Original Research Paper

Determination of Diplotypes Associated with Meat Productivity in Cattle Breeds Common in the Territory of the Republic of Kazakhstan

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Abstract: Technologies for genetic labeling of economically useful traits using polymorphic variants of genes that control the rate of growth and development of animals make it possible to assess the genetic potential of an animal immediately after birth, which significantly reduces time and financial costs. This study aimed to identify paired combinations of the genes growth hormone, growth hormone receptor, and insulin-like growth factor-1 associated with meat productivity in related breeds of cattle meat direction: Hereford, Kazakh white-headed, Aberdeen Angus, Auliekol. The materials for the study were blood and hair follicles samples of animals born in 2015, aged 18 and 24 months. The animals were selected from farms in northern Kazakhstan with equal feeding and housing conditions. The PCR-RFLP method was used to determine the genotypes of animals. According to the results of this study, the associations of phenotypes with the genotypes of the *bGH*, *bGHR*, and *bIGF-1* genes in the studied cattle breeds were revealed.

Keywords: Cattle, Meat Productivity, *bGH* (Growth Hormone) Gene, *bGHR* (Growth Hormone Receptor) Gene, *bIGF-1* (Insulin-Like Growth Factor-1) Gene

Introduction

Animal husbandry in the Republic of Kazakhstan is the main branch of agriculture, which faces the important task of providing the population with food, processing, and light industry with raw materials. To do this, it is necessary not only to improve the technology of raising animals and preparing feed but also to develop and introduce new promising methods for determining and increasing the productivity of animals, which allow them to meet the new requirements for evaluating animals and reduce economic costs by reducing the investment period.

Per the challenges of our time for the intensive development of the meat industry in Kazakhstan, along with the purchase of elite livestock of highly productive breeds, there is an increasing need to develop and master modern breeding methods that allow for forming a highly productive herd of its selection, quickly and efficiently, based on the purchased livestock. This highly productive herd is adapted to the local infectious background, climate, and conditions of keeping, feeding, and breeding.

Such fast and effective tools are provided to breeders of the Republic of Kazakhstan by a marker-accompanying selection. This technology makes it possible to accelerate the rate of selection and reduce the financial cost of classical breeding activities. The MAS -breeding allows for estimating the genetic potential of animal productivity at the early stages of postnatal development (Khare and Khare, 2017; Salisu *et al.*, 2018; Beishova *et al.*, 2019; Dushayeva *et al.*, 2021).

Is a chain of sequential interactions between The Growth Hormone (GH), and somatotropin, which is known to be the most important growth regulator in mammals. The synthesis of somatotropin and the realization of its physiological effects on protein and receptor (somatotropin cascade). Important components of this chain are the growth hormone receptor (*bGHR*), which transmits the humoral somatotropin

signal to target cells, and insulin-Like Growth Factor-1 (*bIGF-1*), which triggers intracellular responses to somatotropin exposure (Parmentier *et al.*, 1999).

In several cases, the data on the somatotropin cascade genes alleles with productivity traits obtained in different breeds are difficult to compare and contradict each other (Boichard *et al.*, 2003) and such studies have not been performed for a significant part of the identified alleles.

Therefore, research to understand the mechanisms of phenotypic effects of candidate genes in different breeds is of great importance. Of particular interest, in this case, are breeds that are related to each other.

This article presents the results of the analysis of gene associations of *bGH*-AluI, *bGHR*-SspI, and *bIGF-1*-SnaBI with phenotypic data on meat productivity in the most widespread breeds in Kazakhstan-foreign Hereford and Aberdeen Angus breeds and local Kazakh Whitehead and Auliekol breeds.

According to the Ministry of Agriculture of the Republic of Kazakhstan as of 01.01.2021, the number of breeding livestock for meat production in the country is more than 682 thousand. Of these, more than 69 thousand are the Hereford breed, more than 393 thousand the Kazakh white-headed, about 113 thousand are Aberdeen Angus breed and more than 60 thousand are the Auliekol breed. Thus, these breeds make up the bulk of beef cattle bred on the territory of the Republic of Kazakhstan and the search for effective ways to increase the productivity of livestock is of strategic importance for the country (MARK, 2022).

This study aimed to identify paired combinations of the genes growth hormone, growth hormone receptor, and insulin-like growth factor-1 associated with meat productivity in related breeds of cattle meat direction: Hereford, Kazakh white-headed, Aberdeen Angus, Auliekol.

Materials and Methods

This study was conducted from January 2016 to December 2021 on the Hereford breed at "Arystan PK" LLP-the village of Sarykol, Sarykolsky district (53°20'19.1"N 65°35'55.2"E), Kazakh white-headed breed at "Zhanabek" LLP-the village of Sverdlovka, Altynsarinsky district (53°07′50″ N 64°39′43″ E), Aberdeen Angus breed at "Sever-Agro N" LLP-the village of Burli, Karabalyksky district (53°36'03.5"N 61°54'30.0"E) and Auliekol breed at "Karkyn" LLP-the village of Rodina (50°15′46″ N 66°53′45″E) (Kostanay region).

The materials for the study were blood and hair follicles samples of animals born in 2015, aged 18 and 24 months. The animals were selected from farms in northern Kazakhstan with equal feeding and housing conditions. Animal productivity data were obtained from the records of the farms that provided the samples. The PCR - RFLP method was used to identify the genotypes of animals. Table 1 shows the primer sequences and PCR conditions for the analysis of each polymorphism.

