The frequency of somatotropic cascade polymorphic genes appearance and the meatiness and health of Auliekol and Kazakh white-headed cattle

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ABSTRACT

Modern cattle breeding is characterised by the need to select specific animals with extraordinary meat performance, as well as an ability to adapt to the natural environment in order to develop new, improved breeds. As Auliekol and Kazakh white-head races are especially interesting to farmers in Kazakhstan, we chose to study three polymorphs of somatotropic cascade genes: bPit-1, bGH and bGHR in the whole blood of such animals, which are known to have an impact on meatiness and good health. The following polymorphic variations were revealed: bPit-1-HinFI and bPit-1-HinF1; bGH-AluIV and bGH-AluIL, as well as bGHR-SspIY and bGHR-SspIF. The agreement of the observed frequencies of genotypes with those theoretically expected according to the Hardy-Weinberg law of balance was also assessed. The final task was to compare the frequency of appearance of polymorphic genes alleles' with somatotropic cascade distribution in the examined animals. Our studies have shown that the frequency of the genotypes' occurrence in both races is in compliance with the frequency based on the law of balance. We suggest that the polymorphisms of the cascade network may result from the breeding progress achieved by directional selection, therefore conditioning high values of meat and health characteristics in the examined cattle.

Key words: meat breed of cattle; polymorphism; somatotropic cascade genes; alleles

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Introduction

The main objective of modern breeding is to improve production efficiency and product quality through planned genetic changes (DISKIN and KENNY, 2016). In the case of cattle, selection of animals with outstanding meat performance and a high degree of adaptation to the natural environment is a priority in order to develop new breeds with improved characteristics. Among such species, Auliekol and Kazakh white-head are of particular interest to livestock farming in the territory of Kazakhstan. The Auliekol breed is the result of crossing Aberdeen Angus (Scotland) and Charolais

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(France) breeds with a local white-headed breed of cows (KAYUMOV et al., 2012; ZHUZENOV et al., 2012). The Kazakh white-headed breed is bred, in turn, by crossing the Kalmyk and Kazakh cow breeds with Hereford bulls (BOZYMOV et al., 2015). High performance of meat, early maturity, the ability to adapt to hot and cold climates, as well as adaptation for use in natural pastures, allow us to recommend these breeds for breeding in countries with similar climatic conditions.

Modern DNA technologies are helping to accelerate breeding and reduce the financial costs of breeding highly productive breeds of farm animals (AHMED and KHOSA, 2010). For example, marker-associated selection (MAS) provides information about the association of polymorphic alleles of genes (candidate genes) responsible for the manifestation of quantitative traits, such as milk and meat productivity, and allows us to estimate the genetic potential productivity of animals in the early stages of postnatal development (REZENDE et al., 2012). For breeding beef cattle, the gene of somatotropin (growth hormone, an essential regulator of growth in mammals) is of great interest and is involved in the work of the whole hormonal cycle of the somatotropic cascade (HU et al., 2016; KANG et al., 2015; KASUYA, 2016; MENSE et al., 2015; MULLEN et al., 2011). This includes genes such as the gene for pituitary growth factor-1 (*bPit-1*) involved in regulating gene expression of growth hormone, and the gene of the growth hormone receptor (*bGHR*) responsible for the mediation of its physiological effects on target cells (BLOTT et al., 2003; DIERKES et al., 1998). Introduction of growth hormone into the diet of meat animal breeds leads to an increase in the rate of growth and intensity of accumulation of muscle mass (GOHARY et al., 2015). However, numerous pieces of evidence suggest that regular consumption of the meat of such animals leads to a number of serious diseases in humans, including cancers (NACHMAN and SMITH, 2015), apart from diseases also caused by the accumulation of pesticides in the body (ŁOZOWICKA et al., 2012). Therefore, the most safe and effective method of intensification of the breeding process is the search for allelic variants of the genes of the

somatotropic cascade associated with increased meat productivity, and their application during the selection process (THOMSEN, 2006).

