Carcass quality traits of beef cattle with different $DGAT1$ genotypes

T A Sedykh¹, L A Kalashnikova² and R S Gizatullin³

¹ Department of Animal Breeding, Ufa Branch of the Russian Academy of Sciences, Bashkir State Agrarian Institute, 71, Prospect Octyabrya, Ufa, Russia, 450054
² Laboratory of DNA technologies, All-Russian Research Institute of Animal Breeding, 13, Lenina St., Lesnye polyany, Pushkinsky district, Moscow region, Russia, 141212
³ Department of Beekeeping, Private Animal Science and Breeding, Bashkir State Agrarian University, 34, 50-letiya Oktyabrya St., Ufa, Russia, 450000

E-mail: nio_bsau@mail.ru

Abstract. The paper presents the research results on carcass quality traits of beef cattle for different $DGAT1$ genotypes. The study aimed to detect the effect of SNP $DGAT1$-$K232A$ on carcass and beef quality of Hereford and Limousine bull calves of different genotypes. The tasks were SNP genotyping of animals by $DGAT1$-$K232A$, detecting the impact of SNP on carcass quality and morphological composition, weight and yield of half carcasses, organoleptic properties of meat, as well as the chemical composition of beef. The method of a polymerase chain reaction with a subsequent restriction fragment length polymorphism analysis was used to genotype fattening bull calves of Hereford (91 heads) and Limousine (109 heads) breeds. The animals were raised until 20 months of age in conditions of a resource-saving indoor and pasture-based system. There was an apparent effect of SNP $DGAT1$-$K232A$ ($DGAT1^{KK}$ > $DGAT1^{AA}$, $P < 0.05$) on the interior raw fat weight and yield indicators, subcutaneous fat tissue thickness, fat content in the rib eye and a sample of minced meat. Thus, genotyping by SNP $DGAT1$-$K232A$ can be used as an additional criterion to improve the quality traits of meat in beef cattle breeding.

1. Introduction
The production of high-quality beef from single-purpose beef cattle is a key focus of agricultural development. One of the important resources to make highly productive herds of beef cattle is the use of marker-assisted selection as an additional criterion for selecting and breeding superior animals. Using genes that control economic traits is an important element in determining the breeding value of animals [1-4].

In references, there are evidences of a positive correlation between the $DGAT1$ enzyme activity and the content of subcutaneous fat, as well as intramuscular fat in the rib eye and semitendinosus. Thus, $DGAT1^{KK}$ genotype animals were found to have a greater fat yield and thicker subcutaneous tissue [5-7]. Sorensen B. M. et al. (2005) proved that animals with the desired $DGAT1^{KK}$ genotype in Holstein-Friesian and Charolais breeds had 5 times greater diacylglycerol acyltransferase activity than $DGAT1^{AK}$ and $DGAT1^{AA}$ genotype animals [8]. The research results of Thaller G. et al. (2003), Pannier
L. et al. (2010), Wu, X. X. et al. (2012), Aviles C. et al. 2015) [5,9-11] showed a significant increase of intramuscular fat in \textit{DGAT1}^{\text{KK}} genotype animals. Anton I. et al. (2011) found high rates of intramuscular fat in the rib eye of AA/AA genotype animals [12].

The study aimed to detect the effect of SNP \textit{DGAT1-K232A} on carcass and beef quality of Hereford and Limousine bull calves of different genotypes. The tasks were SNP genotyping of animals by \textit{DGAT1-K232A}, detecting the impact of SNP on carcass quality and morphological composition, weight and yield of half carcasses, organoleptic properties of meat, as well as the chemical composition of beef.

2. Materials and methods

SNP \textit{DGAT1-K232A} genotyping was performed on one month aged Hereford and Limousine bull calves. Ninety-one young Hereford bulls were descendants of animals imported to private farm "SAVA-Argo-Usen" from Australia in 2009. 114 Limousine bull calves were the offspring of animals, bred at "SAVA-Agro-Yapryk" farm by accumulation cross-breding of Simmental cattle with servicing bulls of French selection. Both farms use a resource-saving indoor and pasture-based system for keeping beef cattle. These are breeding farms that maintain fattening animals. Bull calves were raised and fattened until 20 months of age [13].

