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ТҮЙІН

Бұл зерттеуде азық протеинінің және рациондардың сапалық параметрлерінің (месқарындағы ерігіштік пен ыдырау, аминқышқылдарының құрамы) месқарындағы синтетикалық процестердің ерекшеліктеріне, аш ішекте ассимиляциялауға болатын протеин мен аминқышқылдарының шығымдылығына, маңызды аминқышқылдарының қорытылу динамикасына әсерін зерттелді және бордақыланған ірі қара малдың тірі салмағының өсуі зерттелді. Протеиннің ерігіштігі Макдугал буферінде анықталды, ыдырауы 6, 12, 24 сағаттық экспозицияда нейлон пакеттерінде "in vivar" әдісімен анықталды. Физиологиялық зерттеулер барысында қарыншалардан аш ішекке түсетін сөл көлемінің тәуліктік динамикасы зерттелді. Аш ішекке түсетін микробтық ақуыздың мөлшері диаминопимелин қышқылымен (dad) есептелді. Аммиактың түзілу динамикасын анықтау үшін азықтандыруға дейін және одан кейін месқарын құрамының үлгілері алынды. Микробтық биомасса дифференциалды центрифугалау әдісімен оқшауланған. Азықтың, нәжістің және сөлдің аминқышқылдарының құрамы Сһromospec автоматты анализаторының көмегімен анықталды.

РЕЗЮМЕ

В данном исследовании изучалось влияние качественных параметров кормового протеина и рационов (растворимость и расщепляемость в рубце, аминокислотный состав) на особенности синтетических процессов в рубце, выход протеина и аминокислот, доступных для усвоения в тонком кишечнике, динамику всасывания незаменимых аминокислот, изучали прирост массы тела у откормленного молодняка крупного рогатого скота. Растворимость протеина определяли в буфере Макдугалла, расщепляемость определяли методом "in vivar" в нейлоновых пакетах при экспозиции 6, 12, 24 часа. В процессе физиологических исследований изучалась суточная динамика объема химуса, поступающего из преджелудочков в тонкую кишку. Количество микробного протеина, поступающего в тонкую кишку, рассчитывали по диаминопимелиновой кислоте (ДАД). Для определения динамики образования аммиака были взяты пробы содержимого рубца до и после кормления. Микробную биомассу выделяли методом дифференциального центрифугирования. Аминокислотный состав корма, фекалий и химуса определяли с помощью автоматического анализатора Chromospec.

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THE INFLUENCE OF SOME POLYMORPHIC GENES ON THE PRODUCTIVE AND BREEDING QUALITIES OF KALMYK CATTLE

ANNOTATION

The article presents the results of a study on the influence of some polymorphic genes on the productive and breeding qualities of Kalmyk cattle. The study was conducted at the premises of Agrofirma Turikpen LLC, located in the Zhambyl region of the Republic of Kazakhstan. The objects of the study were Kalmyk breed bulls and heifers up to 18 months of age.

The total number of Kalmyk cattle in TOO Agrofirma Turikpen is 6961 heads. The herd is characterized by a rational structure, which reflects the strategic focus of the farm on reproduction, selection and breeding work and commercial meat production. Analysis of the weight and exterior characteristics showed that the animals are in good physiological condition, and their parameters correspond to those expected for this breed and age. The results obtained allow us to assert that the created conditions of keeping and feeding on the farm contribute to the stable growth and development of animals, which lays a solid foundation for further analysis of their genetic potential.

Based on the results of the conducted research, it becomes clear that further research aimed at developing fundamental principles of zootechnical science within the framework of studying new polymorphisms of candidate genes will contribute to the development and optimization of gene identification methods, the formation of meat productivity and meat quality, as well as the commercial value of livestock. The results of such research allow for the early selection of promising animals for meat breeding and making decisions on the feasibility of using animals with the necessary genotypes for the selection process.

Key words: Kalmyk breed, productive indicators, breeding qualities, polymorphic genes, molecular genetics.

Introduction. Beef cattle breeding is becoming one of the most profitable sectors of the agroindustrial complex today not only in Kazakhstan but also abroad. One of the main areas of selection work in beef cattle breeding is to increase the meat productivity of various cattle breeds. To solve this problem, marker-associated selection of farm animals is used [1; 2; 3; 4].

One of the key and complex tasks in the agricultural sector is to increase the production of highquality beef [1,2].

The urgent need to increase beef production highlights the importance of expanding the country's export potential, which in turn contributes to food security. To achieve these goals, specialized beef cattle breeding must be strengthened as soon as possible [3].

