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Effectiveness of the Use of Genetic Markers of Meat Productivity in the Kazakh White-Headed Breed Identified Using Genome-Wide Association Study

¹Indira Beishova, ¹Askar Nametov, ¹Alzhan Shamshidin, ²Alena Belaya, ¹Tatyana Ulyanova, ¹Alexandr Kovalchuk, ³Ivan Tegza, ¹Baluash Traisov, ⁴Yusupzhan Yuldashbaev, ¹Aliya Akhmetaliyeva, ⁵Aizhan Abylgazinova, ³Rustem Beishov and ¹Yerkingali Batyrgaliyev

¹Zhangir Khan West Kazakhstan Agrarian Technical University, Uralsk, Kazakhstan

²Belarusian State Pedagogical University Named after Maxim Tank, Minsk, Belarus

³Akhmet Baitursynuly Kostanay Regional University, Kostanay, Kazakhstan

⁴Russian State Agrarian University-Moscow Timiryazev Agricultural Academy, Moscow, Russia

⁵Scientific and Production Center of Animal Husbandry and Veterinary Medicine, Astana, Kazakhstan

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Corresponding Author:

Tatyana Ulyanova
Zhangir Khan West
Kazakhstan Agrarian Technical
University, Uralsk, Kazakhstan
Email: tatyana.poddudinskaya@gmail.com

Abstract: The study aimed to determine the effectiveness of the use of genetic markers in cattle of the Kazakh white-headed breed identified using a genome-wide association study. The object of the study was the livestock of 790 Kazakh white-headed bulls bred in breeding farms of the Republic of Kazakhstan. The study adheres to rigorous ethical standards, with all procedures approved by the national scientific council of the national center for state scientific and technical expertise of the science committee of the ministry of science and higher education of the Republic of Kazakhstan, ensuring the welfare and ethical treatment of all animals involved. Genotypes of Kazakh white-headed breed animals were determined using gene seek GGP Bovine 150 K (Neogen) chips. Data processing was carried out using Genome Studio and Plink software. Seven genotype markers associated with an increase in live weight at the age of 12 months were found in cattle of the Kazakh white-headed breed and the greatest phenotypic effect was found in the genotype rs42549324/EPHA8/GG. Evaluation of the phenotypic effects of single nucleotide polymorphisms on the average daily weight gain of Kazakh white-headed breed animals showed that 13 genotypes that increased this trait, as well as 38 genotypes that decreased it, were associated with this trait. Analysis of the growth intensity and economic efficiency of breeding Kazakh white-headed breed animals showed that animals carrying the rs109490287/CC genotype had the largest absolute gain compared to the total sample; and animals with the rs136460595/SEMA6D/GG genotype, on the contrary, were characterized by the smallest absolute gain compared to the total sample. According to the results of the median test, 39 diplotypes were found in the Kazakh white-headed breed that increased live weight at the age of 12 months, of which 18 diplotypes had a more pronounced phenotypic effect than the separate genotype rs42549324/EPHA8/GG. The median test also allowed for revealing 53 diplotypes associated with increased average daily gain, of which 12 were characterized by a more pronounced phenotypic effect compared to individual marker genotypes, as well as 26 diplotypes affecting reduced indicators of average daily gain. Our findings contribute significantly to the field by identifying specific genetic markers that can be used to predict and improve meat productivity in the Kazakh white-headed cattle breed. This research not only adds to the genetic knowledge base of this particular breed but also offers practical applications for breeders aiming to enhance meat production efficiency through genetic selection.

Keywords: Cattle, Live Weight, Average Daily Gain, Quantitative Trait Locus, Single Nucleotide Polymorphisms

Introduction

Cattle breeding is an important branch of agriculture, making a significant contribution to the economic development of many countries (Akhazhanov *et al.*, 2023; Boranbayeva *et al.*, 2023; Nasiyev *et al.*, 2023). Optimization of production processes and increase of livestock productivity are priorities for farmers and agricultural enterprises (Dushayeva *et al.*, 2021). In recent years, genetic research has begun to play an increasingly important role in achieving these goals (Ulyanov *et al.*, 2021; Beishova *et al.*, 2023; Shevchenko *et al.*, 2023).