Blood samples were collected from the jugular vein. DNA was isolated from whole blood stabilized with sodium citrate using a set of "DNA-Extran" ("Syntol"). Genotyping was performed by the PCR-RFLP method [14] using primers: F: 5'–gca-cca-tcc-tct-tcc-TCA-ag-3' and R: 5'–gga-agc-gct-ttc-tcc-gga-tg-3'. Amplifiers were cleaved by the CfrI endonuclease. The number and length of the obtained restriction fragments were determined electrophoretically in 7.5% PAGE in UV light after staining with ethidium bromide. Gel visualization was analyzed with the Gel Doc XR system and the attached Image Lab 2.0 "DNA-analyser" software. Sizes of restriction fragments: 411 KK; 411, 208, 203 KA and 208, 203 AA base pairs.

Sample slaughter of animals and meat sampling was carried out in SAVA meat processing plant. Depending on the \textit{DGAT1} genotypes carcasses were divided into three groups: group I (n=20) - \textit{DGAT1}^{\text{KK}}; group II (n=20) - \textit{DGAT1}^{\text{KA}}; group III (n=10)–\textit{DGAT1}^{\text{AA}}.

Statistical processing of the research results was carried out by standard methods using Microsoft Excel.

3. Results and discussion

SNP \textit{DGAT1-K232A} genotyping proved that genotype distribution in cattle of both breeds is very similar. In bull calves of both breeds, the \textit{DGAT1}^{\text{KK}} genotype is more common (51.65% and 50.46%), the \textit{DGAT1}^{\text{AK}} genotype is in second place (35.16% and 38.53%), and the \textit{DGAT1}^{\text{AA}} genotype is in third place (13.19% and 11.01%). Allele frequencies are the same in both breeds: \textit{DGAT1}^{\text{K}} (0.64) and \textit{DGAT1}^{\text{A}} (0.36). The results of the given studies are consistent with the data obtained by Aviles C. et al. (2015). Genotyping commercial beef breeds Charolais (n=98) and Limousine (n=99) distinguished between the following allele frequencies - \textit{DGAT1}^{\text{K}} – 0.82 and 0.84, \textit{DGAT1}^{\text{A}} – 0.18 and 0.17, respectively [5]. Genotype and allele frequencies depend on the cattle type and breed. Thus, other researchers found that the \textit{DGAT1}^{\text{GC}} allele (encoding alanine) frequency is significantly higher than that of the \textit{DGAT1}^{\text{AA}} allele (encoding lysine) when genotyping beef cattle [11,12]. The allele encoding alanine is found only in \textit{Bos taurus taurus} cattle and is absent in \textit{Bos taurus indicus}, \textit{Bos grunniens}, and \textit{Bubalus bubalis} animals [14].

Carcasses from \textit{DGAT1}^{\text{KK}} genotype Hereford and Limousine bull calves significantly (P<0.05) exceeded carcasses from \textit{DGAT1}^{\text{KA}} genotype animals in terms of the weight of internal raw fat by 4.34% and 2.86%, fat yield by 0.25% and 0.15%, and the thickness of subcutaneous fat by 11.05% and 11.67%, respectively. There is a trend to increase the slaughter indicators in the direction of \textit{DGAT1}^{\text{KK}}→\textit{DGAT1}^{\text{KA}}→\textit{DGAT1}^{\text{AA}}. The data obtained are consistent with the results of Aviles C. et al. (2014). They revealed that AA genotype animals have 2.46 cm thick subcutaneous fat. It is significantly less (p<0.01) than in the KA (2.98) and KK (3.37) genotypes by 16.8% and 27.0 % [5].
Higher fat yield and subcutaneous tissue thickness in animals with the $DGAT1^{KK}$ genotype also agree with the results of Gill J. L. et al. (2011) [6]. This dependence was not found in other studies [9,15].

The morphological composition of carcasses is shown in table 1.