The formation of meat productivity is determined by a complex of morphological and physicochemical transformations in the body of livestock during its growth and fattening. The main factors influencing this process are the quality of feeding, genetic predisposition, gender, age, nutritional status, housing conditions and individual characteristics of animals [4, 5].

Important consumer characteristics of meat products, such as taste, aroma, tenderness, marbling and juiciness, play a key role. During post-slaughter decomposition, glycogen is converted into lactic acid, which contributes to the softening of connective tissue during long-term storage. As animals age, there is a decrease in moisture content and an increase in fat content in meat, which leads to changes in protein composition and an increase in the amount of connective proteins. In the connective tissue of adult animals, the content of elastin increases, and collagen fibers acquire increased rigidity. Muscle proteins are subject to denaturation and proteolytic cleavage with varying degrees of intensity [4,10,11,12].

Thanks to advances in modern molecular genetics, it has become possible to identify genes that regulate both quantitative and qualitative characteristics of the productivity of farm animals. This advance is of particular importance in the field of breeding cattle specialized in meat production. Identifying promising genotypes early in the life of animals is becoming a key point in breeding work. This enables targeted selection and individual selection of the most suitable individuals as parent pairs, thereby accelerating the selection process and increasing the efficiency of livestock productivity [5].

When analyzing the meat productivity of farm animals during their life, the key indicator is growth energy, and after slaughter, the quantitative and qualitative characteristics of muscle and fat tissue, as well as their ratio in the carcass, become important factors [4,6].

The characteristics of animal fat metabolism, which are reflected in the energy of growth, play an important role in the development of animal husbandry. The direction and intensity of lipid metabolism have a significant impact on the quality characteristics of livestock products. A particularly important productivity indicator characterizing fat metabolism is meat marbling [4,8].

Research conducted by Phillips JA III points to the importance of growth hormone and a number of other proteins that directly or indirectly participate in its functioning [7].

Over the past several decades, cattle breeding programs have increasingly used molecular genetic technologies to achieve sustainable and efficient genetic progress in economically important traits.

Traditional breeding systems are slow due to the time lag associated with progeny testing. Characterization of quantitative trait loci allows the use of biomarkers to select for economically important traits and provides faster genetic gain if candidate genes correlate with these traits [13].

The Kalmyk breed of cattle is one of the oldest breeds of cattle, representing significant breeding and economic importance. Kalmyk cattle are distinguished by a strong constitution, harmonious physique and high meat productivity.

Animals of this breed can reach a live weight of: cows - 450-480 kg, bulls - 800-950 kg, and calves at birth - 20-25 kg. Kalmyk cattle have good reproductive capacity, easily tolerate calving and are characterized by high fertility. The average calf yield is 89 per 100 mothers, which exceeds similar indicators of other meat breeds [14,15,16].

One of the effective approaches to assessing the intensity of fat metabolism in animals and their subsequent selection is the use of DNA markers. The development of methods for analyzing potential DNA markers of fat metabolism and studying the influence of various variants of these markers on productivity indicators is a pressing issue in modern zootechnics [9].

The use of DNA markers to improve carcass and meat quality characteristics of cattle has been identified as a useful and effective tool for genetic gain. Quantitative body and carcass traits of cattle are determined by multiple genes, so screening of candidate genes is necessary to understand the relationship between gene variation and these traits [17,18,19,20].

In recent decades, genetic research in animal husbandry has become increasingly important, especially in the context of gene polymorphism. These studies allow us to understand how genetic variations affect various aspects of animal production, such as growth, reproduction and product quality.

The study of gene polymorphisms allows the identification of genetic markers associated with desired characteristics, such as improved growth performance or meat quality.

A study by HC Xu and colleagues found associations of CRTC2 gene polymorphisms with growth performance and meat quality in Qingchuan cattle. The results showed that SNP g.3001 C>T and g.3034 G>A are amino acid substitutions, and SNP g.3034 G>A and g.3467 T>C have a medium level of polymorphism[21].

The observed associations between these SNPs and growth and meat quality parameters indicate the potential importance of the CRTC2 gene in marker-assisted selection of Qingchuan cattle for improving production characteristics and meat quality [22].

A study conducted by a group of scientists led by Sedykh examined the effect of TG5 and LEP gene polymorphisms on meat composition in Hereford and Limousin calves. As a result, significant genetic potential for improving the taste and nutritional value of beef was revealed, mainly due to the high frequency of the desired TT genotype in the TG5 gene. Links were also found between polymorphisms in the TG5 and LEP genes and the main parameters of meat composition [22].

Many foreign scientists analyze the influence of gene polymorphism on beef quality. In these studies, special attention was paid to the polymorphism of the genes of myostatin (MSTN), thyroglobulin (TG), calpine (CAPN) and calpastatin (CAST) [20, 21, 22].

