5)	VV (n=3)
Pre-slaughter liveweight,kg	561,5 ±9,21*	552,1 ±9,68	535,8 ±8,11	587,6 ±8,02*	578,0 ±7,29	561,5 ±7,01
Hot carcass weight, kg	332,9 ±7,61	325,7 ±7,42	312,0 ±7,51	353,6 ±7,12*	346,0 ±7,01	329,6 ±6,57
Carcass output, %	59,3 ±0,31*	59,0 ±0,39	58,2 ±0,30	60,2 ±0,42*	59,9 ±0,51	58,7 ±0,54
Internal raw fat weight, kg	19,1 ±0,15	19,3 ±0,17	18,8 ±0,22	17,1 ±0,27	16,9 ±0,21	16,7 ±0,45
Fat output, %	3,40 ±0,07	3,50 ±0,08	3,50 ±0,07	2,90 ±0,08	2,92 ±0,07	2,97 ±0,14
Post-slaughter weight, kg	352,0 ±8,18	345,0 ±7,11	330,8 ±7,02	370,7 ±8,81	362,9 ±9,11	346,3 ±8,51
Post-slaughter output, %	62,7 ±0,34*	62,5 ±0,34	61,7 ±0,30	63,1 ±0,42*	62,8 ±0,31	61,6 ±0,41

*P<0,05

According to the given table one can see that the studied bull calves of *LL genotype exceed those of VV* genotype (P<0,05) in following indicators: Pre-slaughter liveweight by 4,57 % (Hereford breed); hot carcass weight at 6,78 % and post-slaughter output by 1,5 % (Limousine breed). True differences in the above mentioned indicators of morphological carcass content show their higher dependence on growth hormone GH gene. Animals of both studied breeds of LL genotype compared to LV and VV genotype cattle have unreliable higher indicators of hot carcass weight, internal raw fat weight, fat output and slaughter weight.

Indicators of post-slaughter estimate of beef production traits of different genotype bull calves in DGAT1 gene are presented in table 7.

ISSN: 0975-8585

Table 7 Slaughter results of different genotype bull calves under experiment in DGAT1 gene, ($X \pm S_x$)

Indicator	Breed/Genotype			
	Hereford		Limousine	
	KK (n=5)	AK(n=5)	KK (n=5)	AK (n=5)
Pre-slaughter liveweight,kg	551,1±8,26	561,5±7,91	572,8±8,34	573,9±7,94
Hot carcass weight, kg	324,3±6,99	332,4±7,12	342,0±7,18	348,0±6,14
Carcass output, %	58,8±0,62	59,2±0,56	59,7±0,55	60,6±0,56
Internal raw fat weight, kg	18,3±0,06	17,63±0,05	17,9±0,11*	17,6±0,06
Fat output, %	3,32±0,02*	3,14±0,01	3,1±0,01*	3,06±0,01
Post-slaughter weight, kg	342,6±5,08	350,6±6,01	359,9±6,05	365,6±5,99
Post-slaughter output, %	62,2±0,16	62,4±0,18	62,8±0,17	63,7±0,15

*P<0,05

The received results on slaughter and morphological carcass content of different genotype bull calves by DGAT1 gene prove tendencies in higher pre-slaughter liveweight, hot carcass weight, carcass output and post-slaughter output of AK genotype animals. The true difference in fat output (P<0,05) is found among KK and AK genotype carcasses of Hereford animals. High fat output of Hereford bull calves is due to their breed characteristics.

Studies on chemical composition of beef make it possible to discuss its nutrient value as well as reflect aging and breed properties of animal body. Chemical composition of the rib eye of different genotype bull calves in GH gene are shown in Table 8.

Table 8 Beef chemical composition of different genotype bull calves in GH gene GH, ($X \pm S_x$)

Indicator	Breed/genotype					
	Hereford			Limousine		
	LL (n=5)	LV (n=5)	VV (n=3)	LL (n=5)	LV (n=5)	VV (n=3)
Total moisture, %	72,48 ±1,29	72,09 ±2,26	71,94 ±1,31	72,76 ±1,83	72,10 ±1,08	71,69 ±2,25
Dry matter, %	27,52 ±0,89	27,91 ±0,76	28,06 ±0,95	27,24 ±0,93	27,90± 1,06	28,31 ±1,12
including, protein	21,24 ±1,33	21,70 ±1,08	21,09 ±1,86	20,86 ±2,60	20,78 ±2,03	21,10 ±1,96
fat	5,32 ±0,37	5,24 ±0,12	6,01 ±0,47	5,42 ±0,11	6,16 ±0,32	6,24 ±0,19*
ash	0,96 ±0,02	0,97 ±0,02	0,96 ±0,02	0,96 ±0,02	0,96 ±0,02	0,97 ±0,02
phosphorus, g/kg	1,18 ±0,02	1,23 ±0,02	1,18 ±0,02	1,14 ±0,02	1,14 ±0,02	1,15 ±0,02

*P<0,05

As the result of chemical composition examination we found association between *VV* genotype and fat deposition in the rib eye of Limousine bull calves, evident difference (P<0,05) between *LL* and *VV* genotypes is 1,22%. There is much intramuscular fat in Limousine bull calves due to their breed characteristics. In terms of other indicators there is less moisture and more dry matter in carcass of both studied animal breeds in the LL→LV→VV line, Hereford animals are characterized by higher content of protein and fat.

Chemical composition of the rib eye of different genotype bull calves in *DGAT1* gene are shown in Table 9.

When chemical composition of the rib eye of different genotype bull calves in *DGAT1* gene was studied we found evident difference (P<0,05) in fat content for KK genotype Limousine animals (6,61%).

