Research Article

Associations of *GH* and *TG5* Genotypes with Carcass Composition and Nutrient Conversion Efficiency in Hereford Bulls

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Abstract | One important approach to improving beef production profitability is enhancing feed conversion efficiency and lean meat yield through genetic selection. The aim of the study was to evaluate the effects of growth hormone (*GH*) and thyroglobulin (*TG5*) gene polymorphisms on the morphological composition and the efficiency of feed energy and protein conversion into meat in Hereford bulls. After weaning, the animals were divided into 6 groups according to the genotypes of the *GH L127V* (LL, LV, VV) and *TG5 C422T* (CC, CT, TT) polymorphisms with 9 bulls in each group. Genotyping was performed by PCR-RFLP. Bulls (21 months old) were slaughtered to determine the morphological composition, and the nutrient and energy content of the carcasses. Data on feed intake, slaughter traits, and chemical composition of meat were used to calculate the efficiency of feed nutrients conversion into protein and energy of edible body parts. *GH-VV* genotype was associated with improved muscle tissue development and reduced fat content ($p < 0.05$). In *GH-LL* genotype bulls, lean accounted for 70.6% of carcass weight, which was 4.7–5.2% ($p < 0.05$) less than in V-allele carriers. A significant difference was found between homozygous genotypes for the *GH* gene in metabolizable energy intake per 1 kg of weight gain at 9.82 MJ ($p = 0.05$). The amount of fat in the carcass was significantly ($p < 0.05$) determined by the *TG5* genotype. The results suggest a potential impact of the GH gene on protein metabolism, muscle synthesis, and tissue formation in cattle. The studied associations may be useful for future genetic evaluations in order to improve Hereford cattle breeding.

Keywords | Crude protein, Genotype, Hereford bulls, Metabolizable energy, Morphological composition, Nutrient conversion

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INTRODUCTION

One of the most pressing issues at present is ensuring the energy and protein needs of the human population. The important biological feature of cattle is their ability to consume and process large amounts of cheap low-nutrient forages, including crop and food industry wastes, and convert it into food valuable to humans (Belous *et al*., 2022). Beef is a rich source of protein, fat, and several essential macro- and microelements. The market volume of beef is expected to reach 76 million tons by 2031, which means a significant 8% increase in production (FAO, 2021). However, at global levels, there is a significant environmental impact due to the greenhouse gas emissions from cattle breeding, which is a constraint on the steady growth of beef production. Despite this, people continue to demand delicious and nutritious foods, and the beef production system is not likely to change significantly in the near future (Mohammadabadi et al., 2021). The development of new approaches to beef cattle breeding focuses on creating highly productive animals that can reach a large live weight at a young age and produce the greatest amount

of nutrients with maximum utilization of feed protein and energy (Gerasimov *et al*., 2023). High productivity is primarily an organism's genetically determined ability to efficiently convert nutrients from feed into the tissues that are used as animal products (Kubatbekov *et al*., 2020). This ability is due to the intensive course of metabolic processes in the body at all stages, from the utilization of energy and feed nutrients in the gastrointestinal tract to biosynthesis of proteins, lipids and other nutrients (Baber *et al*., 2019; Ryazanov *et al*., 2022). During the growing period, young animals are highly capable of building muscle mass and utilizing feed protein to form muscle tissue, and also demonstrate high gains with relatively efficient energy and protein utilization (Lebedev *et al*., 2021; Dzhulamanov *et al*., 2022). The widely known methods of evaluating animal meat productivity and determining feed utilization efficiency do not adequately characterize their ability to maximize nutrients production. In this case, the most objective assessment of the animal is provided by indicators of the conversion and transformation of feed nutrients into meat (Valoshin and Glazkov, 2022; Pristupa *et al*., 2025).

The most effective way to increase the profitability of beef production is to improve the efficiency of bioconversion of feed nutrients into products, primarily by enhancing the genetic potential of beef cattle (Ghavi Hossein-Zadeh, 2024). The further development of beef cattle breeding and the intensification of agricultural production impose new requirements on cattle breeds. Fundamental knowledge of molecular genetic mechanisms that determine the specifics of feed utilization for beef production will provide a basis for directed breeding of beef cattle with specified productivity parameters (Abo-Ismail *et al*., 2018). The high correlation between live weight, lean weight and feed costs suggests that these traits are influenced by the same genes. Several studies have reported the effects of growth hormone (*GH*) and thyroglobulin (*TG5*) genes polymorphisms on feed utilization efficiency, weight gain, slaughter performance, and chemical composition of beef, suggesting that genetic variations in these genes may influence the efficiency of feed conversion to body weight in cattle (Gorlov *et al*., 2023; Bila *et al*., 2024). The results of the study on the morphological composition of half-carcasses have shown a significant impact of *GH* gene on chilled carcass weight and lean content (Sedykh *et al*., 2020). Dolmatova *et al*. (2020) found that the *TG5* polymorphism in cattle affects indicators of fat metabolism, such as fat yield and fat content in the longissimus muscle and ground beef. Ardicli *et al*. (2022) showed the significant impact of the *TG* marker on fattening performance, including final weight, hot carcass weight, chilled carcass weight, and total weight gain. Based on the limited information available on the relationship of these genes with the conversion of feed nutrients into body tissues, we have hypothesized that the *GH* and *TG* genes could also be useful for cattle selection due to their regulatory role in metabolism. Animals with a desirable genetic background would be able to convert feed more efficiently (Kostusiak *et al*., 2024). Therefore, studying the genetic aspects of the transformation of feed energy and protein into meat product energy and protein has high theoretical and practical significance for agricultural science. Considering genetic markers in the development of breeding methods can create the basis for early prediction of economic traits. This could help determine the potential for selection and reduce the time between generations (McPhee *et al*., 2020; Kolpakov *et al*., 2025).

The aim of the research was to evaluate the effects of *GH* and *TG5* gene polymorphisms on the morphological composition and the efficiency of feed energy and protein conversion into meat in Hereford bulls.