The MSTN polymorphism is associated with a mutation causing muscle hypertrophy, which allows the identification of the "double muscle" phenotype, widespread in European breeds such as the Belgian Blue. The TG5 polymorphism determines meat marbling, allowing the identification of individuals with different muscle fat content, which is important for adapting breeding to market

requirements. The CAPN1 and CAST genes affect beef tenderness, improving the organoleptic quality of meat during maturation [19, 20, 21].

FABP4, a protein expressed in adipocytes and macrophages, plays a key role in fatty acid transport and lipid hydrolysis. Polymorphisms in the FABP4 gene have been associated with meat quality characteristics, especially in Asian feedlot cattle breeds. Goszczynski et al. investigated the genetic variation of FABP4 in different breeds and assessed the effect of genotype on fat content in a crossbreeding population (Angus-Hereford-Limousin).

The authors Raza, Sayed Haidar Abbas et al. studied the influence of PLIN1 gene polymorphism and its relationship with body characteristics of Qingchuan cows to identify molecular genetic markers.

The PLIN1 gene creates a protein that resides inside fat cells and helps them utilize fat. The expression level of the PLIN1 gene was determined in various tissues using the quantitative reverse transcriptase polymerase chain reaction (qRT-PCR) method. The results showed that the highest level of PLN1 expression was found in subcutaneous fat, followed by the heart and longus dorsi muscle, and the lowest level was found in the kidneys.

Previous studies have shown that information on the effects of some polymorphic genes on fat content in Kalmyk cattle in Kazakhstan is insufficient.

In this context, the focus of the research project on improving the quality of meat in beef cattle by using effective selection methods and techniques, as well as creating new polymorphisms in candidate genes, contributes to the development and optimization of methods for identifying genes responsible for the formation of meat productivity and quality. The aim of this study is to determine the effect of certain polymorphic loci in the CRTC2 and ELOVL6 genes on the fat content in the muscles of Kalmyk cattle[19].

The ELOVL6 gene is one of the candidate genes that has been identified as regulating meat and carcass traits through metabolic control, fatty acid oxidation, fat deposition and lipid synthesis. Especially with respect to lipid metabolism, the ELOVL6 gene in Kalmyk cattle appears to be a key metabolic regulator that modulates fat deposition [21].

Junjvlieke, Zainaguli et al., note that the ELOVL6 gene plays an important role in the synthesis and elongation of fatty acids, which contributes to the formation of fats and the regulation of fat metabolism in the body [20]. The influencing factor of the ELOVL6 gene on fat metabolism in bovine fat cells was analyzed. By introducing adenoviruses, the ELOVL6 gene was activated in fat cells, after which RNA sequencing was performed. The results showed that the activation of the ELOVL6 gene led to changes in the fatty acid composition in fat cells: a decrease in the proportion of myric and palmitic acids and an increase in stearic and arachidic acids. In addition, more than two thousand genes were found whose expression was altered.

A study by Xu, HC and colleagues examined the role of CRTC2 gene in regulating growth and meat quality in Qinchuan cattle [21]. Growth and meat quality genes are key factors in assessing cattle performance and are affected by genetic and environmental conditions. CRTC2, as a recently discovered obesity-related gene, may influence fat deposition.

The researchers analyzed the polymorphisms of the CRTC2 gene in Qinchuan cattle and investigated their association with various growth and meat quality characteristics. As a result, three single nucleotide polymorphisms (SNPs) associated with these traits were identified. These results confirm the involvement of the CRTC2 gene in the regulation of growth and meat quality in Qinchuan cattle and indicate the potential for using CRTC2 as a candidate gene for marker-assisted selection in livestock breeding development programs [21, 22].

The main sources of fat in the body of mammals are subcutaneous, visceral, intramuscular and intermuscular fat [13; 14].

According to scientists Martins et al.; Gui et al.; Raza et al., intramuscular fat is the main factor determining the quality of meat in meat-producing animals. However, increasing intramuscular fat deposition without increasing the other three fat reserves is one of the main challenges facing the meat industry [11; 12; 13]. In addition, the composition of fatty acids in adipose tissue is closely related to meat quality. This is due to their effect on meat quality, especially on nutritional value and taste [14].

In connection with the above, the study of the influence of polymorphic genes on fat content and its relationship with meat quality in the Kalmyk breed in the conditions of Kazakhstan is an urgent task of interest both for science and for practice. Understanding the genetic features that affect the meat characteristics of cattle will help to develop effective selection methods aimed at improving the productivity and quality of animal meat.

The purpose of this study is to establish the influence of individual polymorphic loci (SNP) in the CRTC2, ELOVL6 genes on the fat content in muscles and its relationship with body growth and meat quality traits in Kalmyk cattle bred in different conditions of Kazakhstan.