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Table 9 Chemical composition of beef of different genotype bull calves in DGAT1 gene, ($X \pm S_x$)

Indicator	Breed/genotype			
	Hereford		Hereford	
	КК (n=5)	АК(n=5)	КК (n=5)	АК (n=5)
Total moisture, %	71,61±3,04	71,78±2,38	71,77±2,44	71,86±2,26
Dry matter, %	28,39±1,18	28,22±1,17	28,23±1,44	28,14±1,24
including, protein	22,04±1,03	21,96±1,14	21,66±1,12	22,03±1,16
fat	5,38±0,18	5,31±0,17	5,21±0,25	5,14±0,14
ash	0,97±0,02	0,95±0,02	0,96±0,002	0,97±0,03
phosphorus, g/kg	1,19±0,02	1,20±0,03	1,14±0,04	1,15±0,02

*P<0,05

When chemical composition of the rib eye of different genotype bull calves by DGAT1 gene was studied no true difference in indicators of the studied animals was found.

There is a stable tendency in higher moisture and lower dry matter and protein content in the rib eye of AK genotype animals as well as lower fat in KK genotype animals. Evident changes in the level of ash and phosphorus aren't observed.

DISCUSSION

An animal breed is one of the key factors having impact on beef production traits. While studying GH gene polymorphism in both studied breeds, we found high frequency of L allele (0,68 and 0,73) compared to allele V (0,32 and 0,27). The resulting data being evidence for breed specificity of growth hormone gene go with research results of GH polymorphism for Hereford and Limousine cattle bred in Tatarstan. In animal populations there is high frequency of L allele (0,61 and 0,85) as well as V allele (0,39 and 0,15), Hereford cattle showed high frequency of heterozygous genotype (44,40%) [29] as it was observed in our studies (42,10%). Though when local Hereford cattle bred in Siberia was studied they found low frequency of heterozygous genotype being 10-34 % [30]. As Gorlov et al. consider [12] C allele of GH gene has a negative effect on meat marbling but promotes higher carcass weight and thus higher beef output. In this regard the authors recommend to think heterozygous genotype of bGH gene as economically profitable in animal breeding as this genotype provides high quality beef (marbling) from the one sight and high beef output from the other one.

Animals of both studied breeds in DGAT1 gene have high frequency of К allele (0,91 and 0,85) and low frequency of А allele (0,09 and 0,05). The resulting data correspond to those of Li et al. [20] that found high frequency of GC allele (1,0 and 0,94) and low one for allele AA (0,00 and 0,06) in Swedish Hereford and Limousine cattle as well as Avilйs C. et al. (2014) found allele К (0,84) and allele А (0,18) in Limousine cattle bred in Spain. There is evidence of no KK genotype in Simmental bull calves [14] and Kazakh white-headed animals [12].

In the available resources there is much information on association of GH gene polymorphism with beef production traits. Balanced growth and development of muscle, connective and bone tissues and fat deposition provide their best proportion in animal carcass and higher beef output being an indicator of high beef production capacity [2,12,20,23,29,30,36].

Analysis of liveweight dynamics at different age periods showed advantage of *LL* genotype animals, there is evident difference in absolute and average daily liveweight gain. The derived data correspond to the results [30,34] and confronts the results of *Lee et al*. [19] that found evident increase (P<0,05) in average daily liveweight gain in GG genotype bull calves of Korean Hanwoo breed.

Bull calves of different genotype in DGAT1 gene didn't show evident difference in liveweight gain at the end of fattening.

Post-slaughter bull calf meat productivity assessment for both studied breed found evident differences (P<0,05) in pre-slaughter liveweight and post-slaughter output between LL and VV genotypes in growth hormone. It is also established that КК genotype bull calves in DGAT1 gene have higher fat output (P<0,05). It indirectly corresponds to the research results *Gill* et al. [10], Curi et al. [5], Avilйs et al. [3] when they are related to the depth of subcutaneous fat. Other studies didn't find this relationship [22,24].

When chemical composition of the rib eye was examined there was evident increase in intramuscular fat (6,61%) in VV genotype Limousine bull calves in GH gene. Most researchers argue that intramuscular fat content has a positive impact on beef marbling and VV genotype is associated with this indicator. Tatsuda et al. [34] found that marbling quality prevails in *GG* (Val/Val) genotype of Japanese black cattle.

Moreover there are facts on positive correlation between DGAT1 enzyme performance and intramuscular fat content in the rib eye and semitendinous muscle. In Holstein-Frisian and Carolas cattle of the desired KK genotype DGAT1 performance was 5 times higher compared to AK and AA genotype bearers [31].

In our research of K232A gene polymorphism in *DGAT1* gene evident difference in the rib eye fat content between КК and АК genotype animals wasn't found. True higher intramuscular fat of KK genotype animals is discussed in Wu et al. [38] and Avilйs et al. [3]. Anton et al. [1] revealed higher indicators for AA/AA genotype animals.

Thus, the analyzed SNP in GH gene of the studied bull calves is apparently associated with liveweight indicators at the end of fattening, absolute and average daily growth, pre-slaughter liveweight (for Hereford breed) and hot carcass weight as well as the rib eye intramuscular fat content (for Limousine breed). When K232A gene polymorphism in DGAT1 gene was studied both populations turned to be out of AA genotypes that maybe due to a small number of studied animals. There is an evident effect of DGAT1 gene polymorphism on fat output for Hereford animals. We find it necessary to continue our research by increasing a livestock number as well as to study other beef cattle bred in the region. The received results can be used to improve genetic potential of beef cattle kept in the Cis-Ural steppe zone.

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