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The impact of diacylglycerol O-acyltransferase 1 gene polymorphism on carcass traits in cattle

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Abstract

The aim of this study was to identify the K232A polymorphism in gene encoding diacylglycerol O-acyltransferase 1 (DGAT1) and to evaluate its effect on carcass traits in population of Slovak Pinzgau steers. The genotyping data were obtained for totally 56 animals by using PCR-RFLP method. The A allele (0.93) was more frequent in analysed population than K allele (0.07). Even if the expected and observed heterozygosity indicated prevalence of homozygotes, the significant effect of inbreeding on population structure wasn't found (F_{IS}=-0.08). The decline in effective allele number (N_a=1.15) as well as polymorphic information content (PIC=0.12) pointed out to significant decrease of locus effectiveness in population. The effect of DGAT1 gene polymorphism on carcass traits was tested by using the GLM procedure adopted in SAS 9.3. In association analysis the proportion of muscle, fat, bone, and drip loss within the beef three-rib section were evaluated. However, the statistical analysis showed only non-significant impact of DGAT1 gene polymorphism on selected production traits in analysed population.

Keywords: association analysis, meat production, Pinzgau cattle, polymorphism

Introduction

Carcass traits are alongside fattening performance one of the most important traits in beef industry. It is generally accepted that the beef production is very complex and time-consuming field of the livestock industry (Gorlov et al., 2014; Ardicli et al., 2017). The majority part of traits associated with carcass quality and meat yield is under the control of polygenic inheritance. Thus, progress in the genetic selection process to improve beef cattle breeds depends on the accuracy of the animals breeding value. Due of this, the value of methods helping to identify the best animals and predict their breeding values at an early age is increasing (Bekseitov et al., 2017). Moreover, the development in the field of molecular genetics make it possible to identify genes controlling the economic important traits and thus increase the accuracy of estimated breeding values. Such candidate gene approach can be used especially if the gene

is located in a region that hosts a QTL or when there is prior information on gene effect on a trait (Borges et al., 2014).

The diacylglycerol O-acyltransferase 1 (DGAT1) gene (GenBank no. AY065621) encodes a microbial enzyme catalysing the last step of the synthesis of triglycerides (Ardicli et al., 2017). During the metabolism of fatty acid, the DGAT1 participates in the conversation of carbohydrates into fat and their storage in the fat depot (Gorlov et al., 2014). In cattle, the DGAT1 gene is localized in the area of centromere of chromosome BTA14. Most often, three polymorphisms in DGAT1 gene are examined in cattle; K232A in the exon 8 (Winter et al., 2002), polymorphism in the promoter region (Kühn et al., 2004), T11993C in the exon 17 (Kong et al., 2007). The most studied SNP K232A is caused by dinucleotide substitution of ApA for GpC (AAG→GCG) in position 10433 and 10434 at the beginning of exon 8 resulting in non-conservative substitution of lysine for alanine (Winter et al., 2002; Sedykh et al., 2017). Many studies demonstrated significant impact of K232A polymorphism on milk production (Citek et al., 2007; Gautier et al., 2007; Cerit et al., 2014; Bekseitov et al., 2017) and meat production traits (Yuan et al., 2013; Tait et al., 2014; Ardicli et al., 2017) in various cattle breeds. The objective of this study was to determine the genetic structure of population based on K232A polymorphism in DGAT1 gene and to analyse its impact on carcass traits in Slovak Pinzgau cattle.

Materials and methods

In total of 56 blood samples of Slovak Pinzgau steers were included in this study. The genomic DNA for animals' genotyping was extracted by using salting-out method according to Miller et al. (1988). The purity and concentration of each DNA sample were tested by the spectrophotometry measurement using optical density at wave length of 260 nm. The PCR-RFLP method was used to identify the K232A polymorphism. The target segment of DNA (411 bp) was amplified by using primers proposed by Winter et al. (2002). The PCR products were then digested using restriction endonuclease *Cfr*I and visualised by horizontal electrophoresis in 3% agarose gel (200 V for 50 min) stained with day GelRed (Biotium).