MATERIALS AND METHODS

Study period and location

The study was conducted from May 2023 to February 2025. The animals were reared at the test station of the "Agrofirma Kalininskaya" LTD (Chelyabinsk Region, Russia). The laboratory tests were conducted at the collaborative center of the Federal Research Center for Biological Systems and Agrotechnologies RAS.

Animals and sampling

A 3 × 3 factorial research design was used to evaluate the effects of polymorphisms in *GH* and *TG5* genes on morphological composition of carcass and the efficiency of feed energy and protein conversion into meat in Hereford cattle. A total of 54 purebred Hereford bulls (~ 7 months of age) after weaning were included in the experiment. The animals were genotyped and divided into 6 groups according to the genotypes of the *GH L127V* (LL, LV, VV) and *TG5 C422T* (CC, CT, TT) polymorphisms with 9 bulls in each group. Bulls of different genotypes were raised under the same feeding and housing conditions from weaning to slaughter at 21 months of age. Schematic diagram of the experimental design is presented in Figure 1.

The rearing of young animals during the suckling period (from birth to approximately 7 months) was carried out according to the cow-calf system. Before weaning, the calves were housed alongside the cows in lightweight buildings with straw bedding in winter and grazed together with cows on pastures in summer. The dry steppe pastures of the Chelyabinsk region cannot provide animals with all the nutrients they need for the entire pasture season, so from mid-summer (end of July) calves were fed in shaded pens

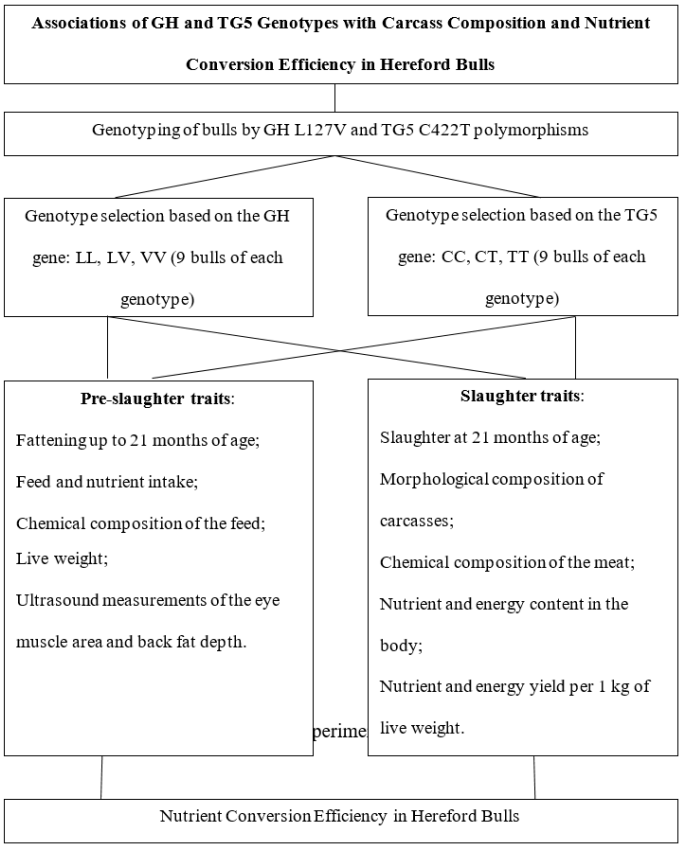

Figure 1: Schematic diagram of the experimental design.

with feeders and water drinkers installed. The young bulls were weaned when they reached a live weight of at least 200 kg and 6-8 months of age. After weaning, the bulls were transferred to a feedlot and fattened from weaning to slaughter at 21 months of age. A semi-open free-stall barns housing system (with straw as bedding) was applied (9 bulls in a pen of 10 m^2 per animal). Each group was kept separately. The bulls were fed *ad libitum* with the same diet and had full access to water. The feeding rations were adjusted based on nutritional needs of animals, taking into account their age, live weight, and the type of housing (winter or summer). The winter ration consisted of 25% roughage, 30% succulent feed, and 45% concentrated feed. They were fed 2.45 to 2.79 kg of dry matter and 24.5 to 27.9 MJ of metabolic energy per 100 kg of live weight. From birth to the end of fattening the proportion of consumed forage by type was as follows: milk 11.3%; hay 17.7%; haylage 7.1%; grain haylage 13.6%; grass 8.2%; and concentrates 42.1% (Table 1). Individual feed intake was determined daily according to the difference between the provided and residue amount of feed using an automated individual feeding system. Chemical analysis of the feed mixture was performed monthly to determine the dry matter content by drying samples (500 g) at 103°C in an oven. Organic matter was determined by ashing the dried sample at 550°C (AOAC, 2000).

A dataset with 54 animal parameters has been created. The data includes RFID-ID numbers, animal weight, feed and nutrition intake, ultrasound measurements of back-fat depth and eye-muscle area. Additionally, the database contains slaughter traits such as pre-slaughter live weight, carcass weight, internal fat weight, content of trim fat, lean, bones and tendons, chemical composition of meat (moisture, fat, protein, ash).

The weight growth of the young animals was monitored monthly during the fattening period until they were 21 months old, on the same date, using electronic scales.

A KX5600G ultrasound device (KAIXIN, PRC) equipped with a 3.5L160E2 linear transducer (frequency of 2.0-5.0 MHz on a scanning area depth of 200 mm) was used to measure the back-fat depth and eye-muscle area. Ultrasound measurements were performed before slaughter on the right side of the animals' bodies in the area of the

Table 1: Feed and nutrient intake for bulls up to 21 months old (per animal).

Indicator	GH			TG5		
	LL	LV	VV	CC	CT	TT
Milk (kg)	1041	1062	1048	1056	1051	1044
Mixed grass hay (kg)	1748	1862	1869	1815	1828	1835
Corn haylage (kg)	1455	1686	1666	1593	1604	1610
Grain haylage (kg)	2642	2821	2870	2761	2780	2792
Concentrates (kg)	2622	2622	2622	2622	2622	2622
Pasture grass (kg)	2504	2458	2460	2479	2477	2466
Feeds contain						
Dry matter (kg)	4539.0	4608.0	4607.0	4557.2	4589.3	4607.6
Metabolizable energy (MJ)	47205.6	47656.0	46584.6	46860.9	47186.5	47398.7
Crude protein (kg)	584.1	621.0	621.6	618.5	604.3	603.9
Concentration of metabolizable energy per 1 kg of dry matter (MJ/kg)	10.4	10.3	10.1	10.3	10.3	10.3

Table 2: Primer sequence, PCR conditions, restriction enzymes used in genotyping.