The work was carried out with financial support within the framework of grant funding for 2024-2026 under the project AP23488071 "The influence of polymorphic genes on the quality of meat of Kalmyk cattle" (State registration number No. 0124PK00251).

Materials and methods. The study was conducted on the basis of TOO "Agrofirma Turikpen", located in the Zhambyl region of the Republic of Kazakhstan. The choice of this farm was due to its specialization in breeding Kalmyk cattle, which created optimal conditions for the implementation of the research objectives.

The object of the study is bulls and heifers of the Kalmyk breed aged 12-24 months. For the experiment, bulls and heifers aged 12 to 24 months were selected in the amount of 300 heads. All animals were kept in identical feeding conditions, which excluded the influence of external factors on the results of the study.

Animals, randomly selected at the age of 12-24 months, are kept in identical conditions and fed an identical TMR (Total Mixed Ration - a ratio of roughage to concentrates of 6:4).

Zootechnical analysis of the herd, determination of the genealogical structure, conditions of maintenance and feeding, as well as growth and development indicators of animals is carried out according to the generally accepted method. Blood is collected from the jugular vein and processed using a reagent kit for DNA extraction. DNA is extracted from the blood using the Blood DNA Kit and DNKExtran1 kits according to the Green and Sambrook method. Amplified DNA fragments were clearly visualized on the gel, and the use of molecular markers confirmed the accuracy of fragment size determination.

The body length, withers height, chest depth, rump height and hip width of the animals are measured. Carcass characteristics such as back fat thickness, ultrasound dry muscle area and intramuscular fat are determined using an ultrasound scanner.

The blood collection procedure was carried out in strict accordance with sanitary norms and standards for working with biological material. Beclab vacuum tubes containing the EDTA anticoagulant were used. This type of tube was chosen for its ability to prevent blood clotting and preserve the biological properties of the material before laboratory processing.

The sequencing results are analyzed using MAFFT and Codon Code Aligner to detect new SNPs. Phylogenetic analysis is performed using the Neighbor Joining method and a tree is constructed using MEGAX. The data are processed using variation statistics methods using Microsoft Excel.

Results and discussion. Agrofirma Turikpen LLP is an important participant in the agroindustrial sector of Kazakhstan, specializing in breeding cattle and producing high-quality beef. The farm was founded in 2000 and is located in the Zhambyl region, which gives it access to the vast pasture lands of the region.

The total number of Kalmyk cattle in Agrofirma Turikpen LLC, located in the Moyynkum district of the Zhambyl region, is 6961 heads. The herd is characterized by a rational structure, which reflects the strategic focus of the farm on reproduction, selection and breeding work and commercial meat production.

The structure of the Kalmyk cattle population in TOO Agrofirma Turikpen is shown in Table 1.

uble 1 Structure of the Kunnyk cuttle population in 100 Agroninia Turkpen				
Animal categories	Number of heads	Share of total livestock, %		
Total population	6961	100%		
Cows	2737	40%		
Heifers up to 18 months	1041	16%		
TV up to 12 months	111	1.5		
Bulls up to 12 months	105	1%		
Bulls up to 24 months	2965	43%		
With tribal status	2846	40%		
No tribal status	4115	59%		

Table 1 – Structure of the Kalmyk cattle population in TOO "Agrofirma Turikpen"

The analysis of the herd structure at TOO Agrofirma Turikpen indicates a high degree of organizational optimization. A significant proportion of cows (39.3%) indicates attention to the reproductive process, ensuring the stability of the number of animals on the farm. Heifers (16.5%) confirm active selection work aimed at rejuvenation and genetic improvement of the herd. Bulls, which make up 42.6% of the total livestock, play a key role in providing the farm with commercial meat products.

This indicates that the company is successfully implementing a commodity production strategy focused on the production of high-quality beef.

The presence of a large group of animals with breeding status (40.9%) emphasizes the importance of breeding work, which is aimed at improving such economically valuable traits as marbling, intramuscular fat content and precocity.

At the same time, a large proportion of animals without breeding status (59.1%) allows for the economic stability of the farm through active participation in the production process.

Thus, the livestock structure in TOO Agrofirma Turikpen is optimally balanced to achieve both breeding and production goals.

Maintaining the breeding part of the herd ensures high genetic potential of animals, while the commercial livestock ensures stable economic results and satisfaction of demand for products both on the domestic and international markets.

The farm's strategy is aimed at further development of selection and breeding work, which indicates its significant contribution to the development of beef cattle breeding in Kazakhstan.