**Table 1. Morphological composition of carcasses of different $DGAT1$ gene genotype bull calves**

| Indicator                        | Hereford $KK$ (n=10) | Hereford $KA$ (n=10) | Hereford $AA$ (n=6) | Limousine $KK$ (n=10) | Limousine $KA$ (n=10) | Limousine $AA$ (n=6) |
|---------------------------------|----------------------|----------------------|----------------------|-----------------------|-----------------------|----------------------|
| The weight of chilled half carcass, kg | 158.8 ±1.64          | 159.5 ±1.31          | 161.3 ±1.91          | 168.6 ±2.07           | 169.8 ±1.40           | 172.6 ±1.48          |
| including flesh, kg             | 114.1 ±1.12          | 114.6 ±0.78          | 116.4 ±1.87          | 122.7 ±1.28           | 123.8 ±0.97           | 126.6 ±1.39          |
| %                               | 71.80 ±1.12          | 71.85 ±0.78          | 72.00 ±1.87          | 72.80 ±1.28           | 72.90 ±0.97           | 73.30 ±1.00          |
| fat, kg                         | 12.0 ±0.15           | 11.8 ±0.33           | 11.3 ±0.20*          | 12.0 ±0.18            | 11.9 ±0.13            | 11.0 ±0.08*          |
| %                               | 7.55 ±0.55           | 7.40 ±0.60           | 6.90 ±1.70           | 7.10 ±0.70            | 7.00 ±0.40            | 6.40 ±0.20           |
| bones, kg                       | 27.9 ±0.26           | 28.3 ±0.37           | 28.5 ±0.69           | 29.4 ±0.89            | 29.5 ±0.37            | 29.9 ±0.17           |
| %                               | 17.60 ±0.40          | 17.70 ±0.45          | 17.70 ±0.40          | 17.40 ±0.37           | 17.40 ±0.37           | 17.30 ±0.17          |
| tendons and ligaments, kg       | 4.8 ±0.08            | 4.8 ±0.13            | 5.1 ±0.13            | 4.5 ±0.10             | 4.6 ±0.13             | 5.1 ±0.17            |
| %                               | 3.00 ±0.00           | 3.00 ±0.13           | 3.10 ±0.10           | 2.70 ±0.20            | 2.70 ±0.13            | 3.00 ±0.00           |
| Meatiness coefficient           | 4.10 ±0.10           | 4.0 ±0.13            | 4.0 ±0.13            | 4.17 ±0.10            | 4.20 ±0.13            | 4.23 ±0.10           |

The table shows that Hereford cattle carcasses contain more fat tissue – 7.55-6.90% compared to 7.10-6.40% in Limousine animals. The fat tissue content in the carcasses of $DGAT1^{KK}$ genotype bull calves was 7.55% and 7.10%, respectively, exceeding the same indicator in the carcasses of $DGAT1^{AA}$ genotype animals by 0.65% and 0.70%. There is an increase in the carcass fleshing index of the Limousine cattle by genotype in the direction of $DGAT1^{KK} \rightarrow DGAT1^{KA} \rightarrow DGAT1^{AA}$. These data comply with the results of Casas E. et al. (2005). They observed no significant association between the $DGAT1K232A$ polymorphism and morphological composition of carcasses in Brahman cattle [16].

The weight and yield of the natural anatomical parts of half-carcasses are shown in table 2.

The table shows that half–carcasses of Hereford cattle with the $DGAT1^{AA}$ genotype had higher weight indices of cuts compared to those of $DGAT1^{KA}$ and $DGAT1^{KK}$. They were 0.4 kg (3.07%) and 0.3 kg (2.31%) for the neck; 0.80 kg (2.72%) for the chuck; 1.20 kg (3.00%) and 1.10 kg (2.74%) for the rib; 0.1 kg (1.32%) for the brisket; 0.30 kg (2.5%) and 0.20 kg (1.67%) for the loin; 1.00 kg (2.07%) and 0.60 kg (1.24%) for the round.

The difference between the cut weights of the $DGAT1^{AA}\rightarrow DGAT1^{KA}$ and $DGAT1^{AA}\rightarrow DGAT1^{KK}$ genotype Limousine bull calves was 0.9 kg (2.93%) and 0.4 kg (1.30%) for the chuck; 0.90 kg (2.13%) and 1.90 kg (4.50%) for the rib; 0.40 kg (3.03%) and 0.20 kg (1.52%) for the loin, 1.40 kg (2.63%) and 1.10 kg (2.07%) for the round respectively. The results are consistent with the data of Karolyi D. Et al. (2012). They found that the $DGAT1^{AA}$ genotype bull calves slightly exceeded $DGAT1^{KK}$ animals by 2.09% in terms of carcass weight and the yield of the most valuable natural anatomical parts of the carcass: the chuck (4.6%), the loin (2.7%) and the round (5.8%) [17].
Table 2. Weight and yield of natural anatomical parts of half-carcasses of different DGAT1 gene genotype bull calves

