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Formation of adipose tissue in Kazakh white-headed bull-calves from sires with a different genotype for the thyroglobulin gene

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Abstract. The improvement of breeding herds is based on the selection and intensive use in reproduction of linear sires with the desired genotype for DNA markers associated with the quality of meat products. The aim of our research was to study the formation of adipose tissue in Kazakh white-headed bull-calves from sires with different genotypes for the TG5 gene. The object of the study were bull-calves the offspring from sires with different genotypes for the thyroglobulin gene: TG5CC (n=6) and TG5CT (n=6). With the same live weight, young animals differed in weight and yield of internal raw fat with the superiority of progeny from heterozygous bulls by 1.8 kg (15.0%; $P = 0.16$) and 0.4% ($P = 0.09$). The TG5CT genotype in sires affected the better development of the subcutaneous fat in the middle of the last rib. The superiority of progeny from homozygous bulls was established by the back fat thickness at the root of the tail. Chemical analysis of slaughter products showed the advantage in fat synthesis of the offspring from sires with the TG5CC genotype. The intensity of fat deposition in sons from bulls with the TG5CC genotype is confirmed by the morphological composition of separate cuts. They exceeded their peers both in absolute mass and in proportion of adipose tissue in cuts. Under the same rearing conditions, the peculiarities in amount and distribution of adipose tissue in carcasses were determined in offspring from sires with different genotypes for the thyroglobulin gene.

1. Introduction

Selection and breeding work with Kazakh white-headed cattle for a long time was based on the sires' selection the leaders in the breed, the creation of a clear genealogical structure in factory herds and linear breeding. This strategy made it possible to breed several intra-breed types in various zones of our country and abroad [1]. At present in addition to the above methods, the improvement of Zavolzhsky factory type is based on selection and intensive use in herds' reproduction of linear sires with a desired genotype for DNA markers associated with the quality of meat products [2, 3, 4].

At the present stage, consumer demand for high quality beef is becoming the main driving force in beef cattle selection. However, selection and breeding work in domestic herds is hampered by the correctness of lifetime assessment and selection of animals in terms of the biological and nutritional value of meat [5, 6]. Currently, this problem is being solved mainly by genotyping the livestock and selecting carriers of the desired genotypes for genes associated with beef quality. Thus, among the numerous hereditary factors in beef cattle, a significant effect on the nutritional properties of meat was



confirmed in μ -calpain, calpastatin, thyroglobulin genes, etc.

The intensity of fat deposition and the peculiarities of lipid metabolism are genetically determined traits that determine the growth rate, early maturity and conformation of animals, and the quality of meat and milk products in cattle [7, 8]. The thyroglobulin gene (TG5) is associated with the features of lipogenesis and the marbling formation in beef cattle [9, 10]. This gene is located in the centromere region of chromosome 14 (BTA14); the entire locus covers more than 200 kb [11]. The C422T polymorphism occurs in the 5'-promoter region of the gene [12]. The nucleotide substitution C \rightarrow T contributes to the appearance of two allelic variants at position 422 of the thyroglobulin gene.

The aim of our research was to study the formation of adipose tissue in Kazakh white-headed bull-calves from sires with different genotypes for the thyroglobulin gene.

2. Materials and methods

The object of the study were Kazakh white-headed bull-calves the offspring from sires with different genotypes for the thyroglobulin gene: TG5^{CC} (n=6) and TG5^{CT} (n=6).

DNA isolation was performed using a standard method. Polymorphism in TG5 gene was investigated by the methods of polymerase chain reaction and DNA restriction fragment length polymorphism (PCR-RFLP) using the following primers: F – 5'-GGG-GAT-GAC-TAC-GAG-TAT-GAC-TG-3; R – 5'-CTG-AAA-ATC-TTG-TGG-AGG-CTG-TA-3 [11]. An annealing temperature of 60°C was used during PCR (30-35 cycles). The resulting amplified fragments were digested with the endonuclease BstX2I. Sizes of amplification products for the TG5 gene 548 - BstX2I restriction fragments for the CC genotype - 295, 178, 75; CT - 473, 295, 178, 75; TT - 473, 75.

Bull-calves of different groups were reared under the same management conditions up to 15 months of age, after which a control slaughter was carried out for 6 animals from each group. Control slaughter of animals was carried out according to the VASKhNIL method (1990) guided by GOST R 54315-2011. General sample of ground beef was taken from the left side of carcass in the amount of 400 g. Before deboning, a sample (200 g) of longissimus dorsi muscle was taken from the same half carcass at the level of the 9-11 ribs by means of a transverse section of the muscle.

The chemical composition of slaughter products were analyzed using the equipment of the Testing Center in Federal Research Centre of Biological Systems and Agro-technologies of the Russian Academy of Sciences (accreditation certificate RA.RU.21ПФ59 from 02.12.2015; [www.цкп-бст.рф; http://ckp-rf.ru/ckp/77384](http://ckp-rf.ru/ckp/77384)).