To assess the breeding qualities of Kalmyk cattle, 200 heads of cattle were rated at the farm of TOO Agrofirma Turikpen. During the grading, the breeding qualities of bulls and heifers of various age groups were assessed, which made it possible to more accurately determine their compliance with the established standards. The assessment of breeding qualities was carried out for the purpose of analyzing and classifying cattle into the categories elite-record, elite and 1st class (table 2).

Group of animals	Total	Class		
Group of animals	Total	elite-record	elite	1st grade
Total	300	101	135	64
Heifers over 18 months	84	31	24	29
Bulls up to 12 months	105	38	49	18
Heifers up to 12 months	111	32	62	17

Table $2 - D$ istribution of probonitized animals by	y classes
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As a result of the probonitization, 300 heads of cattle were distributed among classes as follows: 101 heads were assigned to the "elite-record" class, 135 heads to the "elite" class, and 64 to the "1st class". This indicates a high level of breeding qualities, since a significant portion of the animals meet the "elite" and "elite-record" standards. Among 84 heifers over 18 months old, 31 heads (36.9%) belong to the "elite-record" class, 24 heads (28.5%) to the "elite" class, and 29 heads (34.5%) belong to the "1st class".

In the age group of bulls up to 12 months, out of 105 heads, 38 (36.1%) correspond to the "elite-record" class, and 49 (46.6%) - to the "elite" class. At the same time, in this group, the bulls classified as "class 1" amounted to 17.3%, which emphasizes the high level of breeding qualities of all bulls in this age category. Heifers aged up to 12 months are represented by 111 heads, of which 32 (28.8%) are classified as "elite-record", 62 (55.9%) - as "elite", and 17 (15.3%) - as "class 1".

Measuring live weight is a key indicator of livestock productivity and health. For the Kalmyk breed, which is known for its high meat productivity, accurate live weight data allows for effective assessment of their development and compliance with breeding standards.

Live weight analysis of bulls and heifers at Agrofirma Turikpen LLC is carried out to determine growth and assess compliance with breeding criteria. Table 3 below illustrates the average live weight of animals depending on their age and compliance with grading classes (Table 3).

Age, months	Total heads, bulls	Average live weight, kg	Bonitivoch class, bulls	Total heads, heifers	Average live weight, kg	Bonitivoch class
7 months	25	195	elite	14	174	elite
10 months	42	224	elite	63	192	elite
12 months	38	337	elite	34	216	elite

Table 3 – Average live weight of bulls and heifers by age groups

The data in the table demonstrate a stable increase in the average live weight of animals with age, which confirms their good development and compliance with age standards.

All groups, regardless of gender and age, belong to the high grading class "elite", which indicates a high level of productivity and breeding quality of the livestock.

Such results indicate effective conditions of feeding, housing and selection work in TOO "Agrofirma Turikpen". At the same time, there is a natural advantage of the average live weight of bulls compared to heifers, which corresponds to their biological characteristics and confirms the high genetic potential of the breed.

Measuring exterior and performance characteristics is an important stage of research aimed at studying the physical development of animals and their compliance with breed standards.

This process allows recording key parameters of body composition, which play an important role in assessing meat productivity and identifying the relationship with genetic factors. The measurement procedure was carried out in specially equipped areas of the farm, which ensured convenience and safety for animals and researchers.

Standard zootechnical instruments were used to record the parameters, including measuring tapes, rulers and electronic scales, which ensured the accuracy of the data. The study recorded such parameters as height at withers, height at sacrum, chest girth, oblique body length, chest width and depth, hip width and pastern girth.

These parameters reflect body proportions, development of the skeletal and muscular systems, as well as the ability of animals to accumulate muscle mass.

Live weight and body measurements were measured from 84 heifers at 18 months of age at Agrofirma Turikpen LLC (Table 4).

Indicator	Average value (cm) (X±Sx)	Standard deviation (σ)	Coefficient of variation (CV, %)
Live weight, kg	322.5 ± 5.56	11.25	3.72
Oblique length of the body, cm	120.4 ± 0.07	1.50	1.25
Height at withers, cm	122.7 ± 0.06	1.25	1.02
Height at sacrum, cm	123.6 ± 0.07	1.50	1.21
Chest circumference, cm	143.5 ± 0.28	5.75	4.01
Chest depth, cm	66.8 ± 0.16	3.25	4.87
Chest width, cm	40.3 ± 0.08	1.75	4.34
Width in laps, cm	38.5 ± 0.15	3.00	7.79
Metacarpus girth, cm	16.1 ± 0.06	1.25	7.76

The data in Table 4 show that the parameters of Kalmyk heifers are characterized by varying degrees of variation. The most stable in terms of the coefficient of variation (CV) are the oblique body length, height at the withers, and height at the sacrum, which indicates the homogeneity of these parameters among animals. Their coefficients of variation do not exceed 1.5%, which indicates a relatively small scatter of data. On the other hand, chest girth, chest depth, and chest width show somewhat greater variability (CV from 4% to 4.87%), which may be due to individual differences in the development of the chest and body width in heifers.