Somatotropin genes, like other genes responsible for the development of quantitative traits, are polymorphic (MOHAMMADABADI et al., 2010). It is known that some alleles of somatotropic genes are associated with a high potential for meat and milk production in cattle (PAWAR et al., 2007). In the literature, a number of positions are dedicated to the association of alleles of genes of the somatotropic cascade (*bPit-1, bGH* and *bGHR*) with the productivity traits obtained in different breeds of cattle (BOICHARD et al., 1997). For example, the most studied polymorphic variant of the gene *Pit-1* is the *Pit1-HinfI*, first described by WOOLARD et al., (1994), and subsequently identified as a silent G→A substitution in the region of the sixth exon. The polymorphisms of GH gene - *bGH*-AluI^L and *bGH*-AluI^V are also associated with performance traits in cattle, as this gene plays an important role during the growth and lactation of animals. With respect to the GHR-AluI polymorphism, MAJ et al., (2006) in the study of the association of the polymorphism of GHR-AluI with the characteristics of meat productivity of Polish black and white breed animals showed that animals which are the carriers of allele AluI (-) had higher rates of parameters such as body weight and the mass of cuttings (MAJ et al., 2006). However, the data obtained on different species are difficult to compare and to some extent contradict each other (BOICHARD et al., 1997). Moreover, for a large part of the identified alleles such studies have not been conducted.

Data on the presence of the marker alleles of the somatotropic cascade of genes, and their association with the characteristics of the meat productivity of Kazakh populations of cattle are missing. At the same time, information about genetic markers of the meat productivity of local breeds is extremely important as local breeds are well adapted to the local climate conditions, prey base, and have resistance to diseases prevalent in the territory of Kazakhstan. This gives them an undoubted advantage as an object of beef cattle breeding. Therefore, the aim of our work was to

conduct DNA typing of samples of meat breeds of the Kazakh white-headed and Auliekol cattle, and to assess the presence and frequency of polymorphic variants of genes of the somatotropic cascade *bPit-1, bGH* and *bGHR*.

Materials and methods

Animal specimens and DNA extraction. Two groups of animals were used in the experiment: the first group consisted of females of the Kazakh white-headed breed (n=25), and the second group of females of the Auliekol breed (n=25). The ages of the examined animals ranged from 2 to 3 years, and the weight of individuals was between 500-600 kg. The animals were kept in stall-pasture conditions. DNA samples were extracted from whole blood of animals using the DiatomTM Prep200 (Lab Isogen, Moscow) kit, according to the manufacturer's instructions.

PCR-RFLP. To identify the polymorphism of the *bPit-1*-HinI we used the following amplification conditions: 94 °C– 1 min; (95 °C – 45 sec; 56 °C – 6 sec; 72 °C– 6 sec) x 35 cycles; 72 °C – 1 min; primer sequences: forward — 5'-aaaccatcatctcccttctt-3', reverse — 5'-ccgtgtctatgagaagc-3'. To identify the polymorphism of the *bGH*-AluI, we used the following amplification conditions: 95 °C – 5 min; (95 °C – 3 sec; 64 °C – 3 sec; 72 °C – 6 sec) x 35 cycles; 72 °C – 1 min; primer sequences: forward — 5'-ccgtgtctatgagaagc-3', reverse — 5'-gttcttgagcagcgcgt-3'. To identify the polymorphism of the *bGHR*-SspI, we used the following amplification conditions: 94 °C – 1 min; (95 °C – 3 h; 60°C – 3 sec; 72 °C – 3 sec) x 35 cycles; 72 °C – 1 min; primer sequences: forward — 5'-aatatgtagcagtgacaatat-3', reverse — 5'-acgtttcactgggttgatga-3'. The resulting PCR amplification products were cut with the help of site-specific restriction enzymes: HinFI (Invitrogen™, USA; to identify gene polymorphisms *bPit-1* in exon 6), AluI (Invitrogen™, USA; to identify gene polymorphisms in *bGH* exon 5) and SspI (Invitrogen™, USA; for detection of *bGHR* gene polymorphism in exon 8). The resulting fragments were separated by the length of the nucleotide sequence using electrophoresis in 2 % agarose gel (SeaKemLEAgarose, Lonza, USA). We used O'RangeRuler™ 50 bp DNA Ladder, Fermentas (Lithuania) as a marker of molecular masses.