SNP	Primer sequence	PCR conditions	Restriction enzymes
GH C2141G	F:5'-GCTGCTCCTGAGCCTTCG-3' R:5'-GCGGCGGCACTTCATGACCCT-3'	Initial heating - at +95 °C for 5 min; 35 cycles: denaturation- at +94°C for 45 s; annealing - at +65°C for 45 s; synthesis- at +72°C for 45 s; primer extension - at +72°C for 7 min	AluI
TG5 C422T	F: 5'-GGGGATGACTACGAGTATGACTG-3' R: 5'-GTGAAAATCTTCTGGAGGCTGTA-3'	Initial heating - at +94°C for 4 min; 35 cycles: denaturation - at +94°C for 60 s; annealing - at +62°C for 60 s; synthesis - at +72°C for 60 s; primer extension - at +72°C for 4 min	BstX2I

SNP=single nucleotide polymorphism, PCR=Polymerase chain reaction, GH=growth hormone, TG5= thyroglobulin.

12th-13th ribs of the thoracic cage. Before scanning, the hair was shaved from the area and treated with ultrasonic gel (Geltek, Russia) for better contact with the ultrasound device.

The animals were slaughtered at an industrial slaughterhouse at the end of the fattening period (at 21 months of age). The young animals were stunned by applying an electric probe to the back of their heads, piercing the skin to a depth of no more than 5 mm, with an electric current of 50 Hz industrial frequency and 120 V voltage. After stunning, the bulls were lifted onto a suspended track using a winch and hung by their hind limbs. During bleeding, a 30–50 mm incision was made at the neck-torso junction along the midline of the esophagus. The animals were identified using RFID chips, and the carcasses were identified by tags and cooled for 24-48 hours after slaughter. Dressing of animals after stunning and bleeding involved dehiding, evisceration, splitting and washing.

After cooling, the carcass was cut into specific anatomical parts and deboned. Pre-slaughter weight, hot carcass weight, perinephric and retroperitoneal fat were recorded at slaughter. Trim fat was defined as the combination of subcutaneous and intermuscular fat deposits. Subcutaneous fat refers to adipose tissue located beneath the skin, while intermuscular fat resides between muscle bundles.

An average of 400 g of ground beef was taken from the left half of each carcass. From the same carcass before deboning, a sample (200 g) of the longissimus dorsi muscle at the level of the 9th –11th ribs was taken by transverse muscle cutting.

The dry matter content was determined by drying the samples in an oven at 103 °C. The organic matter content was determined by incinerating the dried sample at 550°C (AOAC, 2000).

According to the postmortem data, we considered the pre-slaughter weight, the weight of the left half-carcass, the morphological composition of the carcasses including lean, trim fat, bones and tendons content, the chemical composition of ground beef and *Longissimus dorsi* muscle. Based on the experimental data, calculations were made about the energy content and conversion protein and energy coefficients.

Genotyping

Blood was collected from the jugular vein of experimental bulls after weaning (8 months of age) after weaning to genotype by polymorphisms of the *GH L127V* and *TG5 C422T* genes. DNA was extracted from whole blood using the "M-Sorb Blood" (Sintol, Russia) genomic DNA extraction kit. The quality of the isolated DNA was checked using a Qubit 4.0 fluorimeter and the Qubit dsDNA HS Assay kit (Invitrogen, USA).

PCR amplification was performed using a Bio-Rad T100 thermocycler (Bio-Rad, Singapore) with a mixture of reagents in a total volume of 15 µl. This mixture contained 1.5 µl of a dinitrophosphate solution, 10x buffer solution, 0.03 µl of each primer at a concentration of 100 mM and 1 unit of *Taq* polymerase. The primers were designed using the online tool BLAST NCBI (https://www.ncbi.nlm.nih.gov/; Altschul *et al*., 1990) (Table 2).

Restriction endonucleases were selected using the NEBcutter v2.0 tool (https://nc2.neb.com/NEBcutter2/). *AluI* and *BstX2I* enzymes (SibEnzyme LLC, Russia) were used. Genotypes were identified by gel electrophoresis and visualized under UV light. The products of the growth hormone gene were identified as follows: GH^{VV} – 223 bp; GH^{LV} – 223, 171, 52 bp; GH^{LL} – 171, 52 bp. For the thyroglobulin gene: $TG5^{TT}$: 473, 75 bp; $TG5^{CT}$: 473, 295, 178, 75 bp; $TG5^{CC}$: 295, 178, 75 bp.

Statistical analysis

The effects of genotype on the traits studied were analyzed using the least-squares method using the general linear model procedure of the Statistica 10.0 software ("Stat Soft Inc.," USA). Model used:

$$Y_{ij} = \mu + A_i + e_{ij}$$

Where, Y_{ij} – represents the studied traits, μ – is the overall mean, A_i – is the fixed effect of the *GH* and *TG5* genotype (1, 2, 3), and e_{ij} – is random error.

Based on the data obtained from chemical research, the energy content of ground beef was calculated using the formula: Energy content of 1 kg of ground beef, MJ = ((P × 4.1) + (F × 9.3)) × 0.04187, where P is the amount of protein, %; F is the amount of fat, % ; 0.04187 – conversion coefficient from kcal to MJ.

The protein conversion coefficient (PCC) was calculated by dividing the protein yield per 1 kg of pre-slaughter weight by the amount of crude protein consumed per 1 kg of live weight gain during the study period. The metabolizable energy conversion coefficient (MECC) was calculated by dividing the metabolizable energy yield per 1 kg of pre-slaughter weight by the metabolizable energy content in fodder consumed per 1 kg of live weight gain during the study period. Crude protein and metabolizable energy intake were measured individually once a month, based on the amount of feed consumed and its chemical composition. The monthly data on protein and energy intake was summarized for the entire period of raising animals, including the stages of suckling and fattening. These calculations provided crucial insights into the protein and energy utilization efficiency of the animals during the study period (Valoshin and Glazkov, 2022; Pristupa *et al.*, 2025).