Data was processed by the methods of basic statistics using the Microsoft Office “Excel 10.0” and the specialized program “Statistica 10” (“Stat Soft Inc.”, USA). The statistical difference between the mean values was assessed using the Tukey’s test.

3. Results

The offspring from sires carrying different genotypes of the thyroglobulin gene did not differ in terms of live weight before slaughter and carcass weight (table 1). However, differences in the development of adipose tissue were more significant. Thus, superiority was established in weight and yield of internal raw fat on the side of sons from sires with the TG5^{CT} genotype with an advantage of 1.8 kg (15.0%; $P = 0.16$) and 0.4% ($P = 0.09$).

The site of localization of subcutaneous adipose tissue determined the intergroup variability in back fat thickness. At the same time, the fat thickness on loin was the same in bull-calves. The TG5^{CT} genotype in sires affected the better development of back fat in the middle of the last rib. The superiority of sons from heterozygous sires was 1.2 cm (30.0%; $P = 0.25$). On the contrary, an advantage of 0.4 cm (2.07%; $P = 0.68$) was determined in young animals from bulls with the TG5^{CC} genotype by measuring the thickness of the subcutaneous adipose tissue at the root of the tail.

Chemical analysis of slaughter products showed the superiority in fat synthesis in progeny from sires with TG5^{CC} genotype. Thus, the content of intramuscular fat in longissimus dorsi muscle and in general sample of ground beef was higher by 0.06% ($P = 0.05$) and 0.49% ($P = 0.40$) than in peers from bulls with a heterozygous genotype for the thyroglobulin gene.

Table 1. Development of adipose tissue in Kazakh white-headed bull-calves, depending on sires' genotype for the gene TG5(X±Sx).

Indicator	Sires' genotype for the gene TG5	
	CC	CT
Live weight, kg	421.7±9.87	423.2±5.41
Carcass weight, kg	242.8±6.60	243.5±3.54
Internal raw fat weight, kg	12.0±0.54	13.8±1.01
Internal raw fat yield, %	2.85±0.075	3.25±0.196
Back fat thickness, mm		
in the middle of the last rib	4.0±0.63	5.2±0.70
on the 3rd lumbar vertebra	10.7±0.49	10.7±0.71
at the root of the tail	19.7±0.56	19.3±0.56
Fat content in longissimus dorsi muscle, %	0.39±0.017	0.33±0.021
Fat content in general sample of ground beef, %	10.56±0.504	10.07±0.222

The intensity of fat deposition is confirmed by the morphological composition of separate cuts in sons from sires with the TG5^{CC} genotype (table 2). They exceeded their peers both in absolute mass and in proportion of adipose tissue in cuts. Thus, the advantage of progeny from homozygous sires in terms of fat mass was 0.40 kg ($P = 0.13$), and the proportion of adipose tissue exceeded by 2.35% ($P = 0.12$) in neck cut. The corresponding indicators in scapular cut were 0.37 kg ($P = 0.17$) and 1.16% ($P = 0.31$), in rib cut - 0.81 kg ($P = 0.16$) and 2.40% ($P = 0.16$), in lumbar cut - 0.07 kg ($P = 0.84$) and 1.11% ($P = 0.74$). Thus, the superiority of progeny from bulls with homozygous genotype of TG5 gene reaches a minimum in the hind third of the half carcass, and the maximum fat deposition in coxal cut was already recorded in sons from heterozygous sires by 0.52 kg ($P = 0.14$) and 0.85% ($P = 0.15$).

Table 2. The adipose tissue content in separate cuts in Kazakh white-headed bull-calves, depending on the sires' genotype for the gene TG5.

Indicator	Sires' genotype for the gene TG5	
	CC	CT
Fat content in neck cut, kg	1.75±0.156	1.35±0.187
%	11.70±0.861	9.35±1.074
Fat content in scapular cut, kg	1.82±0.192	1.45±0.154
%	7.64±0.748	6.48±0.784
Fat content in rib cut, kg	1.93±0.435	1.12±0.322
%	5.72±1.228	3.32±0.980
Fat content in lumbar cut, kg	1.05±0.163	0.98±0.274
%	12.72±1.888	11.61±2.650
Fat content in coxal cut, kg	2.50±0.188	3.02±0.261
%	6.28±0.268	7.13±0.466

A total of 9.05 kg or 7.55% of fat was obtained from the sons of bulls with the TG5^{CC} genotype when deboning all anatomical parts of half carcass, that is 1.13 kg and 0.97% more than their peers.

4. Conclusion

Under the same rearing conditions, the peculiarities in amount and distribution of adipose tissue in carcasses were determined in offspring from sires with different genotypes for the thyroglobulin gene. Wherein, the superiority was established on the side of sons from bulls with heterozygous genotype in terms of mass and yield of internal raw fat. The advantage in fat content in longissimus dorsi muscle and in general sample of ground beef was noted in offspring from homozygous sires for the studied gene.

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