The Kazakh white-headed cattle breed is one of the most common breeds in Kazakhstan and other Central Asian countries (Aitzhanova *et al.*, 2022). It is characterized by high adaptability to harsh climatic conditions and good adaptation to local pasture systems. However, as in any breed, animals have differences in individual productivity (Nametov *et al.*, 2022).

Modern research in the field of cattle genetics has established that Single Nucleotide Polymorphisms (SNPs) are one of the factors affecting productivity in animals (Beishova *et al.*, 2022). SNPs are genetic variants that can influence phenotypic characteristics. Studies have shown that certain SNPs can be associated with dairy or meat productivity, disease resistance, or other signs (Beishova *et al.*, 2022; 2023). While genetic markers have been increasingly used to inform breeding decisions across cattle breeds, the specific genetic basis of meat productivity traits in the Kazakh white-headed breed remains underexplored.

This study presents a study aimed at evaluating the economic effect of raising Kazakh white-headed cattle, considering SNPs that affect the Live Weight (LW) at the age of 12 months and the Average Daily Gain (ADG). The paper shows the relationship between genetic markers and productive indicators of livestock, as well as an assessment of the impact of these markers on economic indicators of breeding. Unlike previous studies that have broadly focused on genetic markers across various cattle breeds, our research uniquely contributes by pinpointing specific SNPs within the Kazakh white-headed breed, thereby offering breed-specific insights that can directly impact breeding programs aimed at enhancing meat productivity.

The study aimed to determine the effectiveness of the use of genetic markers in cattle of the Kazakh white-headed breed, identified using Genome-Wide Association Study (GWAS).

Materials and Methods

All procedures performed in this study followed ethical standards. The research work was approved by the national scientific council of the national center for state

scientific and technical expertise of the science committee of the ministry of science and higher education of the Republic of Kazakhstan in the priority field "sustainable development of the agro-industrial complex and safety of agricultural products" (minutes of meeting No. 6 dated August 04, 2021 and meeting No. 1 dated April 13, 2020).

In this study, the genetic material was sourced from blood samples collected from 790 Kazakh white-headed bull breeding farms in the Republic of Kazakhstan. Data on the number of samples in the context of farms used for the study are given in Table 1.

The efficiency of breeding animals with preferred genotypes was evaluated by LW at the age of 12 months, as well as by ADG.

Feed consumption for each animal was systematically recorded to calculate Feed Conversion Ratios (FCR). Feed intake was measured by the difference in feed mass provided and the leftovers, recorded daily. This method enabled us to determine the actual feed intake for each animal, which was crucial for accurately assessing the efficiency of feed conversion into body weight gain.

SNP Genotyping

Blood samples were drawn from the jugular vein of each animal using a sterile technique to minimize stress and contamination.

Nucleic acid extraction and SNP genotyping were performed in the Neogen Agrigenomics laboratory (Lincoln, NE, USA). The GeneSeek GGP Bovine 150K DNA chip (Neogen Corporation Company, Lincoln, NE, USA), including about 150,000 SNPs, was used for genotyping.

The extraction of nucleic acids was conducted using the DNeasy blood and tissue kit (Qiagen, Hilden, Germany), following the manufacturer's protocol. This method was chosen for its efficiency in extracting high-quality genomic DNA from blood samples, which is crucial for accurate SNP genotyping.