Amplified PCR products of the bovine *bGH* gene (428 bp) were digested using the restriction enzyme AluI. The digested *bGH*-AluI^{LL} PCR product exhibited four fragments of 265, 96, 51, and 16. For the *bGH*-AluI^{LV} genotype were exhibited five fragments of 265, 147, 96, 51, and 16 bp. For the *bGH*-AluI^{VV} genotype were exhibited three fragments of 265, 147, and 16 bp.

Amplified PCR products of the bovine *bGHR* gene (182 bp) were digested using the restriction enzyme SspI. The digested *bGHR*-SspI^{FF} PCR product exhibited two fragments of 158 and 24. For the *bGHR*-SspI^{FY} genotype were exhibited three fragments of 182, 158, and 24 bp. For the *bGHR*-SspI^{YY} genotype exhibited undigested one fragment of 182 bp.

The nucleotide sequence polymorphism of the insulin-like growth factor-1 gene *bIGF-1* in the P1 promoter region was identified by Hines H.C. (Ulyanov *et al.*, 2021). Amplified PCR products of the bovine *bIGF-1* gene (249 bp) were digested using the restriction enzyme SnaBI. The digested *bIGF-1*-SnaBI^{AA} PCR product exhibited two fragments of 223 and 23. For the *bIGF-1*-SnaBI^{AB} genotype exhibited three fragments of 249, 223, and 23 bp. For the *bIGF-1*-SnaBI^{BB} genotype exhibited an undigested fragment of 249 bp.

Evaluation of *bGH*-AluI, *bGHR*-SspI, and *bIGF-1*-SnaBI somatotropin cascade genes polymorphisms as genetic markers of meat productivity in animals included:

1. Comparison of productivity indicators among themselves to determine the preferred and alternative genotypes in the corresponding animal groups
2. Comparison of productivity indices in groups of animals with preferred and undesirable genotypes relative to the total sample and assessment of the significance of the observed differences

The ordinal numbers of the sample values, which are the Lower (L) and Upper (U) limits, were determined by formulae 1 and 2:

$$L = n/2 - \left(Z_{1-\alpha} * \sqrt{n/2} \right) \qquad (1)$$

$$U = 1 + n/2 + \left(Z_{1-\alpha} * \sqrt{n/2} \right) \qquad (2)$$

where, Z is the value of the normal distribution for the selected probability. For a confidence level of 95%, $Z = 1.96$ (Nametov *et al.*, 2018).
n is the sample size.

All animals met at least class I of their breed standard. The minimum live weight requirements for young animals of the Hereford, Kazakh White-headed, Aberdeen Angus, and Auliekol breeds for class I certification are shown in Table 2.

Table 1: PCR modes for the studied polymorphic loci of the studied genes

Polymorphism	Amplification conditions	Primer sequences
bGH-AluI (Skinkytė *et al.*, 2005)	95°C-5 min; (95°C-30 sec; 64°C-30 sec; 72°C-60 sec) x 35 cycles; 72°C-10 min	AluI –F: 5′-ccgtgtctatgagaagc-3′ AluI-R: 5′-gttcttgagcagcgcgt-3′
bGHR-SspI (Fontanesi *et al.*, 2007)	95°C-5 min; (95°C-30 sec ; 60°C-30 sec; 72°C-30 sec) x 35 cycles; 72°C-10 min	SspI-F: 5′- aatacttgggctagcagtgacaatat -3′ SspI-R: 5′- acgtttcactgggttgatga -3′
bIGF-1-SnaBI (Siadkowska *et al.*, 2006)	95°C-5 min; (95°C-30 sec; 64°C-30 sec; 72°C-30 sec) x 35 sec; 72°C-10 min	SnaBI-F: 5′-attcaaagctgcctgcccc-3′ SnaBI-R: 5′-acacgtatgaaaggaact-3′

Table 2: Minimum live weight requirements for the Hereford, Kazakh white-headed, Aberdeen Angus, and Auliekol breeds for assigning animals to the first class when grading (kg) (MARK, 2014)

	Breeds			
Age	Hereford	Kazakh white-headed	Aberdeen Angus	Auliekol
18 months	350	350	330	360
24 months	400	400	380	415

The results were processed using Microsoft excel 2010 software (Microsoft Corp., USA) and Statistica 6.0 (Stat Soft, Tulsa, USA).

Results

Appendix 1 shows that the ratio of genotypes of the same polymorphism differs considerably between breeds. On the one hand, the observed phenomenon may testify in favor of their association with economically useful traits and the pressure of artificial selection. On the other hand, it allows one to assess the prospects for the use of genetic markers in breeding programs.

The generally accepted minimum value of the relative frequency of a minor allele in the population for the genetic marker is 5%. From the data in Appendix 2, it can be seen that the alleles of all three polymorphisms can be used as genetic markers in breeding programs if a statistically significant association with the trait of live weight is found. The exception is the allele *bGHR*-SspI[Y] in animals of the Auliekol breed.

The data presented in Appendix 3 and Fig. 1 suggest that there is a difference in live weight performance between animals at the age of 18 and 24 months in the Kazakh white-headed and Auliekol breeds of polymorphisms *bGH*-AluI, *bGHR*-SspI, and *bIGF-1*-SnaBI. In turn, the same cannot be said for Hereford and Aberdeen Angus animals.

From the data shown in Table 3, a significant difference between the animals' groups of *bIGF-1*-SnaBI polymorphism in Kazakh white-headed and Auliekol animals at the age of 18 and 24 months should be noted.