Correlation coefficients between traits were calculated using Pearson's method

The Shapiro-Wilk test was used to check if a dataset follows a normal distribution. Measured data were expressed as mean ± standard error, and a posteriori Fisher's criterion (F-test) was used for data that met normal distribution, while Mann–Whitney U rank-sum test was used for statistical analysis if the data did not meet normal distribution. $p \leq 0.05$ was considered statistically significant. An integrated approach was used to verify the reliability of the results, despite the small sample size. The Mann-Whitney U-test was chosen for the main comparisons as it is robust to deviations from normal distribution. A posteriori power analysis showed that for most significant effects, the power was above 80%. In order to test for the influence of outliers, we conducted an influence analysis, which demonstrated the stability of the results when each individual was consistently excluded from the analysis.

RESULTS

In vivo ultrasound measurements of carcass traits

In vivo evaluation of meat traits using ultrasound measurements indicated the effect of the GH gene polymorphism on muscle tissue development (Figures 2 A, C). The largest area of the *longissimus dorsi* muscle was recorded in bulls with the GH-VV genotype, which exceeded the measurement of LL-genotype by 8.1 cm^2 (14.0%; $p = 0.10$). In addition, this group was characterized by comparatively less subcutaneous adipose tissue formation than their counterparts with the alternative homozygous genotype, at a difference of 0.43 mm (6.69%; $p > 0.05$). The heterozygous bulls exhibited an intermediate phenotype in terms of ultrasonically measured meat traits.

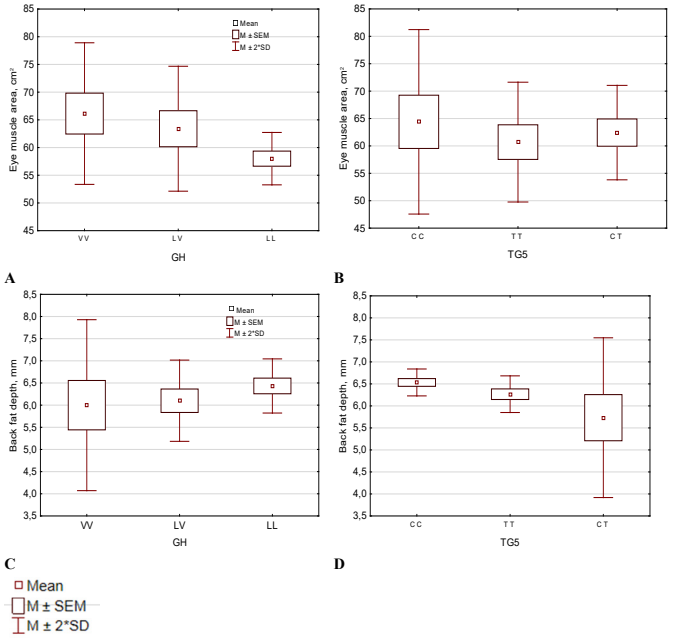

Figure 2: Effect of GH and TG5 gene polymorphisms on eye muscle area (cm^2) and back fat depth (mm) at the level of 12^{th}-13^{th} rib in Hereford bulls: A: variability of eye muscle area (cm^2) depending on GH genitype; B: variability of eye muscle area (cm^2) depending on TG5 genitype; C: variability of back fat depth (mm) depending on GH genitype; D: variability of back fat depth (mm) depending on TG5 genitype.

Trend-level differences ($p = 0.12$) in adipose tissue development were noted between homozygous and heterozygous carriers of the C-allele (Figure 2D). Thus, the difference in subcutaneous fat thickness was 0.8 mm (13.96%) in favor of the CC genotype.

Post-slaughter morphological composition of carcasses

The deboning of half-carcasses revealed significant variations in the content of specific body tissues depending on the genotype of the *GH* gene (Table 3). The LL-genotype was characterized by minimal lean and bone mass and maximum fat mass. The difference in muscle tissue weight between the groups of V allele carriers and LL genotype was 19.8-25.6 kg (17.3-22.4%; $p < 0.05$).

Table 3: Effects of GH and TG5 gene polymorphisms on morphological composition of half carcasses in Hereford bulls (M±SEM), kg.

Trait	GH			TG5		
	LL	LV	VV	CC	CT	TT
Half-carcass weight (kg)	161.7±6.69	178.0±7.77	184.3±3.18	179.0±8.19	171.2±8.88	173.3±9.56
Lean weight (kg)	114.2±5.94[a]	134.0±5.18	139.8±3.70[a]	137.0±6.44	126.1±8.21	124.9±10.09
Fat weight (kg)	22.7±1.04[ab]	15.6±2.00[a]	16.3±1.23[b]	14.3±1.72[a]	18.5±1.21	21.8±1.95[a]
Bone weight (kg)	22.4±0.80[ab]	25.5±0.52[a]	25.5±0.30[b]	25.0±0.26	24.4±1.75	24.1±0.93
Tendons weight (kg)	2.3±0.30	2.9±0.20	2.8±0.09	2.7±0.06	2.7±0.15	2.6±0.47

[a, b] Values in a row with the same indexes differ with significance $p < 0.05$. GH=Growth hormone gene, TG5=Thyroglobulin, SE=Standard error.

Bulls with the LL genotype exhibited significantly greater fat accumulation in the half carcass, with an increase of 6.4-7.1 kg (39.3-45.5%; $p < 0.05$) compared to those with the V allele. The rank distribution of genotypes for the *GH* gene for bone content corresponded with the development of the lean part of the carcass, with an average difference of 3.1 kg (13.8%; $p < 0.05$) between groups. The *GH* gene had no significant effect on the variability of chilled carcass weight in Hereford bulls. However, differences at the trend level ($p = 0.09$) were established between carriers of both alternative homozygous genotypes, reaching 22.6 kg (14.0%).