Table 1: Information about the number of samples studied at the farms

Breed	Farm	Region	Number, heads
Kazakh white-headed	Adlet-T LLP	Kostanay region, Taranovsky District	284
	Plemzavod Alabota LLP	North Kazakhstan region, Tayynshinsky District	315
	Shalabay LLP	Abai region, Zharminsky District	191

Processing of SNP Genotyping Data

The received data were processed using the GenomeStudio software and converted to the Plink format (.bed, .bim, .fam) (Belaya *et al.*, 2022). Thus, the standard format of A/B genotypes was modified into a nucleotide format that corresponded to specific nucleotide variants. Then some procedures were implemented to control the quality of genetic data using the Plink software. The data was filtered according to the following criteria: (1) The call frequency for all polymorphisms for a separate sample is not lower than 90%; (2) For all genotyped samples, the frequency of occurrence of each of the polymorphisms is not less than 90%; (3) For each of the studied polymorphisms, the frequency of the minor allele is not lower than 5%; (4) The deviation of genotypes from the Hardy-Weinberg equilibrium with a significance of $p < 10^{-6}$. As a result, after filtering, the number of SNPs for further analysis was 85,533.

Genome-Wide Associative Study

The Plink software was used to conduct a GWAS. All phenotypes were quantitative and linear regression was used for analysis. Determination coefficients were also calculated. The statistical significance of the regression coefficients of polymorphisms was evaluated using the Wald test. The polymorphisms with a p-value higher than the quotient of the significance level (0.05) by the number of the polymorphisms with a p-value of the Wald test was less than 0.05 were taken as potentially significant. Processing and visualization of associative analysis were carried out using quartile-quartile graphs and the λ coefficient (Purcell *et al.*, 2007; Pickrell, 2014).

The λ coefficient was used to estimate the acceptable level of statistical significance of SNPs. A value of this coefficient exceeding 1 indicates that a model using certain p values of selected polymorphisms is trustworthy.

The single-locus linear model is calculated by the formula $y = \Sigma Mxbx$; where y is a vector with predicted de-regression genotypes (predicted transmitting abilities); m is the SNP candidate genotype (the allelic dose is encoded as 0, 1, or 2) for each animal; b is the regression coefficient of the SNP candidate. For each candidate, the Wald test was used to evaluate the alternative hypothesis $H1: b \neq 0$ compared to the null hypothesis $H0: b = 0$.

Quantitative Analysis of Phenotypic Effects of Genotypes by Polymorphisms Associated with Productivity Traits

The statistical significance of the difference in productivity characteristics in the group with a specific genotype (diplotype) from the total sample under study was assessed using a nonparametric median test. This method allows the analysis of small samples when the feature does not have a normal Gaussian distribution and the evaluation of the statistical significance of the

differences between a part of the sample and the entire sample as a whole. To do this, 95% Confidence Intervals (CIs 95%) were calculated for the Median (Me) of the analyzed group and the total sample under study and then the boundaries of these CIs were compared with each other. The results are shown in the form of Me (25; 75), CI 95% (Abdullayev *et al.* 2024).

To characterize the phenotypic effects of preferred and undesirable genotypes, we calculated the difference between the average values of the studied indicators in groups of animals of specific genotypes with the average values of the total sample. Statistical processing of the results was carried out using the Microsoft Excel 2010 software.

The dynamics of the LW and growth intensity of the Kazakh white-headed breed were evaluated by indicators of absolute gain, relative gain and ADG, as well as Feed Conversion (FC) at the age of 12 months (Mussayeva *et al.*, 2021). The economic efficiency of breeding animals of different genotypes was calculated considering all costs and the difference in the cost of products sold.

Results

Using GeneSeek GGP Bovine 150 microchip technology, 83 SNPs were identified that were statistically significantly associated with Quantitative Trait Loci (QTL) in Kazakh white-headed cattle. These SNPs showed high ($p \leq 0.0000001$) and borderline ($p \leq 0.000001$) degrees of significance for phenotypic traits. Of the identified SNPs, two polymorphisms with borderline statistical significance were associated with LW at the age of 12 months; 36 polymorphisms with high statistical significance were associated with an average daily LW gain, and 45 polymorphisms had borderline significance.