Since the character of the distribution of the trait in the studied groups was different from the normal one and in the future, groups with less than 20 animals were included in the analysis of diplotypes, a nonparametric method for calculating 95% confidence intervals for the median was used to assess the difference between the group and the sample. For a group of animals of the Kazakh white-

headed breed, interval estimation was also carried out relative to the total sample (Fig. 2).

The results of the assessment of the nature of the association of the genotype association concerning the total sample for the Auliekol animals are shown in the diagrams in Fig. 3.

The paired-combination analysis in the breed study followed the same research pattern as the individual genotype analysis.

In animals of the Kazakh white-headed breed, two genetic markers of increased live weight and two markers of decreased live weight were identified at 24 months. Diplotypes with an increasing phenotypic effect include *bGH*-AluI[LV]-*bIGF-1*-SnaBI[AB] and *bGH*-AluI[LV]-*bIGF-1*-SnaBI[BB]; diplotypes with a decreasing phenotypic effect on the trait of live weight include paired combinations *bGH*-AluI[LL]-*bIGF-1*-SnaBI[AA] and *bGH*-AluI[LL]-*bIGF-1*-SnaBI[BB] (Fig. 4).

From the data given in Table 4, it can be noted that the diplotype *bGH*-AluI[LL] - *bIGF-1*-SnaBI[AA] has the most pronounced decreasing effect on the live weight of the Kazakh white-headed breed at the age of 24 months, which is characterized by the decrease in the indicator concerning the standard by 37 kg (9.00%). The frequency of diplotype in the studied sample is approximately 3.05%.

Graphical evaluation of the statistical significance of phenotypic effects of paired combinations of the somatotropin cascade genes in the Auliekol animals at the age of 24 months revealed the diplotypes marking both increased and decreased body weight (Fig. 5).

From the graphical data shown in Fig. 5, it can be seen that among the paired combinations of polymorphisms of the studied genes, 2 genetic markers of reduced live weight were revealed in animals of the Auliekol breed at the age of 24 months - *bGH*-AluI[LL]-*bIGF-1*-SnaBI[AB] and *bGH*-AluI[LL]-*bIGF-1*-SnaBI[BB] and 3 genetic markers of increased live weight *bGH*-AluI[LV]-*bIGF-1*-SnaBI[AA], *bGH*-AluI[LV]-*bIGF-1*-SnaBI[AB], and *bGH*-AluI[LV]-*bIGF-1*-SnaBI[BB].

In the phenotypic effects' analysis of paired combinations of the studied polymorphisms on the trait of live weight at 24 months in Aberdeen-Angus animals, a significant upward phenotypic effect was found for the paired combination of *bGH*-AluI^{VV}-*bIGF-1*-SnaBI^{BB}.

Figure 6 shows that the boundaries limits of the confidence interval for the median of the diplotype group from 420 to 431 kg and fall outside the confidence interval for the median sample of 415-418 kg for this trait.

A comparison with the Aberdeen Angus breed standard revealed that the live weight of animals with the *bGH*-AluI^{VV}-*bIGF-1*-SnaBI^{BB} diplotype at the age of 24 months exceeded the live weight of the Aberdeen Angus breed standard by 45 kg (12%) and 12.52 kg (3%) when compared with the total sample (Table 4). This indicates that the *bGH*-AluI^{VV}-*bIGF-1*-SnaBI^{BB} diplotype is the recommended genetic marker to increase the live weight of Aberdeen Angus animals at the age of 24 months.

The frequency of diplotype in the studied sample is approximately 5.08%.

Studies have shown that there were no marking diplotypes found in the Hereford breed.
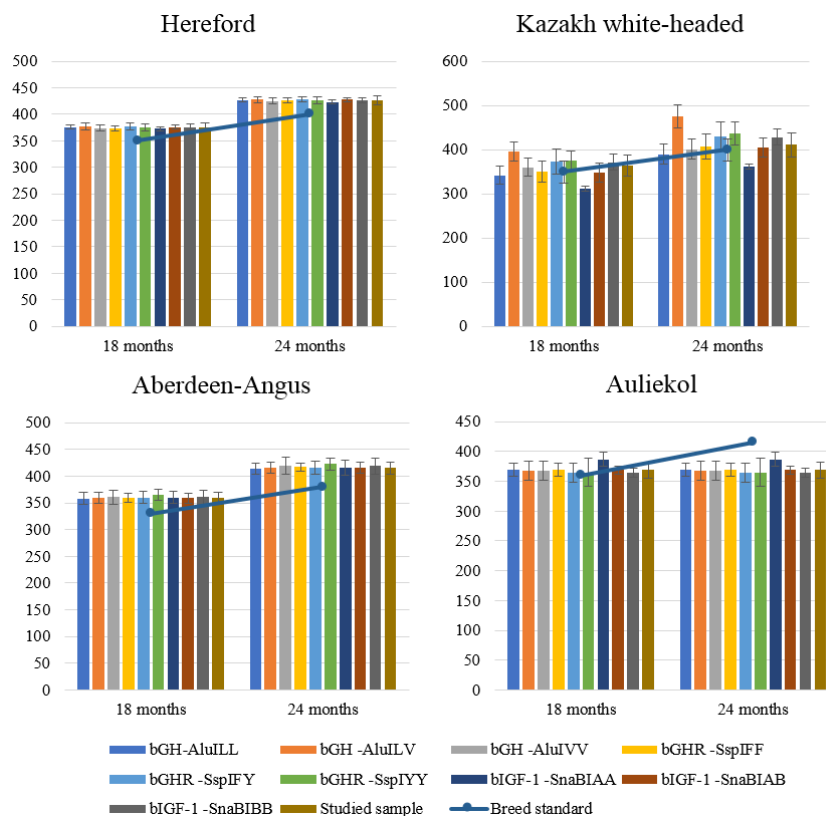