The effect of the TG5 genotype on the mass of individual body tissues was less pronounced than that of the GH gene. Significant differences in the amount of fat were found between the both homozygous groups, which was 7.5 kg (52.4%; $p < 0.05$), with a predominance of the TT genotype. Carriers of the CC genotype tended to outperform their peers in terms of other indicators of the carcass's morphological composition.

The peculiarities of body tissue development are better characterized by analyzing the relative content of separate parts of the half-carcass in Hereford bulls (Figure 3). Muscle tissue formation is significantly determined by the genotype for the *GH* gene. In LL-genotype carriers, it was 70.6% of carcass weight, which was 4.7-5.2% ($p < 0.05$) less than in heterozygous and homozygous peers with the V allele. The reverse ranking of genotype distribution was observed for adipose tissue content. The V allele was associated with lower fat deposition intensity and contributed to a 5.3-5.4% ($p < 0.05$) reduction in carcass fat percentage relative to the LL genotype.

The *TG5* gene polymorphism also influenced the variability in the morphological composition of the half-carcasses of Hereford bulls. Trend-level differences were observed in lean content of 4.6% ($p= 0.09$) and adipose tissue content of 4.8% ($p= 0.08$) between alternative homozygous genotypes. Furthermore, the T allele was linked to increased fat deposition, while the C allele was associated with enhanced muscle development. The combination of alleles resulted in intermediate expression of body tissue development in the heterozygous genotype.

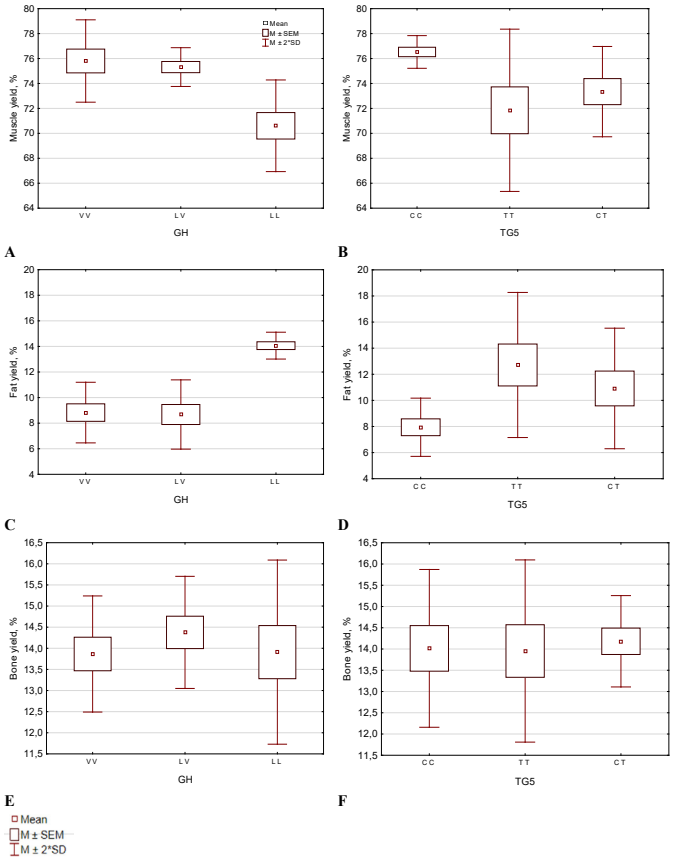

Figure 3: Tissue content in half-carcasses of Hereford bulls of different genotypes by GH and TG5 genes, %: A: variability of muscle yield (%) depending on GH genitype; B: variability of muscle yield (%) depending on TG5 genitype; C: variability of fat yield (%) depending on GH genitype; D: variability of fat yield (%) depending on TG5 genitype; E: variability of bone yield (%) depending on GH genitype; F: variability of bone yield (%) depending on TG5 genitype.

Nutrient and energy content of meat

Table 4 presents the ability of Hereford bulls to synthesize nutrients in the body depending on the genotype of the *GH* and *TG5* genes. Despite the significantly higher protein content in meat compared to fat, the contribution

of fat to the energy value of meat was higher in bulls of all genotypes. Furthermore, the ratio of fat and protein energy differed between animal groups. The highest ratio of fat and protein energy among the genotypes for the *GH* gene was recorded in LL-genotype carriers at 1.41:1, while the lowest ratio was found in heterozygous young animals at 1.12:1. Among the *TG5* genotypes, the extreme variants of this index were the alternative homozygous genotypes, which showed maximum expression in TT carriers (1.37:1) and minimum expression in CC individuals (1.12:1).

Feed intake and nutrient conversion efficiency

The crude protein intake per unit of weight gain depended on the GH genotype (Table 5). VV-genotype carriers consumed the least amount of crude protein, which was 37-44 g (3.4-4.0%) less than their peers. The rank distribution of metabolizable energy intake per 1 kg gain was identical, with a significant difference of 9.82 MJ (11.1%; p = 0.05) between homozygous genotypes. The *TG5* gene polymorphism had no effect on the variability of the requirements for feed crude protein and metabolizable energy per unit of live weight gain.

The body of bulls with the LL genotype contained the least amount of protein, with differences at the trend level compared to heterozygous (LV) animals being 8.8 kg (15.7%; p = 0.12) and homozygous V allele carriers 10.0 kg (17.9%; p = 0.08). A lower proportion of protein was recorded in the live weight gain of young animals with the LL genotype. They were inferior to VV animals by 6.2 g (5.9%; p = 0.20) and to their heterozygous peers by 7.6 g (7.1%; p = 0.12). There were no significant differences in the amount of accumulated body fat or its yield per 1 kg of live weight gain between genotypes for the *GH* gene.

No significant intergroup differences were found when analyzing the nutrient content of the bodies per 1 kg of live weight of bulls genotyped for the *TG5* gene. The CC-genotype carriers were the leaders in dietary protein yield per unit of growth with an advantage of 2.5-4.7 g (2.4-4.7%) over T allele carriers (CT and TT). With regard to body fat produced per 1 kg of live weight, the TT group outperformed the others by 3.0-6.9 g (3.9-9.6%).