Statistical analysis. The comparison of the samples was performed according to the distribution of the allele frequencies of the studied genes, and assessment of the conformity of the actual distribution of genotypes theoretically expected according to the law of Hardy-Weinberg equilibrium ($p^2 + 2pq + q^2 = 1$ where p^2 is the proportion of homozygotes for one allele; p - the frequency of this allele; q^2 is the proportion of homozygotes for the alternative allele; q is the frequency of the corresponding allele, 2pq is the proportion of heterozygotes) was performed using the χ^2 criterion. The differences were considered statistically significant when probability was P < 0.05.

Results

Analysis of single-nucleotide polymorphisms (SNP) of genes bPit-1-HinFI, bGH–AluI and bGHR-SspI. Gene polymorphism *bPit-1* in exon 6 is determined by A→G nucleotide substitution that does not cause a change in amino acid sequence. The recognition site for HinFI restrictase is the sequence G↓ANTC. A cut fragment during fermentation includes A nucleotide corresponding to allele *bPit-1*-HinFI*^B*, which is the most common. In more rare cases, the nucleotide sequence contains the nucleotide G and therefore, the restriction site is absent. In this study we investigated polymorphic variants of the gene *bPit* in populations of the Auliekol and Kazakh white breeds. Using PCR-RFLP we showed that the length of the amplificative gene fragment *bPit-1* was 451 BP, and the length of fragments after restriction - 244 and 207 BP. On the electrophoretogram (Fig. 1 (A) options bands are visible that are typical for genotypes *bPit-1*-HinFI*^{AA}* (one lane 451 BP), *bPit-1*-HinFI*^{BB}* (two bands of 244 and 207 BP), and *bPit-1*-HinFI*^{AB}* (three lanes 451, 244 and 207 BP).
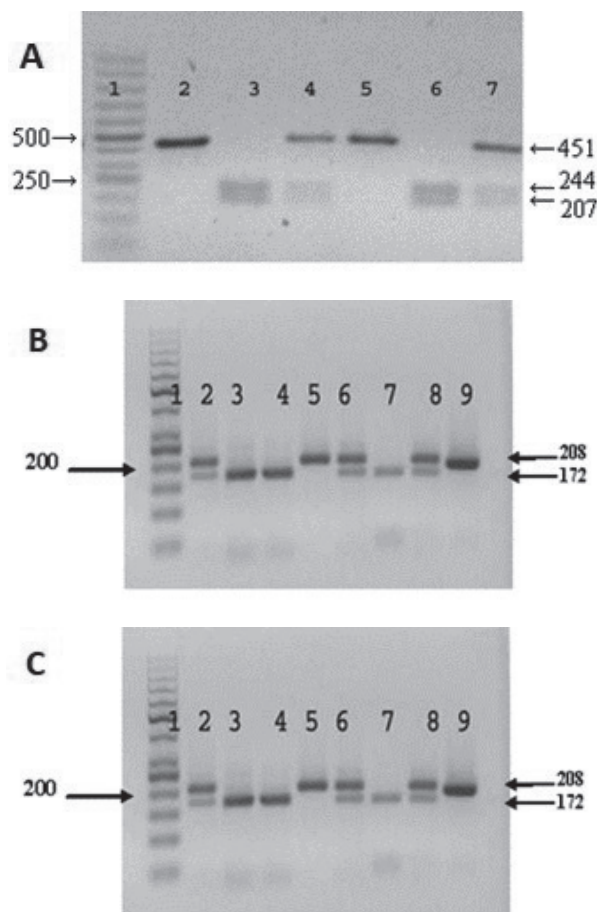
Fig. 1. Electrophoretogram DNA typing of
polymorphisms bPit-1-HinFI, bGH-AluI, bGHR-SspI