Fig. 1: Mean live weight values (kg) at 18 and 24 months of age are given for animals with different genotypes for *bGH*-AluI, *bGHR*-SspI, and *bIGF-1*-SnaBI polymorphism (m ± σ)
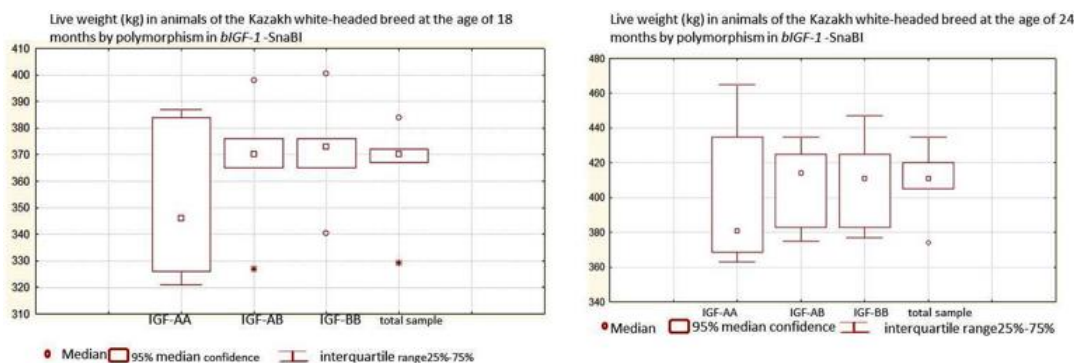

Fig. 2: Live weight (kg) in animals of the Kazakh white-headed breed at the age of 18 and 24 months by a polymorphism in *bIGF-1*-SnaBI
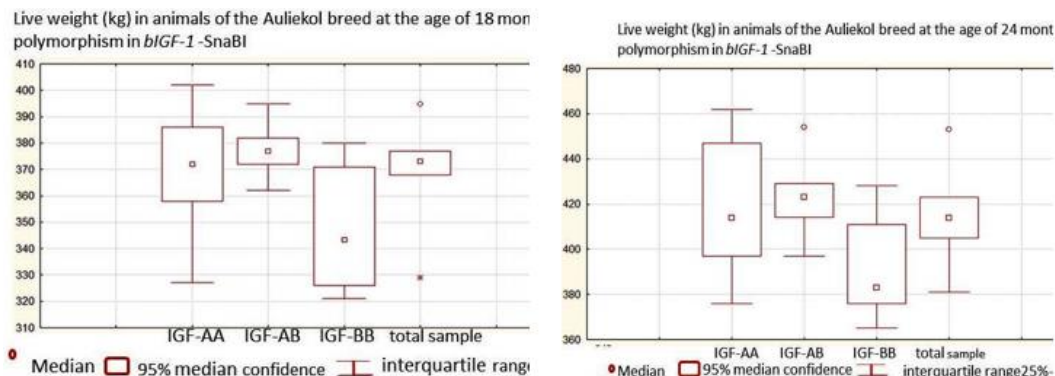
Fig. 3: Live weight (kg) animals Auliekol animals 18 and 24 months of age according to the *bIGF-1*-SnaBI polymorphism
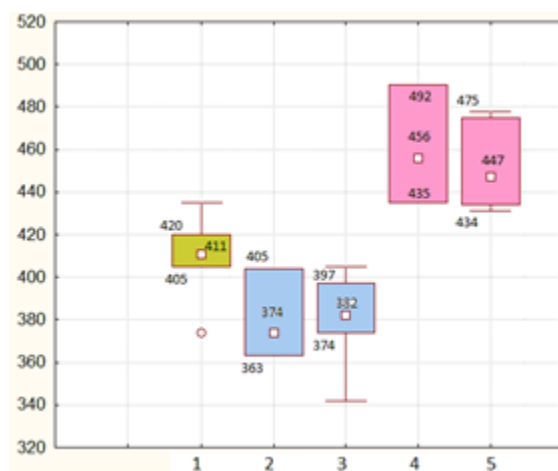
Fig. 4: Graphical evaluation of the statistical significance of phenotypic effects of paired combinations of the studied genes marking increased and decreased live weight at the age of 24 months in animals of the Kazakh white-headed breed; 1 -General sample; 2 -*bGH*-AluI^{LL}-*bIGF-1*-SnaBI^{AA}; 3 -*bGH*-AluI^{LL}-*bIGF-1*-SnaBI^{BB}; 4 -*bGH*-AluI^{LV}-*bIGF-1*-SnaBI^{AB}; 5 -*bGH*-AluI^{LV}-*bIGF-1*-SnaBI^{BB}
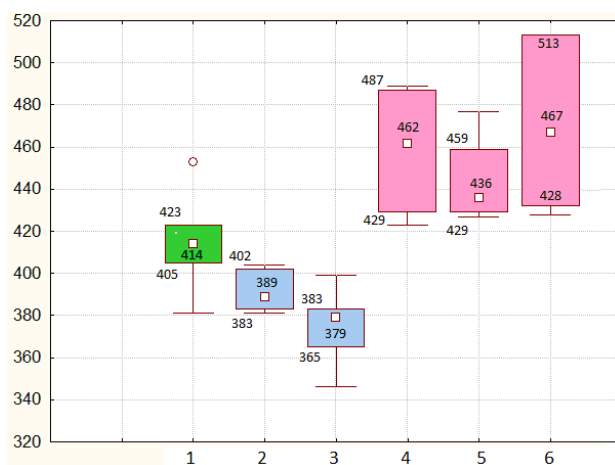
Fig. 5: Assessment of the phenotypic effects of paired combinations of somatotropin cascade genes, marking increased and decreased body weight at the age of 24 months in animals of the Auliekol breed. 1 - General sample; 2 - *bGH*-AluI^{LL}-*bIGF-1*-SnaBI^{AB}; 3 - *bGH*-AluI^{LL}-*bIGF-1*-SnaBI^{BB}; 4 - *bGH*-AluI^{LV}-*bIGF-1*-SnaBI^{AA}; 5 - *bGH*-AluI^{LV}-*bIGF-1*-SnaBI^{AB}; 6 - *bGH*-AluI^{LV}-*bIGF-1*-SnaBI^{BB}
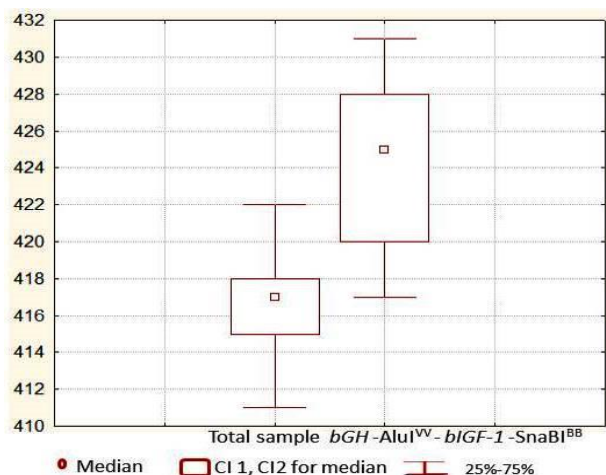
Fig. 6: Graphical evaluation of the phenotypic effect of the *bGH*-AluI^{VV}-*bIGF-1*-SnaBI^{BB} diplotype on the trait of live weight in Aberdeen Angus animals at the age of 24 months