The maximum values of the variation coefficient are observed for the width at the hips and the circumference of the metacarpus (7.79% and 7.76%, respectively). This indicates a significant scatter of data and, possibly, the influence of both genetic and external factors (e.g., housing conditions and nutrition), which can affect the variability of these indicators.

As for the live weight, it averages 322.5 kg with a variation coefficient of 3.72%, which also indicates a certain homogeneity among animals. The standard deviation of 11.25 kg indicates that the live weight of heifers is within the range, which may be due to genetic factors, feeding and housing conditions.

Thus, the measurement data indicate a high homogeneity of the body structure of the Kalmyk breed in terms of the main parameters of length and height, while some transverse measurements are characterized by more significant fluctuations. Live weight and body measurements of bulls at 12 months of age were also studied (Table 5)

Indicator	Average value (cm) (X±Sx)	Standard deviation (σ)	Coefficient of variation (CV, %)
Live weight, kg	302.4 ± 3.53	11.25	3.72
Oblique length of the body, cm	131.2 ± 0.1	1.5	1.14
Height at withers, cm	118.8 ± 0.08	1,2	1.01
Height at sacrum, cm	119.6 ± 0.09	1.3	1.08
Chest circumference, cm	158.5 ± 0.12	1.7	1.07
Chest depth, cm	69.8 ± 0.18	2.5	3.58
Chest width, cm	38.3 ± 0.06	0.9	2.35
Width in laps, cm	31.7 ± 0.06	0.8	2.53
Metacarpus girth, cm	18.1 ± 0.06	0.9	4.97

Table 5 – Body measurements of Kalmyk breed bulls

The analysis of the table shows that most of the measured parameters of the Kalmyk bulls are highly uniform, which is confirmed by the low values of the standard deviation and the coefficient of variation. The oblique body length, height at the withers and chest width are particularly stable, which indicates the consistency of the animal sizes. More pronounced variability is observed in the chest depth and live weight, which may indicate the influence of various factors, such as nutrition and housing conditions. In general, the data indicate good health and condition of the bulls, which is important for further breeding programs.

Based on the obtained body measurements, the body constitution indices of the animals were calculated (Table 6).

Body composition index	Indicators, %		
	Heifers 18 months	Bulls 12 months	
Leg length index	101.91	90.5	
Stretching index	98.13	110.4	
Index of confusion	116.95	227.5	
Bone index	11.22	20.0	

Table 6 – Body condition indices of heifers and bulls of the Kalmyk breed

According to Table 6, the leg length index of bulls is 90.5%, which is below the norm. This may indicate insufficient growth or an incorrect ratio between height and body length. The stretch index of bulls is 110.4%, which is a positive sign and indicates a good proportion between body length and height.

All data were entered into specially prepared protocols, which made it possible to systematize the results obtained and ensure their further processing.

The data collected at this stage are key to analyzing the impact of genetic markers on performance characteristics. Exterior parameters such as chest depth and width or hip width are directly related to meat performance, as they reflect the animals' ability to accumulate mass and develop muscle tissue.

For example, a developed chest indicates good capacity of internal organs, and wide hips indicate high potential for development of the rear part of the body, which is especially important for meat breeds.

The obtained results are used for comparison with genotyping data, which allows establishing possible correlations between the physical development and genetic characteristics of animals. These indicators are also important for selection work, as they make it possible to select animals with the most promising productive characteristics.

Thus, measurements of conformation and body weight provide an important link between the physical and genetic aspects of the study, ensuring its comprehensiveness and reliability.

Collecting blood from animals was an important step in providing sufficient biological material for molecular studies.

Blood was collected from the jugular vein using vacuum tubes with an anticoagulant, which allowed the integrity of the samples to be maintained until they were analyzed.

The blood processing included extraction of genomic DNA using the phenol-chloroform method. This method has proven its reliability, providing high-quality DNA with a concentration exceeding the minimum required for molecular analysis. The purity of the extracted DNA was confirmed using a spectrophotometer, with the A260/A280 ratio indicating the suitability of the samples for further genotyping.

All isolated samples were placed in low-temperature storage conditions, which guaranteed the preservation of their properties. The polymerase chain reaction performed allowed for the amplification of target DNA regions associated with the study of single nucleotide polymorphisms. The reaction results were tested by agarose gel electrophoresis, which demonstrated the high efficiency of the chosen method.