Analysis of the influence of individual genotypes by QTL-associated polymorphisms on productivity compared with the total sample of the Kazakh white-headed breed showed only two genotypes associated with an increase in LW at the age of 12 months. Therefore, to search for associations of paired combinations of genotypes (diplotypes) by polymorphisms associated with this indicator, 10 additional SNPs with the highest values of β with the pre-threshold level of association were also analyzed (Table 2). The characteristics of the LW at 12 months in cattle of the Kazakh white-headed breed with genotypes that increase this indicator about the total sample are shown in Table 3.

Of the polymorphisms used to search for diplotypes of the pre-threshold significance level, seven genotype markers associated with an increase in LW at the age of 12 months in Kazakh white-headed cattle were found of the identified markers, the greatest phenotypic effect was observed in the rs42549324/EPHA8/GG genotype. For example, the average LW of carriers of this genotype was 337 ± 11 kg, which is 4.98% more than in the total study sample.

Table 2: SNPs of pre-threshold significance level associated with LW at the age of 12 months in the Kazakh white-headed breed

RS	BTA	p-value	β	Alleles 0/1	ω A-0	G-0/0 (%)	G-0/1 (%)	G-1/1 (%)
rs110794170	12	6.70E-05	7.633	C/T	0.305	4.2	34.1	61.7
rs110044335/SCAI	11	5.87E-04	7.011	G/A	0.259	7.6	38.6	53.8
rs137106352	16	1.27E-05	6.847	C/T	0.297	6.7	42.8	50.4
rs41659799	9	8.87E-05	8.015	G/A	0.207	2.2	24.8	73.0
rs42549324/EPHA8	9	4.41E-04	8.779	A/G	0.144	1.4	23.7	74.9
rs134633932	14	7.52E-04	6.243	A/G	0.347	11.4	45.6	43.0
rs134498295/GBA4	6	3.83E-04	9.451	T/C	0.140	1.4	14.6	84.0
rs109861235	19	6.03E-05	6.156	A/G	0.299	7.9	42.0	50.2
rs110524569	16	7.98E-05	6.103	A/G	0.334	8.7	42.5	48.8
rs133267258	12	4.64E-04	6.483	C/A	0.318	5.2	33.2	61.5

Table 3: Characteristics and indicators of LW at 12 months in the Kazakh white-headed breed with increasing* genotypes according to SNP of pre-threshold significance

RS	p-value	β	Alleles0/1	GT	%	M \pm σ , kg	% Δ	Me (25; 27)/ CI 95%
rs110899754	1.39E-06	7.805	A/C	AA	126	328 \pm 3.3	2.07	329 (320; 335)/(322; 330)
rs110794170	6.70E-05	7.633	C/T	TT	61.7	333 \pm 07	3.72	330 (320; 339.5)/(324; 335)
rs137106352	1.27E-05	6.847	C/T	TT	50.4	332 \pm 07	3.33	332 (320; 341)/(324; 336)
rs42549324/EPHA8	4.41E-04	8.779	A/G	GG	74.9	337 \pm 11	4.98	331.5 (328; 346)/(328; 350)
rs134633932	7.52E-04	6.243	A/G	GG	43.0	330 \pm 05	2.90	329.5 (315; 340)/(322; 330)
rs134498295/GBA4	3.83E-04	9.451	T/C	TC	14.6	329 \pm 04	2.48	330 (315; 340)/(328; 332)
rs109861235	6.03E-05	6.156	A/G	GG	50.2	330 \pm 04	2.81	330 (320; 339)/(325; 333)
rs133267258	4.64E-04	6.483	C/A	AA	61.5	332 \pm 07	3.57	330 (320; 335)/(324; 330)
Total sample	-	-	-	-	-	321 \pm 02	-	320 (309; 332)/(320; 324)

Note: * Increasing phenotypic effect according to the results of the median test

Table 4: The ADG in the Kazakh white-headed breed with genotypes characterized by the most pronounced increasing and decreasing phenotypic effects