Table 3: Statistical significance of the difference between groups of animals with alternative genotypes of *bGH*-AluI, *bGHR*-SspI, and *bIGF-1*-SnaBI polymorphic genes for live weight at 18 and 24 months of age

Breed	*bGH*-AluI	*bGHR*-SspI	*bIGF-1*-SnaBI
18 months			
Hereford	0.40	0.22	0.79
Kazakh white-headed	0.07*	0.52	0.02*
Aberdeen-Angus	0.32	0.48	0.47
Auliekol	0.32	0.14	0.01
24 months			
Hereford	0.68	0.07	0.19
Kazakh white-headed	0.08*	0.67	0.04*
Aberdeen-Angus	0.06	0.12	0.31
Auliekol	0.62	0.18	0.01

Notes: * -the comparison was made using the Mann-Whitney U-test (for two independent samples); with statistically significant differences at P<α; α = 0.05

Table 4: Characteristics of the selection significance of marking diplotypes in animals of the Kazakh white-headed, Auliekol, and Aberdeen Angus breeds at the age of 24 months*

Diplotype	Phenotypic effect	% Diplo-type	% Genotype 1	% Genotype 2	Average m	Difference in relation to the total sample		Difference in relation to breed standard	
						kg	%	kg	%
Kazakh white-headed breed (* n total sample 295; m ± σ of the total sample 411 ± 18 kg; breed standard 400 kg)									
bGH-AluI^{LL} - *bIGF-1*-SnaBI^{AA}	decreasing	3.05	67.12	11.53	374.0	-37	-9.00	-26	-6.50
bGH-AluI^{LL} - *bIGF-1*-SnaBI^{BB}	decreasing	13.90	67.12	43.73	376.3	-35	-8.44	-24	-5.93
bGH-AluI^{LV} - *bIGF-1*-SnaBI^{AB}	increasing	9.49	31.19	44.75	457.3	46	11.27	57	14.33
bGH-AluI^{LV} - *bIGF-1*-SnaBI^{BB}	increasing	8.81	31.19	43.73	452.0	41	9.98	52	13.00
Auliekol breed (* n total sample 286; m ± σ of the total sample 417 ± 16 kg; breed standard 415 kg)									
bGH-AluI^{LL} - *bIGF-1*-SnaBI^{AB}	decreasing	12.24	44.76	36.36	391.3	-26	-6.16	-24	-5.71
bGH-AluI^{LL} – *bIGF-1*-SnaBI^{BB}	decreasing	9.44	44.76	43.36	374.6	-42	-10.17	-40	-9.73
bGH-AluI^{LV} - *bIGF-1*-SnaBI^{AA}	increasing	8.04	43.71	20.28	458.0	41	9.83	43	10.36
bGH-AluI^{LV} - *bIGF-1*-SnaBI^{AB}	increasing	18.53	43.71	36.36	446.6	thirty	7.10	32	7.61
bGH-AluI^{LV} - *bIGF-1*-SnaBI^{BB}	increasing	3.85	43.71	43.36	462.3	45	10.86	47	11.40
Aberdeen Angus breed (* n total sample 192; m ± σ of the total sample 415 ± 12 kg; breed standard 380 kg)									
bGH-AluI^{VV} - *bIGF-1*-SnaBI^{BB}	increasing	5.08	26.56	20.83	425	ten	2.41	45	11.84

Discussion

Any population that is in constant flux. Breeding processes occurring in herds and populations through gene migration, their elimination due to various circumstances, as well as emerging mutations and recombination, change their genotypic structure, which makes it possible to analyze and control the breeding process.