Table 4: Nutrient yield and energy value of carcass from Hereford bulls of different genotypes according to the GH and TG5 genes (M±SEM).

Genotype	Content in 1 kg of flesh (g)		Energy contained in 1 kg of flesh (kJ)	Including energy (kJ)		Total energy in carcass flesh (MJ)
	Protein	Fat		Protein	Fat	
GH						
LL	181.1±7.91	110.6±17.43	7414.5±563.87	3109.3±135.71	4305.2±678.57	2026.9±152.25
LV	193.6±2.74	96.4±15.57	7076.1±653.10	3323.9±47.09	3752.2±606.14	2121.6±240.62
VV	189.3±1.39	99.5±10.41	7123.2±426.37	3248.9±23.79	3874.3±405.48	2226.9±173.42
TG5						
CC	190.3±1.07	94.4±12.36	6943.1±495.63	3266.1±18.44	3677.0±481.41	2112.2±244.02
CT	190.2±4.54	103.8±12.03	7308.5±546.51	3265.5±77.94	4043.0±468.61	2125.0±244.14
TT	183.5±8.68	108.2±19.06	7362.2±602.93	3150.5±149.04	4211.7±742.00	2138.1±42.85

GH=Growth hormone gene, TG5=Thyroglobulin, SE=Standard error.

Table 5: Bioconversion of feed protein and energy into the edible body parts of Hereford bulls of different genotypes by GH and TG5 genes (M±SEM).

Indicator	GH			TG5		
	LL	LV	VV	CC	CT	TT
Intake per 1 kg of live weight gain						
Crude protein (g)	1092±29.5	1085±32.6	1048±11.4	1083±34.2	1074±21.6	1067±30.5
Metabolizable energy (MJ)	88.39±3.622	83.30±3.346	78.57±0.547	82.22±3.804	84.06±3.939	83.98±4.208
Protein content in the body (kg)	56.0±4.67	64.8±3.36	66.0±1.77	64.3±3.27	61.7±4.05	60.8±5.94
Fat content in the body (kg)	45.5±4.19	45.5±5.49	47.1±3.93	44.6±5.25	46.1±5.26	47.3±2.61
Yield per 1 kg of live weight						
Protein (g)	98.7±4.30	106.3±1.90	104.9±2.29	105.7±1.54	103.2±3.21	101.0±5.06
Fat (g)	80.6±8.26	74.5±7.81	74.7±5.58	73.0±6.35	76.9±6.61	79.9±8.75
Energy (MJ)	5.51±0.250	5.45±0.348	5.42±0.257	5.37±0.282	5.47±0.336	5.53±0.229
The protein conversion coefficient (PCC) (%)	9.1±0.63	9.8±0.43	10.0±0.18	9.8±0.40	9.6±0.39	9.5±0.72
The metabolizable energy conversion coefficient (MECC) (%)	6.2±0.36	6.6±0.55	6.9±0.38	6.6±0.59	6.5±0.57	6.6±0.08

GH=Growth hormone gene, TG5=Thyroglobulin, SE=Standard error.

The variations of nutrient synthesis in the edible body parts of bulls of different genotypes by the *GH* gene resulted in differences in the conversion coefficients of feed protein and energy into dietary protein and the energy of meat products. The difference between the both homozygous genotypes for protein bioconversion was 0.9% (p= 0.19), while the difference for metabolizable energy was 0.7%. Bulls with VV-genotype were characterized by the highest efficiency of feed nutrient utilization. Heterozygous (LV) animals had intermediate conversion rates.

When bulls were grouped according to their *TG5* genotype, the variability in the conversion of feed nutrients into products was within narrow limits. Across genotypes, 9.5-9.8% of crude protein and 6.5-6.6% of metabolizable energy of feed were spent on body tissue formation. While extreme variants of protein conversion ratio among Hereford bulls reached 8.05-10.29%, metabolizable energy - 5.55-7.65%.

Correlation analysis between traits

The prerequisites for creating a highly efficient Hereford herd is a reasonable selection of animals based on the study of the relationship between productive traits (Table 6). Significant positive correlations were found between live weight and lean amount ($r = 0.93$, $p < 0.001$), protein conversion ratio ($r = 0.91$, $p < 0.001$), and energy conversion ratio ($r = 0.69$, $p < 0.05$). The prediction of meat productivity using ultrasound measurements was highly accurate for determining eye muscle area. The correlation between the morphometric parameters of the *longissimus dorsi* muscle and lean weight was $r = 0.83$ ($p < 0.01$), with protein and energy bioconversion were $r = 0.74$ ($p < 0.05$) and $r = 0.80$ ($p < 0.01$), respectively.

Table 6: Correlation of lifetime productivity traits with carcass lean and fat content and conversion of feed protein and energy into edible body parts.

Correlated traits	Live weight	Eye muscle area	Back fat depth
Lean weight	0.93***	0.83**	0.24
Lean yield	0.64	0.57	-0.07
Fat weight	-0.20	-0.19	0.02
Fat yield	-0.48	-0.42	0.13
The protein conversion coefficient	0.91***	0.74*	-0.30
The metabolizable energy conversion coefficient	0.69*	0.80**	-0.27

Significance of correlation coefficient: * - $p < 0.05$; ** - $p < 0.01$; *** - $p < 0.001$

There was a positive correlation between lean yield and live weight, as well as between lean yield and eye muscle area. The correlation coefficients ranged from 0.57 to 0.64 ($p = 0.06$-0.10). However, there was a negative correlation between fat yield and live weight ($r = -0.48$; $p = 0.19$), as well as between fat yield and the morphometric parameters of the *longissimus dorsi* muscle ($r = -0.42$; $p = 0.25$). Against the background of ultrasound measurements of the eye muscle area, the assessment of subcutaneous fat development is an unreliable method of predicting the morphological composition of carcasses and the feed utilization efficiency of bulls.