Polymorphism	Genotype	n	M \pm σ , kg	% Δ	Me (25; 75)	CI 95%	MT
rs109490287	CC	011	896 \pm 24.5	11.63%	896 (856; 936)	822; 973	P
	TC	143	819 \pm 12.1	02.00%	815 (777; 864)	800; 825	-
	TT	635	798 \pm 04.5	-00.58%	800 (764; 836)	797; 805	-
rs136460595/SEMA6D	GG	021	724 \pm 17.5	-09.86%	729 (689; 755)	649; 775	N
	AG	164	793 \pm 12.1	-01.25%	792 (753; 849)	773; 800	-
	AA	605	807 \pm 04.6	00.48%	805 (767; 838)	803; 811	-
Total sample			803 \pm 4.4	-	803 (764; 838)	800; 808	-

Evaluation of the phenotypic effects of SNP on the ADG in Kazakh white-headed breed animals showed that 13 genotypes that increased this trait, as well as 38 genotypes that decreased it, were associated with this trait. The characteristics of the ADG in animals of genotypes with the most pronounced phenotypic effects are given in Table 4.

Animals with the rs109490287 genotype predominated the most over the total sample/SS. Thus, their average daily weight gain rate was 11.63% higher than that of the total study sample and amounted to 896 \pm 24.5 g. Animals with the rs136460595/SEMA6D/GG genotype were characterized by the lowest value of this indicator (724 \pm 17.5 g), which is lower than the total studied sample by 9.86%. Table 5 shows the characteristics of the growth intensity and economic efficiency of breeding Kazakh white-headed breed animals that are carriers of genotype markers with the most pronounced phenotypic effects on the LW at the age of 12 months.

From the data in Table 5, it can be seen that animals who carried the rs109490287/CC genotype had the greatest absolute gain compared to the total sample. The FC rate in such animals was 5.20 feed units, which is only 0.05 feed units lower than in the total studied sample of Kazakh white-headed cattle and nevertheless, the CE of breeding animals with the rs109490287/CC genotype was 43.3%, which exceeds the average CE of the total sample by 7.1%.

Animals with the rs136460595/SEMA6D/GG genotype, on the contrary, were characterized by the smallest absolute gain in comparison with the total sample. For this group, the FC was 5.30 feed units, which is 0.05 feed units less than the total studied sample of the Kazakh white-headed breed. As a result, the breeding of animals carrying the rs136460595/SEMA6D/GG genotype leads to a decrease in CE by 7.8% compared to the total sample and amounts to 28.4%.

Table 5: Growth and development of Kazakh white-headed breed animals with genotypes characterized by the most pronounced increasing and decreasing phenotypic effects on LW at 12 months

Genotype	AG, kg	ADG, g	FC, feed units	P, thousand rubles	CE, %
rs110899754/AA	299	819	5.24	23.3	37.8
rs109490287/CC	327	896	5.20	30.0	43.3
rs136460595/SEMA6D/GG	264	724	5.30	15.0	28.4
Total sample	292	801	5.25	21.8	36.2

Note: here and further in Table 6 AG, kg is the absolute gain, kg; ADG, g is the average daily gain, g; FC, feed units is the feed conversion, feed units; P, thousand rubles is the profit in thousands of rubles; CE, % is the cost-effectiveness

Table 6: Growth and development of Kazakh white-headed breed animals with genotypes characterized by the most pronounced increasing and decreasing phenotypic effects on LW at 12 months

RS 1-RS 2	LW, kg	AG, kg	ADG, g	FC, feed units	Δ P, thousand rubles	CE %
Diploypes associated with LW at 12 months						
rs42549324/EPHA7/GG-rs109861235/GG	370±3.3	341	935	4.05	11.6	45.6
rs42549324/EPHA7/GG-rs41659799/AA	370±3.3	341	935	4.05	11.6	45.6
rs42549324/EPHA7/CC-rs134498295/GBA3/AG	309±1.9	280	768	5.47	-02.9	33.2
rs110524569/GG-rs137106352/CC	270±1.7	241	661	6.36	-12.2	20.3
Diploypes associated with ADG						
rs110622349/CC-rs43359785/ST3GAL3/AA	384	355	973±13.1	5.16	14.9	47.5
rs109464179/AA-rs43359785/ST3GAL3/AA	384	355	973±7.5	5.16	14.9	47.5
rs43525779/AA-rs43359785/ST3GAL3/AA	384	355	973±5.6	5.16	14.9	47.5
rs134258946/OR7E200/TT-rs136617917/DNAJC24/GG	315	286	784±6.0	5.26	-01.5	34.7
rs136531048/ADGRF2/TT-rs109464179/GG	315	286	784±11.2	5.26	-01.5	34.7
rs134258946/OR7E200/TT-rs136531048//ADGRF2/TT	315	286	784±7.7	5.26	-01.5	34.7
rs134258946/OR7E200/TT-rs109464179/GG	315	286	783±5.3	5.26	-01.6	34.6
Total sample	321±1.76	292	803±4.4	5.25	-	36.2