We selected the sequences of the forward and reverse primers: LEFT PRIMER – AAACTTCGGCTGGCATACAC and RIGHT PRIMER – TCGAGTGCTCCGAGATGAAT, the annealing temperature of the forward primer is 58.83°C, the annealing temperature of the reverse primer is 58.61°C, the GC content in the sequence of both primers is 50.0%, the size of the obtained amplification product is 220 bp. Next, to detect the point mutation, we searched for the desired restriction enzyme, using a computer program, the BfaI restriction enzyme with the CTAG recognition site was determined. Amplification was carried out using primers: LEFT PRIMER - AAACTTCGGCTGGCATACAC and RIGHT PRIMER - TCGAGTGCTCCGAGATGAAT, the length of the resulting PCR product will be 220 bp, after restriction with BfaI endonuclease, depending on the genotype, the following fragments are formed: 220 bp, 144 bp, 76 bp, which are well visualized in 4.0% agarose gel.

Forward and reverse primers (LEFT PRIMER – AAACTTCGGCTGGCATACAC and RIGHT PRIMER – TCGAGTGCTCCGAGATGAAT) were synthesized in the amount of 10 picomoles and BfaI restriction enzyme with the C/TAG restriction site was used to identify the CRTC2 gene alleles. After restriction of the amplification, fragments are formed depending on the genotype of the animals: in individuals with the homozygous GG genotype 144 bp, 76 bp, since there is a restriction site, the amplification is cut into two fragments, 144 bp in size. and 76 bp, in heterozygous individuals with the GA genotype, fragments of 220 bp, 144 bp, 76 bp appear on the electropherogram, in homozygous AA genotype, the amplification is not cut by the BfaI restriction enzyme and we can visualize only one fragment, 220 bp in size (Table 7).

The temperature regime of amplification was: initial denaturation step I – $95^{\circ}C$ – 5 minutes, step II, denaturation at $94^{\circ}C$ – 30 sec, primer annealing at $60^{\circ}C$ – 30 sec and elongation at $72^{\circ}C$ – 30 sec, the number of cycles was 35, III final synthesis at $72^{\circ}C$ – 5 min.

As a result of amplification, a fairly good quality amplification product was obtained; the size of the obtained PCR product corresponds to the expected results, 220 bp (Fig. 2).

To identify genetic variants of the CRTC2 gene (g.3034 G>A SNP polymorphism), we performed restriction of the PCR product with BfaI restriction enzyme at 37°C for three hours and after visualization of the restriction results on the electropherogram, a fragment of only one size, 220 bp, was detected, which corresponds to the homozygous genotype AA. Here are possible options, all DNA samples are homozygous or we have not accurately established the location of the point

mutation g.3034 G>A SNP polymorphism in the coding part of the CRTC2 gene (GCCTA[G>A]CCGAG).

Table 7 – Composition of the reaction mixture for amplification of the CRTC2 gene region of Kalmyk cattle

Components of the PCR reaction	For 1 reaction mixture, µl	For 30 reaction mixture, µl
10x PTR KCl buffer	2.5	75.0
dNTP mixture	2.0	60.0
Direct Primer F	1.0	30.0
Reverse primer R	1.0	30.0
25 mM MgCl2	1.5	45.0
Taq polymerase enzyme	0.2	6.0
Deionized water	13.8	414.0
DNA sample	3.0	-
Volume of the reaction mixture	25.0	



Figure 1 – Electropherogram of the CRTC2 gene amplification of Kalmyk cattle, 3.0% agarose, wells 1-7, 8-14, PCR product size 220 bp, M-DNA marker pUC19/MspI



Figure 2 – Electropherogram of the CRTC2 gene amplification after restriction with BfaI endonuclease, 3.0% agarose, wells 1-7, 8-14 homozygous genotype AA, fragments of 220 bp, M-DNA marker pUC19/MspI

We have conducted a literature review to determine the localization of the following (SNPs); g.3001 C>T; g.3034 G>A; g.3467 T>C polymorphisms in the coding part of the CRTC2 gene, however, the available literature does not contain information on the localization of these mutations that are associated with meat productivity in cattle. A similar situation is in determining the localization of the point mutation in the coding part of the ELOVL6 gene in cattle.

Conclusion. The obtained results allow us to state that the created conditions of keeping and feeding on the farm contribute to the stable growth and development of animals, which lays a solid foundation for further analysis of their genetic potential. Exterior parameters, such as the depth and width of the chest or the width of the hips, are directly related to meat productivity, as they reflect the ability of animals to accumulate mass and develop muscle tissue. The obtained results are used for comparison with genotyping data, which allows us to establish possible correlations between the physical development and genetic characteristics of animals. These indicators are also important for breeding work, as they make it possible to select animals with the most promising productive characteristics.