DISCUSSION

This study proposes to evaluate the effects of *GH* and *TG5* genes polymorphisms on the morphological composition of carcasses, as well as the efficiency of feed protein and energy utilization for nutrient synthesis of edible body parts of Hereford bulls. Anatomical and morphological characterization were assessed *in vivo* using ultrasound measurements of the area of the *longissimus dorsi* muscle area and the subcutaneous fat thickness, and also after slaughter by deboning the carcasses. Sood *et al.* (2023a) found that the heritability of carcass lean and fat content was high (h^2 = 0.41-0.61 and 0.46-0.62, respectively), while the heritability of bone tissue content was moderate (h^2 = 0.22-0.48). These results indicate that genetic factors influence tissue development in beef cattle. In our work, the high correlation ($r=0.91$-0.93; $p < 0.001$) between live weight, lean weight and protein conversion ratio indicates that these traits are influenced by a similar set of genes. The identification of a stable correlation between genotype and easily assessed traits with carcass composition would increase fattening efficiency and optimize resource costs. Raza *et al.* (2020) provide evidence of different QTLs associated with carcass formation and individual body tissues in animals. In particular, 41 genes involved in carcass lean synthesis were identified at the BTA4, BTA13 and BTA25 sites (Sood *et al.*, 2023b). The TG5 and GH gene polymorphisms were selected due to their previously identified associations with the dynamics of carbohydrate, lipid, protein, and mineral metabolism. These metabolic processes and their related biological pathways are essential for understanding the physiological basis of fattening in beef cattle. Thyroglobulin is a glycoprotein hormone synthesized by the thyroid gland's follicular cells and serves as a carrier for triiodothyronine (T3) and thyroxine (T4), which play an important role in lipid metabolism (Zhang *et al.*, 2015). They determine the growth and differentiation of adipocytes and help maintain homeostasis in the fat depot. The most significant molecular genetic regulator of these processes is the TG5 gene. It has been shown to be associated with carcass composition and nutrient conversion efficiency, making it an important factor in determining the quality of beef. Growth hormone affects various tissues and metabolism of all nutrients, influencing

the growth and development of animals. These systematic processes in tissue metabolism affect the distribution of nutrients and, therefore, play a significant role in the morphological characteristics and feed efficiency traits in beef cattle (Miroshnikov *et al*., 2021).

Zhang *et al*. (2015) observed a significant effect ($p < 0.05$) of thyroglobulin (*TG*) gene polymorphisms on lean yield and eye muscle area. In our studies, lean yield ($p= 0.09$) and fat yield ($p= 0.08$) were determined at the level of trend by genetic features of Hereford bulls for *TG5 C422T* polymorphism. The associations at the trend level may be related to the small sample size (n= 54) in this study, so some significant associations affecting carcass composition may not have been detected. While the amount of fat in carcass was significantly ($p < 0.05$) determined by the *TG5* genotype. Due to the important role of the 5' untranslated region of thyroglobulin in the regulation of gene transcription, variation TG5 C422T polymorphism has a significant relationship with fat metabolism and intramuscular fat content in beef cattle (Anwar *et al*., 2017). According to Dolmatova *et al*. (2020) and Sycheva *et al*. (2023), animals with the TT genotype exhibited more intensive fat deposition, and the T allele was associated with higher carcass and meat fat content. These results are fully consistent with those of our study: TT-genotype carriers accumulated 7.5 kg ($p < 0.05$) more fat by the age of 21 months compared with peers who had the CC variant of the gene. However, the CC-genotype was superior in terms of subcutaneous fat deposition, outperforming heterozygous bulls by 0.8 mm ($p = 0.12$). The heterozygous genotype in Herefords resulted in minimal subcutaneous fat development compared to their homozygous counterparts, suggesting a dominance effect. Bennett *et al*. (2013) also observed a dominance effect ($p = 0.06$) in the *TG5* gene for subcutaneous fat thickness, but heterozygous animals differed in maximum expression of the trait.

The *GH L127V* polymorphism had a greater impact on the morphological composition of Hereford bulls. At the same time, significant differences ($p < 0.05$) were observed in the weight and yield of the major tissues in the carcass. Lee *et al*. (2013) explain the differences in carcass composition of bulls depending on the GH genotype by different of the plasma hormone concentrations. Thus, Ardiyanti *et al*. (2009) recorded the association of the GH L127V polymorphism with changes in the growth hormone concentration in the blood of heifers, which contributed to differences in body weight and carcass traits between the genotypes. In this case, heifers with the VV genotype had the highest concentration of growth hormone in the blood. Sasazaki (2021) observed an association between the *GH L127V* polymorphism and carcass and lean yield in beef cattle. According to Zalewska *et al*. (2021) and Romero *et al*. (2024), genetic variants in the growth hormone (*GH*) gene are responsible for variations in meat production parameters, including carcass weight, eye muscle area, subcutaneous fat thickness and carcass fat content. In our study, due to the small sample size, we observed differences at the trend level ($p= 0.10$) between homozygous genotypes in ultrasound measurements of eye muscle area. However, intra-breed variability was not significant for subcutaneous fat development. Homozygous carriers of the L allele were found to have superior carcass fat accumulation. This is consistent with the slaughter results for Kazakh White-Headed steers obtained by Selionova and Plakhtyukova (2020). The V allele in Hereford cattle was associated with increased muscle weight and skeletal development. Meanwhile, heterozygous animals exhibited intermediate tissue development. Conversely, Sedykh *et al*. (2020) found that Limousin steers with the LL genotype had significantly greater lean weight and eye muscle area. Thus, numerous studies have confirmed that the *GH* gene determines the weight and ratio of individual tissues in cattle. The inconsistency in data on allelic association can be explained by breed and population specificity.

Heine *et al*. (2021) found a positive correlation between the crude protein content in the diet and body tissue development in cattle. In our studies, V allele carriers consumed 6.4% ($p = 0.09$) more feed crude protein during the rearing period, which was accompanied by improved muscle and skeletal development. However, crude protein and energy consumption per 1 kg of live weight gain had an inverse ranking of the *GH* genotype distribution, and a significant difference ($p= 0.05$) was found between homozygous bulls for metabolizable energy intake of the diet. These results are consistent with the data of high efficiency of feed utilization by V allele carriers obtained on young Kazakh white-headed cattle (Gerasimov *et al*., 2023).