The allele and genotype frequencies were calculated using Genalex v6.1 (Peakall and Smouse, 2012). The impact of factors affecting the genetic structure of population (inbreeding, artificial selection, migration, etc.) were tested by Chi-square ($\chi 2$) test based on the differences between observed and expected genotype frequencies. In terms of genetic diversity, the effective allele number (N_a), the polymorphic information content (PIC) and the Wright's fixation index (F_{IS}) were determined using Genalex v6.1 (Peakall and Smouse, 2012).

In association analysis the proportion of muscle, fat, bones, and drip loss within the beef three-rib section were tested. Those parameters of carcass value (proportion of fat and bones) and quality of beef meat (drip loss) were measured according to Honikel (1998). The effect of DGAT1 gene polymorphisms on meat production traits was tested by using the GLM (one-way ANOVA) procedure implemented in SAS 9.3.

Results and discussion

In population of 56 Slovak Pinzgau steers only AA and KA genotypes for SNP K232A of gene DGAT1 were identified. The presence of homozygous AA genotype was detected based on two fragments with length 203 bp and 208 bp, whereas heterozygous KA genotype was represented by three fragments with length 411 bp, 208 bp and 203 bp. Due to the prevalence of homozygous AA animals (85.71%), the superiority of A allele across animals in population was found (A=0.93, K=0.07). Such a low frequency of K allele was reported for various breeds of beef or dual-purpose cattle, including Charolais (Ripoli et al., 2006), Angus (Kaupe et al., 2007), Simmental (Ardicli et al., 2017), and Russian beef cattle (Gorlov et al., 2014). On the other hand, the dairy cattle (Holstein, Jersey) showed much higher frequency of K allele (Kaupe et al., 2004; Casas et al., 2005; Citek et al., 2007).

Both observed and expected heterozygosity indicated the significant decrease of diversity level in population (H_o=0.14; H_e=0.13). Despite that, the F_{IS} index (F_{IS}=-0.08) did not show such a rapid decrease of heterozygosity across animals and indicated relative balanced proportion of homozygotes and heterozygotes. In addition, the F_{IS} value close to zero signalized only low impact of inbreeding on the population genetic structure. The Hardy-Weinberg equilibrium in population confirmed also the Chi-square test (P=0.57). The effectiveness of allele impact of locus in population was expressed by the effective allele number. The observed decline in N_a value (1.15) pointed out mainly to decrease of locus effectiveness in population that confirmed also the value of polymorphic information content (0.12).

Table 1 shows the summary statistics for analysed production traits and Table 2 summarizes the average values for each trait with respect to specific DGAT1 genotypes. The differences between evaluated carcass traits depending on the K232A genotypes were very low. Due to this and the fact, that the statistical analyses showed only non-significant effect of DGAT1 polymorphism on the variability of analysed traits, it can be concluded that obtained results have only informative character. Generally, it seems to be that the AA genotype is favourable for all of analysed traits. In previous studies the A allele was significantly associated with intramuscular fat content (Thaller et al., 2003; Li et al., 2013), taste qualities (Dunner et al., 2013), and marbled meat (Gorlov et al., 2014).

Table 1. Basic statistical variation measurements of analysed carcass traits

Trait	Mean ±SD[a]	Lower 95% CI[b]	Upper 95% CI[b]
Percentage of muscle	60.62 ±6.71	58.83	62.42
Percentage of fat	17.38 ±6.65	15.6	19.16
Percentage of bones	21.99 ±2.46	21.34	22.66
Percentage of drip loss	2.38 ±1.82	1.89	2.87

[a] Standard deviation; [b] Confidence interval.

Table 2. Average values of carcass traits in consideration depending on the DGAT1 genotype

Genotype	Percentage of muscle	Percentage of fat	Percentage of bones	Percentage of drip loss
AA	60.63 ±6.84	17.54 ±6.83	21.83 ±2.25	3.36 ±1.65
KA	60.56 ±6.28	16.41 ±5.72	23.03 ±3.48	2.51 ±2.78

Conclusions

Despite the fact that presented study did not confirm the role of DGAT1 gene in genetic control of carcass traits, such analyses of SNPs in genes affecting the economically important traits are still very usable for identification of genetic markers that can be applied in gene assisted selection of cattle. The obtained results could be affected mainly by the sample size and polygenic effects associated with expression of analysed traits. To obtain more reliable results in the future is therefore necessary to increase the sample size (including breeds with different genetic composition) as well as number of loci in the panel of candidate genes.

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