A. lane 1 – molecular mass marker; lane 2 – PCR product of a fragment of the gene *bPit-1*-HinFI 451 BP; lanes 3 and 6 restriction fragments of 244 and 207 BP, corresponding to genotype *bPit-1*-HinFI^{BB}; lanes 4 and 7 — restriction fragments of 451, 244 and 207 BP, corresponding to genotype *bPit-1*-HinfI^{AB}; lane 5 – a restriction fragment of 451 BP, the corresponding genotype *bPit-1*-HinFI^{AA}. **B.** Lanes 2 and 6 —fragments of the restriction 208, 172, 35 BP, corresponding to the genotype *bGH*-AluI^{LV}; lanes 3, 4 and 7 – restriction fragment of 172 BP, corresponding to the genotype *bGH*-AluI^{LL}; lane 5 – a restriction fragment of 208 BP corresponding to the genotype *bGH*-AluI^{VV}; lane 9 – the PCR product is 208 BP gene fragment of the *bGH*-AluI. **C.** lane 1 – PCR product of 182 BP fragment of the gene *bGHR*-SspI; lanes 2, 3 and 4 – a restriction fragment of 158 BP, corresponding to genotype *bGHR*-SspI^{FF}; lane 5 – a restriction fragment of 182 BP corresponding to the genotype *bGHR*-SspI^{YY}; lane 6 – fragments of the restriction of 182 and 158 BP, corresponding to genotype *bGHR*-SspI^{FY}. The 24 BP fragment was not visualized.

The polymorphism of the nucleotide sequence of *bGH* gene in exon 5 is due to the C→G transition resulting in amino acid replacement of leucine for valine in the protein sequence. The recognition site for AluI restrictase is the AD↓ST sequence. The enzyme recognizable allele contains a nucleotide C and is referred to as *bGH*-AluI^L. In the case of the presence of G the nucleotide restriction site disappears and this allele is referred to as *bGH*-AluI^V. In our work it was shown that the length of the amplificated *bGH* gene fragment was 208 BP. The length of fragments after restriction was 172 and 35 BP. The electrophoretogram (Fig. 1B) showed versions of the visible bands of a certain length characteristic of the genotype *bGH*-AluI^{VV} (one lane 208 BP) *bGH*-AluI^{LL} (two strips 172 and 35 BP) and *bGH*-AluI^{LV} (three stripes 208, 172 and 35 BP). The restriction fragment of 35 BP was not visualized on agarose gel.

In the exon of the 8 bGHR gene a single-nucleotide polymorphism was found, which led to the replacement of a neutral phenylalanine at position 279 of the protein polar, although with uncharged residue tyrosine. The recognition site for SspI restrictase is the sequence AAT↓ATT. The cut fragment contained thymine and corresponded to the allele *bGHR*-SspI^F. If adenine is in this position, – the restriction site is absent and the allele is referred to as *bGHR*-SspI^Y. In our work it was shown that the length of the amplified *bGHR* gene fragment was 182 BP. The length of fragments after restriction was 158 and 24 BP. On the electrophoretogram (Fig. 1C) bands of a specific length were visible, typical for the genotypes *bGHR*-SspI^{YY} (single band of 182 BP), *bGHR*-SspI^{FF} (two bands 158 and 24 BP) and *bGHR*-SspI^{FY} (three bands – 182, 158 and 24 BP). No fragment of 24 BP was visualized on agarose gel.

Evaluation of the conformity of the observed genotype frequencies with those theoretically expected according to the law of Hardy-Weinberg. We investigated the genetic structure of populations of Auliekol and Kazakh white-headed cattle using the method of genotyping, comparing this observed frequency of genotypes and the theoretically expected equilibrium distribution, calculated in accordance with the law of the Hardy-Weinberg equilibrium (Table 1).

Table 1. The distribution of genotype frequencies in the samples of animals of Auliekol
and Kazakh white-headed breeds

Polymor-phism	Genotype	Auliekol breed (n=25)			Kazakh white-headed breed (n=25)		
		n observed	n expected	χ^2	n observed	n expected	χ^2
bPit-1-HinFI	bPit-1-HinFI^{AA}	3	4	0.69	6	6	0.004
	bPit-1-HinFI^{AB}	14	12		12	12	
	bPit-1-HinF1^{BB}	8	9		7	7	
bGH-AluI	bGH-AluI^{VV}	9	10	1.16	18	17	2.60
	bGH-AluI^{LV}	14	12		5	7	
	bGH-AluI^{LL}	2	3		2	1	
bGHR-SspI	bGHR-SspI^{YY}	21	20	2.78	13	14	2.49
	bGHR-SspI^{FY}	3	5		12	9	
	bGHR-SspI^{FF}	1	0		0	1	

Note: The deviation of observed genotype frequencies from the theoretically expected according to the law of Hardy-Weinberg equilibrium is significant at $\chi^2 \geq 3.84$

From the data given in the Table it is understood that in both populations the observed frequencies of genotypes correspond to the theoretically expected frequencies on the basis of the law of the Hardy-Weinberg equilibrium. This suggests that the polymorphisms *bPit-1*-HinFI, *bGH*-AluI and *bGHR*-SspI can be associated with economically useful traits in Auliekol and Kazakh white-headed cattle. Most likely, they were subjected to the indirect pressure of artificial selection, but the nature of this selection was not directional.