Kostusiak *et al*. (2024) found no significant effect of *TG* gene polymorphism on dry matter live weight gain and metabolizable energy live weight gain. Our studies are in full agreement with these data, the *TG5* genotype of Hereford bulls did not determine the variability in the net accumulation of the structural and functional components of the body based on the intake of dietary dry matter and energy. Conversely, individuals with the V allele of the *GH* gene showed a tendency towards increased protein accumulation in the body and a higher protein yield per unit of live weight gain. Hashizume *et al*. (2005) reported that the GH polymorphism effects on endocrine function that promotes protein accretion and synthesis. V-allele was associated with the highest concentration of growth hormone in the blood (Ardiyanti *et al*., 2009).

A key indicator of the efficiency of beef cattle breeding is the ability of the animals to convert the protein and energy in feed into the nutrients in the edible parts of the carcass (Valoshin and Glazkov, 2022). Pristupa *et al.* (2025) observed that, under the same feeding and housing conditions, the efficiency with which steers convert feed into body weight is determined by genetic factors. In our study, genetic variation in the *GH* gene was found to have a greater impact on young animals' ability to utilize feed protein for synthesizing body tissue than *TG5* gene polymorphisms. Plasma hormone activity, influenced by genetic variations in the GH gene, affects protein metabolism, muscle synthesis, and tissue formation in cattle (Ardiyanti *et al.*, 2009). Thus, during the rearing period, an intake of 621.6 kg of crude protein resulted in a live weight gain of 593 kg for VV genotype carriers, and the edible parts of their bodies contained 66.0 kg of protein. These indicators were 10.6% ($p = 0.09$) and 17.9% ($p = 0.08$) higher than the corresponding traits for LL genotype peers. At the same time, 10% of the feed crude protein in bulls with the VV variant of the *GH* gene was used for building body tissues, which was 0.9% ($P= 0.19$) higher than in their peers. Grouping bulls according to their *TG5* genotype showed no significant differences between groups in the efficiency with which they utilized crude protein and metabolizable energy.

The polymorphism of the TG5 gene was weakly correlated with the variability in live weight and carcass weight in bull calves. A correlation analysis of our data suggests a significant relationship between these traits and the conversion rates of protein and feed energy. Therefore, the thyroid hormone precursor, the TG gene, has a greater impact on the variability in fat metabolism than on the efficiency of nutrient utilization. In turn, the genetic variants of the GH gene significantly determine differences in live weight and carcass weight, which is consistent with the data from Lee *et al.* (2013) and Plakhtyukova and Selionova (2022). These variations in the gene also cause changes in endocrine function, which regulates the intensity of protein metabolism and tissue formation in cattle, as described by Hashizume *et al.* (2005). Under the same feeding conditions, these factors determine the different efficiency of feed protein and energy conversion.

CONCLUSION

Our study revealed significant associations of *GH* and *TG5* gene polymorphisms with carcass characteristics, and the ability to convert feed into edible tissues in Hereford bulls. The V allele of the *GH* gene was found to have a significant effect on parameters associated with high lean yield, lower fat deposition and low feed energy requirements per 1 kg of weight gain compared to homozygous carriers of the LL genotype. Similarly, variations in fat deposition in carcasses were found to be correlated with the TT genotype of the *TG5* gene. The results suggest a potential impact of the GH gene on protein metabolism, muscle synthesis, and tissue formation in Hereford cattle. On the other hand, further work will be necessary to confirm the significant effects of the genes studied in a larger population. The introduction of accurate prediction methods and *in vivo* assessment of meat productivity will enable the selection of the most valuable animals for the herd without the need for slaughter. Marker-assisted selection using genetic variations in the *GH* and *TG5* genes can improve quantitative and qualitative indicators of meat productivity in Hereford cattle.

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NOVELTY STATEMENT

New data on the association of the GH and TG5 genes with the phenotypic variability of carcass composition and feed nutrients conversion into edible body parts of Hereford bulls are presented. The prospects of using genotyping based on the studied genes in the formation of highly efficient herds of Hereford cattle are substantiated. The V-allele carriers of the GH gene exhibited a high efficiency of protein metabolism and the ability to better develop muscle tissue. The TT genotype of the TG5 gene was associated with an increased fat content. The development of new methods for selecting and evaluating the genetic potential of animals with the desired tissue ratio in the body will contribute to the rational use of available resources.

AUTHORS' CONTRIBUTION

Kinispay Dzhulamanov, Nikolay Gerasimov contributed equally to the experimentation. Kinispay Dzhulamanov designed and conducted the experiment. Nikolay Gerasimov wrote and edited the article. Kinispay Dzhulamanov and Nikolay Gerasimov studied scientific literature about the topic. All authors read and approved the final manuscript.

Ethical approval

Treatment of animals and experimental studies were conducted in accordance with the instructions and recommendations provided by the Model Law of the Inter-Parliamentary Assembly of Member States of the Commonwealth of Independent States "On the Treatment of Animals," Article 20 (Resolution No. 29-17 of the MA of CIS Member States dated 31 October 2007). The experimental methods were approved by the Ethics Committee of the Federal Research Centre of Biological Systems and Agrotechnologies of the Russian Academy of Sciences under Protocol No. 1, dated 02/22/2024 (http://fncbst.ru/?page_id=3553). The study was conducted to minimize animal suffering and reduce the number of samples. This association study has a limitation. Due to the small sample size (n = 54), some differences between genotypes for carcass traits and feed conversion may not have reached a statistically significant level. The animals were slaughtered according to the method specified in State Standard R 34120-2017 (2018).

Generative AI and AI-assisted technology statement

The authors declare that no generative AI or AI-assisted technologies were used to generate, analyze, or interpret the research data. Generative AI tools were used only to assist in improving the grammar and readability of the manuscript during the revision stage, and all scientific interpretations and conclusions are entirely the authors' own.

Conflict of interest

The authors have declared no conflict of interest.

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