| Indicator                      | Hereford | Limousine |
|--------------------------------|----------|-----------|
|                                | KK (n=10) | KA (n=10) | KK (n=10) | KA (n=10) | AA (n=6) | AA (n=6) |
| The weight of chilled half carcass after fat removal, kg | 146.8 ±3.17 | 147.4 ±3.56 | 150.4 ±3.88 | 157.0 ±4.15 | 157.8 ±3.28 | 160.7 ±2.99 |
| including the neck, kg         | 12.6 ±0.11 | 12.7 ±0.16 | 13.0 ±0.18 | 13.3 ±0.06 | 13.2 ±0.16 | 13.3 ±0.30 |
| %                              | 8.6       | 8.6       | 8.7       | 8.5       | 8.5       | 8.3       |
| chuck, kg                      | 28.6 ±0.14 | 28.6 ±0.29 | 29.4 ±0.15 | 29.8 ±0.11 | 30.3 ±0.10 | 30.7 ±0.22 |
| %                              | 19.5      | 19.5      | 19.5      | 19.0      | 19.2      | 19.1      |
| rib, kg                        | 38.9 ±3.14 | 39.0 ±3.22 | 40.1 ±2.96 | 41.3 ±3.25 | 40.3 ±3.61 | 42.2 ±4.31 |
| %                              | 26.6      | 26.5      | 26.6      | 26.3      | 26.2      | 26.3      |
| brisket, kg                    | 7.5 ±0.15 | 7.6 ±0.11 | 7.6 ±0.10 | 8.0 ±0.09 | 7.9 ±0.18 | 8.0 ±0.15 |
| %                              | 5.2       | 5.1       | 4.9       | 5.1       | 5.0       | 5.0       |
| loin, kg                       | 11.7 ±1.31 | 11.8 ±1.08 | 12.0 ±1.15 | 12.8 ±1.14 | 13.0 ±1.24 | 13.2 ±1.31 |
| %                              | 8.0       | 8.0       | 8.0       | 8.1       | 8.2       | 8.2       |
| round, kg                      | 47.3 ±3.61 | 47.7 ±4.10 | 48.3 ±4.05 | 51.8 ±3.88 | 52.1 ±3.36 | 53.2 ±4.00 |
| %                              | 32.2      | 32.4      | 32.1      | 33.0      | 33.0      | 33.1      |

The organoleptic evaluation of meat for processing demonstrated no effect of gene polymorphism on the indicators of visual appearance, smell, taste, consistency and juiciness of meat. On average, the overall quality of meat is high being 8.49-8.51 points and 8.58-8.59 points for the broth.

The content of intramuscular fat in the rib eye of the DGAT1KK genotype bull calves is significantly higher (P<0.05) by 0.18% and 0.29%, respectively, than that of the DGAT1AA genotype animals. There was a significant increase in this indicator (P<0.001) in the general sample of minced meat from the DGAT1KK genotype Hereford bull calves by 0.58%; Limousine animals by 0.18% (P<0.05). The content of tryptophan and protein quality indicator increases in the direction of DGAT1KK →DGAT1KA →DGAT1AA. The received data correspond to the findings of Aviles C. et al. (2015). They confirmed that the intramuscular fat content in the DGAT1KA genotype animals is significantly lower (P<0.01) by 2.38% than in the DGAT1KK genotype, and higher (P<0.05) by 6.28% than in the DGAT1KK genotype [5] contradicting the results of D. Karolyi, (2012). The latter established that the carcasses of the AA genotype animals have a higher intramuscular fat content by 2.75 g/kg [17].

4. Conclusion

Thus, studies on the quality of carcasses and beef in Hereford and Limousine bull calves of different DGAT1 gene genotypes showed a reliable influence of SNP DGAT1-K232A on the weight and yield of internal raw fat, subcutaneous fat thickness, the fat content in the rib eye and a sample of minced beef. Thus, genotyping by SNP DGAT1-K232A can be used as an additional criterion to improve the quality traits of meat in beef cattle breeding.
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