Comparative analysis of the allele frequencies of polymorphic genes of somatotropiccascade distribution in representatives of the Auliekol and Kazakh white-headed breeds. Differences in the relative frequency of the alleles of genes *bPit-1*, *bGH* and *bGHR*in the population of Auliekol and Kazakh white-headed cattle are shown in Table 2. It is revealed that HinFI-allelic versions of the gene *bPit-1* in representatives of the Auliekol breed make up 0.400 to 0.600 alleles for *bPit-1*- HinFI^A and *bPit-1*-HinFI^B respectively. At the same time, for the Kazakh white-headed, the ratio is almost 1:1 (0.480:0.520).

Table 2. The distribution of relative frequencies of the studied genes alleles in populations of Auliekol
and Kazakh white-headed cattle (Q ±SQ)

Polymorphism	Allele	The observed frequency of Alleles		Relative frequencies of Alleles		χ^2
		Auliekol breed	Kazakh white-headed breed	Auliekol breed	Kazakh white-headed breed	
bPit-1-HinFI	bPit-1-HinFI^A	20	24	0.400±0.02	0.480±0.02	0.442
	bPit-1-HinFI^B	30	26	0.600±0.02	0.520±0.02	
bGH-AluI	bGH-AluI^V	18	9	0.360±0.02	0.180±0.02	0.0454
	bGH-AluI^L	32	41	0.640±0.02	0.820±0.02	
bGHR-SspI	bGHR-SspI^Y	5	12	0.100±0.01	0.240±0.02	0.0654
	bGHR-SspI^F	45	38	0.900±0.01	0.760±0.02	

Note: the difference between breeds is significant at P<0.05.

The alleles *bGH*-AluI^V and *bGHR*-SspI^Y were more rare for both breeds of animals. Their frequency in representatives of the Auliekol breed amounted to 0.100 and 0.360 respectively, and for the Kazakh white-headed breed — 0.180 and 0.240, respectively.

Discussion

The number of known genes that have an impact on the specific quantitative features has not been finally determined, which is why the genotyping of animals based on the newly discovered SNP is important, connected to gathering information allowing them to be linked with usability. It is an important element of strategy determined as the search for (choice of) candidate genes, in which protein products play a direct role in specific physiological processes. Many studies indicate (PARMENTIER et al., 1999; CASTIGLIEGO et al., 2010; RENAVILLE et al., 2002) that various genes coding the elements of the somatotropic axis are directly matched with cow usability. The center of the somatotropic axis consists of a growth hormone peptide, which controls metabolism and growth in vertebrates. GH actions are mediated and regulated by many proteins, which together create a comprehensive system of interrelated interactions called the somatotropic axis. GH is secreted to the system via the frontal lobe of the hyphophysis. Secretion is controlled via the two hypothalamic neuropeptides: somatoliberin (GHRH, stimulation of secretion) and somatostatin (SRIF, inhibition of secretion) (SALVATORI, 2004). After GH secretion into the circulatory system, it quickly binds with GH-binding proteins (GHBP) into a complex that increases its half-life (BAUMAN, 1994). In target tissues, after separation from the GH complex, it binds to a specific receptor on the surface of the target cell (GHR). The largest clusters of these receptors are found in hepatocytes, but they have also been found in other organs and tissues, including the mammary glands of cows (SINOWATZ et al., 2000; PLATH-GABLER et al., 2001). Due to the catalytic properties of the intracellular domain of the GHR (tyrosine kinase activity), a signaling cascade is triggered, as a result of which the transcription factors of genes mediating the GH signal are activated. Its further transmission is mediated primarily by insulin-like growth factor I (IGF-I) together with its receptor - IGF-IR. Molecular analysis of genes encoding the major components of the somatotropic axis, as well as a number of other important intracellular mediators associated with them, can provide a great deal of valuable information related to the performance and health of cattle.