Note: ±σ values are given for those parameters with which a statistically significant association of the diplotype has been established

The analysis of paired combinations of genotypes QTL-associated with SNP included 1,551 diplotypes, of which 397 were associated with LW at the age of 12 months and 389 with ADG.

According to the results of our median test, 39 diplotypes were identified in the Kazakh white-headed breed that increases LW at the age of 12 months, of which 18 diplotypes had a more pronounced phenotypic effect than the separate genotype rs42549324/EPHA8/GG, where the average LW of carrier animals was 337±11 kg. Furthermore, 48 diplotype markers associated with reduced LW at the age of 12 months were identified in Kazakh white-headed cattle (no separate genotype markers that lowered the LW of animals at this age were identified).

The median test also let us identify 53 diplotypes associated with increased ADG, of which 12 were characterized by a more pronounced phenotypic effect compared to individual marker genotypes; as well as 26 diplotypes affecting reduced ADG, but their phenotypic effect found for the rs136460595/GG genotype did not exceed-9.86%.

The characteristics of productivity, intensity of growth and economic effect of breeding animals of the Kazakh white-headed breed with diplotypes having the greatest increasing and decreasing effects are given in Table 6.

Among the diplotypes associated with the LW at the age of 12 months, the groups with the diplotypes

rs42549324/EPHA7/GG-rs109861235/GG and rs42549324/EPHA7/GG-rs41659799/AA have the most pronounced increasing effect (Table 6). Thus, the LW of these groups is 370±3.3 kg, which is more than the total studied sample by 49 kg. The ADG in animals of these diplotypes is 935 g. As a result, this gives an additional 49 kg of absolute gain. FC in such animals is reduced and amounts to 4.5 feed units, which is less than the total sample by 0.75 feed units. Breeding animals of the rs42549324/EPHA7/GG-rs109861235/GG and rs42549324/EPHA7/GG-rs41659799/AA diplotypes brings an additional P of 11.6 thousand rubles and the CE of production is 45.6%, which exceeds the total sample by 9.4%.

The lowest LW was found in animals with the rs110524569/GG-rs137106352/CC diplotype: The LW of such animals was 270±1.7 kg, which was less than the total sample by 51 kg or 15.9%. The animals with this diplotype had a greater feed consumption per 1 kg of weight gain than the total sample by 1.1 feed units. As a result, the breeding of such animals led to a loss of P equaling 12,162 rubles and a decrease in CE by 20.3%.

Among the animals of the Kazakh white-headed breed, according to the ADG, the maximum increasing phenotypic effect was found in animals with the diplotypes rs110622349/SS-rs43359785/ST3GAL3/AA,rs109464179/AA-rs43359785/ST3GAL3/AA and rs43525779/AA-

rs43359785/ST3GAL3/AA. The LW of such animals reaches 355 kg compared to the average of 321 ± 1.76 kg for the sample. The ADG in young animals with these diplotypes reached 973 g and resulted in an additional 63 kg of absolute gain. Against the background of a decrease in FC in such animals (5.16 feed units compared to 5.25 feed units of the total sample), the additional P compared to the total sample was 14.9 thousand rubles and the CE of production increased to 47.5%, compared with 36.2% of the CE of the total sample.