As a result of amplification, a fairly good quality amplification product was obtained, the size of the obtained PCR product corresponds to the expected results, 220 bp. The results indicate the possibility of using marker-associated selection to increase animal productivity.

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ТҮЙІН

Мақалада кейбір полиморфты гендердің қалмақ тұқымды ірі қара малының өнімділік және асыл тұқымдық қасиеттеріне әсері туралы зерттеу нәтижелері берілген. Зерттеу Қазақстан Республикасының Жамбыл облысында орналасқан «Агрофирма Түрікпен» ЖШС базасында жүргізілді. Зерттеу объектісі ретінде 18 айға дейінгі қалмақ тұқымының бұқашықтары мен қашарлары алынды.

«Агрофирма «Түрікпен» ЖШС-дегі қалмақ тұқымдас ірі қара малының жалпы саны 6961 басты құрайды. Табын малы шаруашылықтың өсімін молайту, селекциялық-асыл тұқымдық жұмыстарға және тауарлы ет өндіруге стратегиялық бағдарын көрсететін ұтымды құрылыммен сипатталады. Зерттеу нәтижелері табындағы малдардың тірі салмағы мен сыртқы пішін сипаттамаларын талдау барысында жақсы физиологиялық күйде екенін және олардың параметрлері осы тұқым мен жас төлдердің өсімі тұқым мал стандартына сәйкес келетінін көрсетті. Алынған нәтижелер шаруашылықта күтіп-бағу мен азықтандырудың жасалған жағдайлары жануарлардың тұрақты өсіп-жетілуіне ықпал ететінін дәлелдеуге мүмкіндік береді, бұл олардың генетикалық әлеуетін одан әрі талдауға берік негіз болды.

Зерттеу нәтижелері бойынша кандидат гендердің жаңа полиморфизмдерін зерттеу аясында малтану ғылымының іргелі принциптерін дамытуға бағытталған әрі қарайғы зерттеулер гендерді анықтау әдістерін әзірлеуге және оңтайландыруға, ет өнімділігі мен ет сапасын, сондай-ақ малдың тауарлық құнын қалыптастыруға ықпал ететіні белгілі болды. Мұндай зерттеулердің нәтижелері етті өсіруге арналған перспективті малдарды ерте кезеңде іріктеуге және асыл тұқымдылық процесінде қажетті генотиптері бар жануарларды пайдаланудың орындылығы туралы шешім қабылдауға мүмкіндік береді

РЕЗЮМЕ

В статье изложены материалы результаты исследования по изучению влияние некоторых полиморфных генов на продуктивные и племенные качества крупного рогатого скота калмыцкой породы. Исследование проводилось на базе ТОО «Агрофирма Турикпен», расположенного в Жамбылской области Республики Казахстан. Объектом исследования являлись бычки и телки калмыцкой породы в возрасте до 18 мес.

Общее поголовье калмыцкого крупного рогатого скота в ТОО «Агрофирма Турикпен», составляет 6961 голову. Стадо характеризуется рациональной структурой, которая отражает стратегическую направленность хозяйства на воспроизводство, селекционно-племенную работу и товарное мясное производство. Анализ массы и экстерьерных характеристик показал, что животные находятся в хорошем физиологическом состоянии, а их параметры соответствуют ожидаемым для данной породы и возраста. Полученные результаты позволяют утверждать, что созданные условия содержания и кормления в хозяйстве способствуют стабильному росту и развитию животных, что закладывает прочную основу для дальнейшего анализа их генетического потенциала.

По результатом проведенным исследованиям становится ясно, что дальнейшие исследования, направленные на разработку фундаментальных принципов зоотехнической науки в рамках изучения новых полиморфизмов генов-кандидатов, будут способствовать разработке и оптимизации методов идентификации генов, формированию мясной продуктивности и качества мяса, а также товарной ценности скота. Результаты таких исследований позволяют на ранней стадии отбирать перспективных животных для мясного разведения и принимать решения о целесообразности использования животных с необходимыми генотипами для селекционного процесса.

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INFLUENCE OF BIOTECHNOLOGICAL METHODS OF FREEZING AND THAWING OF SEMEN OF PRODUCING RAMS ON SEMEN PRESERVATION AND INSEMINATION RESULTS

ANNOTATION

The article presents materials on improving biotechnological methods of freezing and thawing sperm of rams - producers of the Ordabasy breed of meat and fat sheep. As a result of the studies, high efficiency of insemination of ewes with thawed sperm, frozen and stored in disposable polypropylene

CONTENT



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