The SNP polymorphism of the gene *bPit-1* was carried in the Holstein-Friesian breed, as well as the meat breeds Belgian blue, Polish black and white, Piemontese and Angus. However, the data obtained in these studies has been inconsistent. A number of studies have been conducted on the relationship of polymorphic gene variants of *Pit-1* with characteristics of meat productivity from representatives of Angus cattle, and have noted that associations of the polymorphisms with growth rate or carcass parameters were virtually absent (GE et al., 1997; RENAVILLE et al., 1997; ZHAO et al., 1992). Other authors (BELAYA et al., 2010) have shown that Holstein cows and Holsteinised black-motley breeds have a tendency to increase their yield of milk, butterfat and protein content in groups with genotype *bPit-1*-HinFI^{BB} compared to groups of cows with genotypes *bPit-1*-HinFI^{AB} and *bPit-1*-HinFI^{AA}. Research carried out by ZWIERZCHOWSKI et al., (2002) on Polish meat breeds of cattle has shown that the genotype *HinF^A* is rare in the studied population, and is associated with higher meat productivity, as well as indirectly with healthiness.

Our research has provided results relating to the distribution of the allele frequencies *bPit-1*-HinFI^A and *bPit-1*-HinFI^B in Auliekol and Kazakh white-headed cattle populations that are the major beef breeds in the territory of Kazakhstan.

The share of alleles of the gene *bPit-1* in representatives of the Auliekol breed comprise 0.400 (*bPit-1*-HinFI^A) to 0.600 (*bPit-1*-HinFI^B). At the same time, for the Kazakh white-headed breed, the ratio is almost 1:1 (0.480:0.520). These results complement the available literature data, and indicate the high frequency of the allele *bPit-1*-HinFI^A, compared to other breeds. For example, in Holstein and Holsteinised black-and-white dairy cattle, the frequency of *bPit-1*-HinFI^A allele

amounted to 0.21 and 0.23, respectively (BELAYA et al., 2010).

The GH gene that plays an important role in the processes of growth and lactation of animals also has several polymorphic variants. Using PCR-RFLP and restriction enzyme AluI, two alleles responsible for two alternative forms of bovine somatotropin with a residue of leucine or valine at position 127 were revealed (JIANG and LUCY, 2001). In most studies, animals with the genotype VV showed lower growth rates than animals with genotype LL and LV. They also had lower weight and daily weight gain. In the work by ZWIERZCHOWSKI et. al., (2002) it was shown that VV meat bulls had higher daily weight gain compared to bulls possessing other genotypes. On the other hand, DI STASIO et al., (2002) studying Piemontese cattle, showed no association between the polymorphism of the GH gene and characteristics of meat productivity.

The distribution of genotype frequencies for the polymorphism of *bGH* gene showed that in both species considered, the allele of *bGH*-AluI*^{V}* is rare. Its frequency among representatives of the Kazakh white-headed and Auliekol breeds amounted to 0.180 and 0.360, respectively. It should be noted that in populations of Holstein cattle this ratio varies for the allele of *bGH*-AluI*^{V}* from 0.07 to 0.25 (BELAYA et al., 2010). Thus, the frequency of this allele in animals of Auliekol breed was higher than that described in the work of other authors.

Data on the distribution of SspI-alleles of *bGHR* gene frequencies demonstrate that *bGHR*-SspI*^{Y}* allele is rare among representatives of the species we studied (0.100 – 0.240 for Auliekol and Kazakh white-headed). These data are consistent with the data of other authors: according to Fontanesy et al. allele *bGHR*-SspI*^{Y}* frequency in the representatives of the Jersey, Holstein-Friesian and Simmental breeds is 0.05, 0.27 and 0.10, respectively. Allele *bGHR*-SspI*^{F}* frequency in representatives of these breeds reaches 0.95, 0.73 and 0.90 respectively (FONTANESI et al. 2007). There are also other GHR gene polymorphisms that were identified using the restriction enzymes AluI, StuI, and AccI. Their association with performance traits was studied subsequently by: RENAVILLE et al. (1997)

- in Holstein-Friesian bulls; MAJ et al., (2006) - in Polish black and white breed; and GE et al., (1997) - in a population of Angus cattle. Thus, the highest results in these symptoms were typical for animals with the genotype of AluI (–/–) [18]. MAJ et al., (2006) also investigated this polymorphism in meat breeds such as Angus, Limousin and Hereford cattle. Another variant of the polymorphism - FLP-NsiI was associated with daily feed consumption. Genotype –/– or +/– was associated with lower feed intake, and animals with NsiI genotype –/– had a higher percentage of lean cuts, compared to other genotypes (MAJ and ZWIERZCHOWSKI, 2008).