Discussion

According to the data obtained by us, for the indicators of LW at 12 months of age and the ADG, the λ value was 1.092 and 1.846, respectively, which indicates the confidence level of the model (Belaya *et al.*, 2022). The analysis of the distribution of statistically significant polymorphisms by chromosomes, carried out using the Python software, pandas, matplotlib and seaborn libraries and visualized in the form of Manhattan plot graphs showed that in cattle of the Kazakh white-headed breed, two polymorphisms of the borderline significance level were associated with the LW at the age of 12 months; 36 polymorphisms of the high significance level and 45 polymorphisms of the borderline the significance levels were associated with ADG (Belaya *et al.*, 2022).

Analysis of the effect of QTL-associated SNPs on LW at 12 months of age compared with the total sample allowed us to establish a slightly increasing phenotypic effect in two genotypes, rs110899754/AA and rs41566580/CC, with the largest gain in LW (2.07%) observed in animals with the rs110899754/AA genotype. Of the two polymorphisms associated with the LW, one was described by a group of scientists (Meredith *et al.*, 2012). They identified the association of the rs41566580 polymorphic site in the Irish population of Holstein-Friesian cattle (Meredith *et al.*, 2012) of the 81 SNPs statistically significantly associated with ADG, 14 polymorphisms were studied by other scientists and of the 36 SNPs of high significance associated with the same indicator, 6 polymorphic sites were studied by other authors. The polymorphic site rs109218410/HERC3 was characterized by Snelling *et al.* (2010) as a QTL, which is significantly ($p < 0.05$) associated with LW at birth in crossbreeds of aberdeen-angus, red angus, simmental, hereford, limousine, gelbvian, pinzhauer and charolais breeds. Kiser *et al.* (2019) showed that the polymorphic site rs110377022/HERC3 was statistically significant ($p < 1.94E-13$) associated with the coefficient of reproductive ability and the age of the first calving in the Holstein breed. Ilie *et al.* (2021) identified rs110749552/HERC3 polymorphism as associated ($p < 4.27E-07$) with LW and somatic cell index in cattle of Romanian brown and Romanian spotted breeds. Olsen *et al.* (2016) showed a

statistically significant ($p < 0.010$) association of rs133157501/FAM13A polymorphism with the percentage of milk protein in Norwegian red cattle. Buitenhuis *et al.* (2015) identified the polymorphic site rs134106481 as significantly associated ($p = 4.90E-02$) with the potassium content in milk in cattle of the Danish populations of Holstein and Jersey breeds. Cole *et al.* (2011) established a statistically significant association ($p < 0.05$) of rs43526428/PWWP2A polymorphism with milk yield, milk protein and fat yield, milk fat percentage, ease of calving, duration of the productive period, sacrum width, udder structure, stillbirth and other signs. Dadousis *et al.* (2017) characterized the polymorphic site rs110435062 as significantly associated ($p = 1.69E-05$) with cheese protein extraction in the Italian population of the brown Swiss breed.

Out of 45 polymorphisms of the borderline significance level associated with the ADG, 8 SNPs were described by other scientists. Thus, Buitenhuis *et al.* (2015) established the association of rs109037411/ENSBTAG00000048421 polymorphism with the percentage of non-glycosylated kappa-casein in milk in cattle of Danish populations of Jersey and Holstein breeds; rs109420069/STK4 polymorphism with the sign of somatic cells in Jersey, Holstein and Yorkshire breeds; rs109719021/BAALC polymorphism with the percentage of protein in milk in American populations of Holstein cattle; and rs137202311/SPAG17 polymorphism with a percentage of protein in milk in the Canadian Holstein population (Buitenhuis *et al.*, 2016; Nayeri *et al.*, 2016; Jiang *et al.*, 2019; Oliveira *et al.*, 2019).