The selection of animals for economically useful traits directly or indirectly leads to changes in the gene pool of

animals and its structure (Piccoli *et al.*, 2017) and, in turn, the genetic structure of the population determines the possibility of using marker-associated selection in breeding programs, as well as to assume the effectiveness of such measures.

Analysis of *bGH*-AluI polymorphism showed a similar distribution of allele frequencies in the studied breeds (Appendix 2). The *bGH*-AluI^L allele occurs with a frequency of 68.43 in the Hereford breed, 51.3 in the Aberdeen-Angus breed, and 66.61 in the Auliekol breed. In the Kazakh white-headed breed its frequency is significantly higher - 83.05. The data obtained agree with the results of Selionova *et al.* (2017), which established a high occurrence of *bGH*-AluI^L allele (0.64; 0.78-0.89) in Hereford, Kalmyk and Kazakh white-headed breeds; Sedykh (2017), who established the frequency of *bGH*-AluI^L allele 0.684 and 0.731, respectively, in Herefords and Limousins; Sharipov *et al.* (2015), who established the frequency of *bGH*-AluI^L allele 0.61 and 0.85 in Herefords and Limousines breed in Tatarstan; Krasnopiorova *et al.* (2012) who found the frequency of *bGH*-AluI^L allele in Charolais, Herefords and Simmentals to be 0.850; 0.900 and 0.563, respectively; Lee *et al.* (2013), who found a high incidence of the *bGH*-AluI^L allele of 0.907 in Hanwoo; Hartatik *et al.* (2013), who found the frequency of the *bGH*-AluI^L allele of 0.830 and 0.910 in Limousins (Limousin); Kostenko and Starodub (2011), who established the frequency of the *bGH*-AluI^L allele in Polis Sian Beef at 0.807; Mokhnachova *et al.* (2016), who found the frequency of the *bGH*-AluI^L allele in Ukrainian Grey cattle to be 0.980. It should be noted that the low frequency of the *bGH*-AluI^L allele is observed in different breeds bred in Russia. This may be due to the long-term selection of local cattle populations. Thus, Sulimova *et al.* (2011) the low frequency of the *bGH*-AluI^L allele in Kalmyk, Kazakh White-headed, and Mongolian breeds -0,117; 0,209, and 0,125 were established. According to the *bGHR*-SspI polymorphism, all the studied breeds showed a clear advantage of the *bGHR*-SspI^F allele (Appendix 2). Thus, its frequency was 95.10 in the Auliekol breed, 91.36 in the Kazakh white-headed breed, and 78.39 in the Aberdeen Angus breed. In the Hereford breed, the frequency of the *bGHR*-SspI^F allele was slightly lower and amounted to 62.12. The data obtained are from the data of other researchers. In their research works the frequency of occurrence of the F allele of the *bGHR* gene in cattle of different breeds was 0,667 (Fedota *et al.*, 2017), Jersey-0,850 (Komisarek *et al.*, 2011), Holstein-0,840 (Rahmatalla *et al.*, 2011), Romanian Black-and-White-0.770 and Romanian Grey Steppe-1.0, respectively (Carsai *et al.*, 2013). The *bIGF-1*-SnaBI polymorphism showed a similar distribution of allele frequencies among the studied breeds (Appendix 2). Thus, the frequency of the *bIGF-1*-SnaBI^B allele in the Kazakh white-headed breed was 66.10, in the Auliekol

breed-61.54, and the Hereford breed-60.61. The exception was the Aberdeen-Angus breed, where the *bIGF-1*-SnaBI^B allele was less common (42.19). Several studies have been devoted to determining the *bIGF-1*-SnaBI polymorphism in cattle. In their works, the frequency of a *bIGF-1*-SnaBI^B allele in Holstein cattle is 0.562 (Yousef *et al.*, 2010), in commercial lines -0,56 (Li *et al.*, 2004), in Aberdeen Angus breed-0,64 (Ge *et al.*, 2001). In M. Szewczuk; E. Siadkowska the frequency of the *bIGF-1*-SnaBI^B allele was lower and was 0.33 for Montbeliarde cattle (Szewczuk, 2016) and 0.48 for the Holstein-Friesian breed (Siadkowska *et al.*, 2006).

The highest live weight according to the *bGH*-AluI polymorphism in the Kazakh white-headed breed at the age of 18 months was observed in the group of animals with the *bGH*-AluI^{LV} genotype (395±27), animals with a lower live weight are observed in the group with the *bGH*-AluI^{LL} genotype (342±29 kg) (Appendix 3). At the same time, according to Fedota *et al.* (2016), animals of Aberdeen-Angus breed with *bGH*-AluI^{LL} genotype were superior to animals with *bGH*-AluI^{LV} and *BGH*-AluI^{VV} genotypes in growth performance. According to Lee *et al.* (2013), Thomas *et al.* (2007), Hartatik *et al.* (2020) and Gill *et al.* (2009) animals with the *bGH*-AluI^{LL} genotype had the highest live weight at birth. In cattle, the *bGH*-AluI^L allele is associated with higher body weight and marbling score. However, Hartatik *et al.* (2020) suggested that the *bGH*-AluI^V allele may be a potential genetic marker in cattle.