On the basis of the above data, we can assume that the continuation of the study of associations of polymorphic variants of genes *bPit-1*, *bGH* and *bGHR* with characteristics of meat productivity in populations of Auliekol and Kazakh white-headed cattle will help breeders in the selection of individuals with genetically generated high meat productivity. In addition, we assume that the cultivation of such highly productive breeds can be implemented not only in Kazakhstan, from where these are derived, but also in other countries with similar climatic conditions and the need for intensification of livestock farming.

Therefore, using DNA-typing of 50 samples of cattle (25 Auliekol and 25 Kazakh white-headed breeds) we established the animal genotypes for the three polymorphic genes of the somatotropic cascade: *bPit-1*, *bGH* and *bGHR*. The samples of both species revealed polymorphic variants such as *bPit-1*-HinFI*^{A}* and *bPit-1*-HinFI*^{A}*, *bGH*-AluI*^{V}* and *bGH*-AluI*^{L}*, , *bGHR*-SspI*^{Y}* and *bGHR*-SspI*^{F}*. It was established that the allele frequency *bPit-1*-HinFI*^{A}* in the investigated samples was slightly higher than the published data for other breeds, and the frequency of the alleles of *bGH*-AluI*^{V}* and *bGHR*-SspI*^{Y}* was comparable with the results of other authors. The distribution of allele frequencies *bPit-1*-HinFI*^{A}* and *bPit-1*-HinFI*^{B}* was 0.400 to 0.600. Kazakh white-headed and Auliekol cattle breeds are promising for further evaluation of the possible application of *bPit-1*, *bGH* and *bGHR* gene polymorphisms as genetic markers for meat productivity coming from healthy animals, which has lately become an important indicator of animal welfare and consumer health.

There is a permanent need for the search for, as well as the identification of genes, whose variability may have a direct or indirect connection to the usability and health characteristics of cattle of both the dairy and beef breeds. Molecular studies of the insufficiently understood elements of the somatotropic axis in the cattle used in Kazakhstan were performed in order to match these to the meat usability characteristics and health condition of the cows. These will be a very useful data in the animal selection and breeding work.

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SAŽETAK

Moderno stočarstvo obilježava potreba da se odaberu određene životinje s obzirom na svojstva njihova mesa i mogućnost prilagodbe prirodnom okolišu kako bi se razvile nove poboljšane pasmine. Budući da su bjeloglave pasmine auliekol i kazakh posebno zanimljive za ugajivače u Kazakhstanu, u ovom istraživanju analizirana su polimorfizmi 3 gena koji sudjeluju u kaskadnim reakcijama somatotropina: bPit-1, bGH i bGHR. Geni su izolirani iz pune krvi, a razlozi njihova odabira za istraživanje su spoznaje da utječu na mesnatost i dobro zdravlje. Utvrđene su slijedeće polimorfne varijante istraženih gena: bPit-1-HinFI i bPit-1-HinF1, zatim bGH-AluIV i bGH-AluIL, te bGHR-SspIY i bGHR-SspIF. U radu je također provjerena podudarnost između opaženih i teoretski očekivanih frekvencija prema Hardy i Weinberg-ovu zakonu o ravnoteži genotipova i gena u populaciji. Konačni zadatak bio je kod istraženih životinja usporediti frekvenciju pojavnosti polimorfnih genskih alela s distribucijom somatotropne kaskade. Rezultati su pokazali da je frekvencija gonotipova kod obje pasmine u skladu s frekvencijam koje se osnivaju na zakonu o ravnoteži. Predlaže se da bi polimorfizam kaskadne mreže reakcija mogao biti rezultat uzgojnog napretka koji je ostvaren izravnom selekcijom usmjerenom prema visokoj razini mesnatosti i obilježjima zdravlja istraženih goveda.

Ključne riječi: mesne pasmine goveda; polimorfizam, geni somatotropne kaskade; aleli