Kim *et al.* (2009) characterized the polymorphic site rs29009651/FRK as QTL which was significantly associated with reproductive traits in North American Holstein cattle; polymorphic site rs41657325/UBE2R2 as the one associated with the fertilization coefficient in Holsteins; rs43629218/MYO1E as the one associated with the percentage of protein in milk in the Dutch population of Holstein-Frisian breed; rs43734039/MARCHF3 as the one associated with protein yield in milk in Holstein-Frisian cattle (Kim *et al.*, 2009; Schopen *et al.*, 2011; Meredith *et al.*, 2012; Gaddis *et al.*, 2016). The association of the remaining 68 polymorphisms with economically useful traits in cattle of the Kazakh white-headed breed has been established in our study for the first time.

The results of our study highlight the significant role of SNP markers in predicting and enhancing meat productivity in the Kazakh white-headed cattle breed. Specifically, we identified critical genetic markers like rs42549324/EPHA8 and rs109490287/CC, which are significantly associated with increased live weight and average daily gain, respectively. While our study provides comprehensive insights into the genetic factors influencing meat productivity, future research should explore the interaction of these SNPs with environmental

variables to fully harness their potential in different breeding contexts.

Conclusion

Analysis of the effect of QTL-associated SNPs on LW at 12 months of age compared with the total sample allowed us to establish a slightly increasing phenotypic effect in two genotypes (rs110899754/AA and rs41566580/CC), with the greatest LW gain observed in animals carrying the rs110899754/AA genotype.

The study of the ADG over the entire growing period showed 13 genotypes that increased this indicator and 38 genotypes associated with its reduced values. Animals with the rs109490287/CC genotype predominated the most over the total sample. Animals with the rs136460595/SEMA6D/GG genotype were characterized by the lowest value of this indicator. Analysis of the effect of paired combinations of polymorphisms with statistical pre-threshold significance on the LW at the age of 12 months in Kazakh white-headed cattle showed 39 diplotypes that increased this indicator. The carriers of the rs42549324/EPHA7/GG-rs109861235/GG and rs42549324/EPHA7/GG-rs41659799/AA diplotypes had the greatest advantage.

We identified 48 diplotypes that statistically significantly decreased the LW in the age period of 12 months. Of these, the lowest LW was observed in animals who had the rs110524569/GG-rs137106352/CC diplotype. 53 diplotypes were associated with an increased ADG, of which 12 diplotypes had a greater phenotypic effect than individual marker genotypes. The most pronounced effect was observed in the diplotypes rs110622349/AA-rs43359785/ST3GAL3/CC, rs109464179/AA-rs43359785/ST3GAL3/AA and rs43525779/AA-rs43359785/ST3GAL3/AA.

Our findings highlight the potential of SNP markers as powerful tools for the genetic improvement of meat productivity in the Kazakh white-headed breed. The identified markers offer breeders the opportunity to incorporate genetic information into selection decisions, enabling the development of more efficient and productive cattle populations. Furthermore, the integration of genetic markers associated with feed conversion efficiency and economic efficiency into breeding strategies has the potential to significantly improve the profitability and sustainability of meat production.

This study has the potential for practical recommendations that may be in demand by farms and farmers engaged in breeding the Kazakh white-headed breed.

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Author's Contributions

Indira Beishova: Written the manuscript.

Askar Nametov, Yusupzhan Yuldashbaev and Aliya Akhmetaliyeva: Conceived of the presented idea.

Alzhan Shamshidin, Alena Belaya and Tatyana Ulyanova: Edited the manuscript.

Alexandr Kovalchuk: Verified the analytical methods.

Ivan Tegza: Acquired funded and developed the theory.

Baluash Traisov: Verified the analytical methods.

Aizhan Abylgazinova: Curated data, derived the models and analyzed the data.

Rustem Beishov: Defined the methodology.

Yerkingali Batyrgaliyev: Curated data, derived the models and analyzed the data.

Ethics

This article is comprised entirely of original content and includes no material previously published elsewhere. The corresponding author affirms that all co-authors have reviewed and approved the final manuscript. Furthermore, we confirm that there are no ethical conflicts associated with this publication.

Conflict of Interest

The authors declare no conflict of interest.

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