The *bGHR*-SspI polymorphism in animals of the Kazakh white-headed breed was the preferred *bGHR*-SspI^{YY} genotype (376±31 kg) (Appendix 3). This agrees with the previously published data of other authors. For example, according to (Fedota *et al.*, 2017) the *bGHR*-SspI^{YY} genotype was also preferred for Aberdeen-Angus breed animals. Thus, the group with this genotype was characterized by a higher Average Daily Gain (ADG) and live weight at 8 months of age (Fedota *et al.*, 2017). The known SNP F279Y is associated with dairy performance and is included in the current Marker-Assisted Selection (MAS) for commercial purposes in several countries (Olenski *et al.*, 2010).

By the *bIGF-1*-SnaBI polymorphism in the Kazakh white-headed breed, the *bIGF-1*-SnaBI^{BB} genotype (371±18 kg) is preferable and with the lowest live weight genotype *bIGF-1*-SnaBI^{AA} (311±17 kg) is observed (Appendix 3).

In animals of the Auliekol breed, the difference in live weight in groups with different genotypes is characteristic of the *bIGF-1*-SnaBI polymorphism and the genotype *bIGF-1*-SnaBI^{AA} is preferred (387±11 kg) (Appendix 3). Other researchers have previously reported that the *bIGF-1*-SnaBI polymorphism affects the growth rate and meat productivity of Angus, Beefbooster, Holstein-Friesian, and Charolais cattle (Li *et al.*, 2004; Siadkowska *et al.*, 2006; De la Rosa Reyna *et al.*, 2010; Ge *et al.*, 2001).

According to Daniela do Amaral Grossi *et al.* (2015), the *bIGF-1*-SnaBI[A] allele was found to be associated with higher live weight at birth, weaning, 12 and 18 months of age in Canchim beef cattle. A. Rogberg-Muñoz *et al.* (2011) identified an association of the *bIGF-1* gene with live weight at weaning in commercial and experimental groups of Hereford breeds.

The trend of increased or decreased live weight in animals of the Kazakh white-headed and Auliekol breeds by preferred or undesired genotypes persists at the age of 24 months. Data for the other genotypes were not considered, since they were approximately equal to the weight of the breed standard.

The diagrams in Fig. 2 show that the groups with the *bIGF-1*-SnaBI[AA], *bIGF-1*-SnaBI[AB], and *bIGF-1*-SnaBI[BB] genotypes are indeed significantly different from each other. However, the group with the genotype is deconsolidated and its range of traits is outside both the upper and lower confidence intervals of the median of the total sample. Moreover, this trend can be traced in all age categories.

Thus, it should be stated that it is not appropriate to use the *bIGF-1*-SnaBI[BB] genotype as a genetic marker for cows of the Kazakh white-headed breed.

The average live weight of animals at 18 months is 365 ± 10 kg and at 24 months 413 ± 7 kg, which is 4 and 3 kg below the breed standard (Appendix 3). Taking into account that this genotype in the studied sample is 43.36%, a decrease in its frequency of occurrence in the course of breeding programs could yield a very tangible result. Thus, it is obvious that the *bIGF-1*-SnaBI[BB] genotype is a genetic marker of the low live weight of the Auliekol breed animals at the age of 18 and 24 months. Work with this genetic marker should not be based on the selection of the preferred genotype but the elimination of the negative *bIGF-1*-SnaBI[BB] genotype.

The most pronounced increasing effect is observed in groups of animals of the Kazakh white-headed breed with the diplotype *bGH*-AluI[LV]-*bIGF-1*-SnaBI[AB] (Fig. 4). In this group of animals, the live weight at the age of 24 months is in the range of 435-492 kg and the most pronounced decreasing phenotypic effect is observed in animals of the Kazakh white-headed breed with the diplotype *bGH*-AluI[LL]-*bIGF-1*-SnaBI[BB] (the median value of live weight according to a group from 374 to 397 kg). While the live weight of animals of the total sample of the Kazakh white-headed breed at the age of 24 months is in the range of 405-420 kg.

The diplotype *bGH*-AluI[LV]-*bIGF-1*-SnaBI[AB], which is characterized by an increase in the indicator relative to the standard by 57 kg (14.33%), has the most pronounced increasing phenotypic effect on the live weight of the Kazakh white-headed breed animals at the age of 24 months (Table 4). The diplotype frequency in the sample studied is approximately 9.49%.

Table 4 shows that the greatest economic effect will be given by animals with the increasing diplotype *bGH*-AluI[LV]-*bIGF-1*-SnaBI[AB] and *bGH*-AluI[LV]-*bIGF-1*-SnaBI[BB]. In this case, animals with the above diplotypes should be left in the herd for further selection.

In turn, animals with downward diplotypes of *bGH*-AluI[LL]-*bIGF-1*-SnaBI[AA] and *bGH*-AluI[LL]-*bIGF-1*-SnaBI[BB] must be excluded from the reproduction cycle.

The most pronounced decreasing effect is observed in the group of animals with diplotype *bGH*-AluI[LL]-*bIGF-1*-SnaBI[BB,] the live weight of animals aged 24 months is in the range of 365-383 kg (Fig. 5). This is significantly lower compared to the general sample, in which the median live weight is in the range of 405-423 kg. The most pronounced enhancing phenotypic effect was observed in the group of animals with diplotype *bGH*-AluI[LV]-*bIGF-1*-SnaBI[BB], where the live weight of animals at 24 months of age is in the range of 428-513 kg, which is considerably higher compared to the total sample, in which the median live weight is in the range of 405-423 kg.

From the data given in Table 4, it follows that the diplotype *bGH*-AluI[LL]-*bIGF-1*-SnaBI[BB] is characterized by the most pronounced decreasing effect on the Auliekol breed animals at the age of 24 months concerning the standard of the breed by 40 kg (9.73%). The diplotype frequency in the studied sample is approximately 9.44%.

The diplotype *bGH*-AluI[LV]-*bIGF-1*-SnaBI[BB] has a markedly pronounced increasing phenotypic effect on the live weight of the Auliekol breed animals at the age of 24 months, which is characterized by a 47 kg (14.40%) increase in the index concerning the standard. The frequency of the diplotype in the studied sample is approximately 3.85%. Animals with this diplotype, as in the case of the Kazakh white-headed breed, should be kept in the herd for further breeding, and animals with the diplotype *bGH*-AluI[LL]-*bIGF-1*-SnaBI[BB] should be excluded from reproduction.

Conclusion

According to the results of this study, the associations of phenotypes with the genotypes of the *bGH*, *bGHR*, and *bIGF-1* genes in the studied cattle breeds were revealed.

We recommend using the identified diplotypes with decreasing or increasing effects on live weight in the studied breeds in the selection of animals within the framework of breeding programs. At the same time, we propose to keep animals with an increasing type of diplotypes in the herd for breeding work and to exclude animals with diplotypes having decreasing effects from reproduction.

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Author's Contributions

Askar Mirzahmetovich Nametov: Developed the concept and design of this study and participated in writing the article.

Indira Saltanovna Beishova and Alena Valentinovna Belaya: Developed the concept and design of the study, performed analysis and interpretation of the data, and participated in writing the article.

Tatyana Vladimirovna Ulyanova: Established the genotypes of cattle, conducted statistical processing and participated in writing the article.

Alexandr Mikhailovich Kovalchuk: Conducted the selection of biological material statistical processing, and participated in writing the article.

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Ethics

This article is original and contains unpublished material. The corresponding author confirms that all of the other authors have read and approved the manuscript and that no ethical issues are involved.

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Appendix 1: Results of genotyping of beef cattle populations by polymorphic genes *bGH*-AluI, *bGHR*-SspI, and *bIGF-1*-SnaBI

| | Breed | | | | | | | |
| | Hereford (n = 198) | | Kazakh white-headed (n = 295) | | Aberdeen-Angus (n = 192) | | Auliekol (n = 286) | |
Genotypes	n	%	n	%	n	%	n	%
bGH-AluI^LL	107	54.04	199	67.12	56	29.17	128	44.76
bGH-AluI^LV	57	28.79	92	31.19	85	44.27	125	43.71
bGH-AluI^VV	34	17.17	5	1.69	51	26.56	33	11.54
bGHR-SspI^FF	72	36.36	253	85.76	130	67.71	264	92.31
bGHR-SspI^FY	102	51.52	33	11.19	41	21.35	18	6.29
bGHR-SspI^YY	24	12.12	9	3.05	6	3.13	43	1.40
bIGF-1-SnaBI^AA	24	12.12	34	11.53	50	26.04	59	20.28
bIGF-1-SnaBI^AB	108	54.55	132	44.75	82	42.71	104	36.36
bIGF-1-SnaBI^BB	66	33.33	129	43.73	40	20.83	124	43.36

Appendix 2: Distribution of relative allele frequencies of *bGH*-AluI, *bGHR*-SspI and *bIGF-1*-SnaBI polymorphisms in the cattle populations studied ($Q \pm S_Q$)

| | Breed | | | |
Allele	Hereford	Kazakh white-headed	Aberdeen-Angus	Auliekol
bGH-AluI^L	68.43	83.05	51.30	66.61
bGH-AluI^V	31.57	17.29	48.70	33.39
bGHR-SspI^F	62.12	91.36	78.39	95.10
bGHR-SspI^Y	37.88	8.64	13.80	4.20
bIGF-1-SnaBI^A	39.39	33.90	47.40	38.46
bIGF-1-SnaBI^B	60.61	66.10	42.19	61.54

Appendix 3: Mean live weight values (kg) at 18 and 24 months of age are given for animals with different genotypes for *bGH*-AluI, *bGHR*-SspI, and *bIGF-1*-SnaBI polymorphism (m ± σ)

Genotype	Breed							
	Hereford		Kazakh white-headed		Aberdeen-Angus		Auliekol	
	18 months	24 months	18 months	24 months	18 months	24 months	18 months	24 months
bGH-AluI^{LL}	376±4	427±40	342±29	390±18	358±10	414±12	370±11	418±12
bGH-AluI^{LV}	377±6	428±60	395±27	475±20	360±90	416±12	368±23	415±12
bGH-AluI^{VV}	374±4	425±10	360±23	401±20	361±80	420±22	368±17	416±19
bGHR-SspI^{FF}	374±4	426±60	351±34	407±17	359±90	417±70	370±12	418±10
bGHR-SspI^{FY}	377±7	428±60	374±42	430±17	360±10	416±14	365±20	401±14
bGHR-SspI^{YY}	375±6	427±80	376±31	437±15	365±10	423±12	365±23	406±27
bIGF-1-SnaBI^{AA}	373±4	423±40	311±17	362±24	360±80	416±18	387±11	439±15
bIGF-1-SnaBI^{AB}	376±4	428±40	348±23	405±21	359±80	416±12	369±90	414±40
bIGF-1-SnaBI^{BB}	376±4	427±60	371±18	428±18	361±90	419±21	365±10	413±00
Studied sample	376±7	427±80	364±32	411±18	359±10	415±12	369±12	417±16
Breed standard	350	400	350	400	330	380	360	415