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THE RELATIONSHIP BETWEEN POLYMORPHISM IN *PPARGC1A* GENE AND CONFORMATION TRAITS OF SALERS COWS BREED

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Abstract. The study analysed two SNP polymorphisms located in intron 9 (1892T>C) and the 3'UTR (3359A>C) region of the *PPARGC1A* gene (GenBank accession number AY321517). The research was conducted in a salers cattle herd. Identification of genotypes of individual individuals was carried out using PCR-RFLP. The *CC* and *AA* genotype determined the largest body mass of the analysed animals. Other traits such as cows' habit, muscularity, cross height and chest circumference were most favourable for heterozygous *CT* individuals concerning the *PPARGC1A*/*Hae*III polymorphism. When analysing the relationship between *PPARGC1A/Nhe*I polymorphism and cow *habitat* characteristics, the genotype was the most beneficial *CC*. The results obtained were not confirmed statistically.

Key words: cow salers, conformation trait, body weight.

INTRODUCTION

The salers breed comes from France and is resistant to harsh environmental conditions. They are great for breeding in more difficult or extensive feeding conditions. This breed is immune to the disease. Cattle salers belong to late ripening breeds that give birth to small but without a significant share of difficult births. One of the elements included in the assessment of the use-value of animals is the assessment of their habit. Based on it, one can conduct the initial selection of animals, as well as select bulls in a herd of beef cattle (Choroszy et al. 2012). Other authors claim that this type of selection provides additional information about the animal's structure and its production predispositions, thus allowing to direct production in a herd of beef cattle. Therefore, it is such an important factor in breeding work (Barham et al. 2009; Choroszy et al. 2010).

Proliferator-activated receptor peroxisomes-gamma (PPARGC1A, also known as PGC-1α), encoded by the *PPARGC1A* gene, is a metabolic switch that regulates metabolic pathways via its pleiotropic interactions with nuclear receptors (NR) and other transcription factors other than NR, such as peroxisomal proliferation receptors (PPAR), nuclear respiratory factors (NRF), thyroid hormone (TR) receptors, estrogen-related receptors (ERRs), CCAAT binding (C/EBP) binding proteins and sterol regulatory element (SREBP). PGC-1α transcriptionally activates the pathways of mitochondrial biogenesis, lipid metabolism and glucose. PPARGC1A, due to its pleiotropic, direct action and significant indirect influence through modulation of cell metabolism, plays a significant and complex role in animal physiology, and learning about this role is of paramount importance for our knowledge of the body's functioning (Li et al. 2014).

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The aim of the study was to estimate the frequency of genotypes and alleles of the polymorphisms studied in the *PPARGC1A* gene and to determine the possible association of particular genotypes with selected parameters of the salers cattle.

MATERIAL AND METHODS

The research was carried out in years 2016/2017 on the salers of the breed maintained in the West Pomeranian Voivodeship and fed normalised dietary doses. The individuals were kept in similar environmental conditions, with access to the pasture during spring and summer, and in the winter to hay and haylage. The use value of meat-type beef cattle was assessed in accordance with Commission Decision 2006/427/EC of 20 June 2006, which establishes methods for evaluating the value in use and methods for determining the genetic value of pure-bred breeding animals of the cattle (Decyzja Komisji ustanawiająca metody… DzU WE L 169 z 22.06.2006).

DNA isolation was performed using the MasterPure™ DNA isolation kit (Epicentre®) according to the isolation protocol included with the package. Peripheral blood as a DNA isolation material was taken from the zygomatic vein into vacuum tubes containing K_3EDTA as an anticoagulant. Genotypes of individual individuals were determined using the PCR-RFL P method. Two SNP polymorphisms localised in intron 9 (1892T>C) and in the 3'UTR region (3359A>C) of the *PPARGC1A* gene were analysed (GenBank accession number AY321517). The PCR reaction was carried out using primers in accordance with the work of Khatib et al. (2007). It then digested with the received amplification product with appropriate restriction enzymes. The fragment about intron 9 (195 bp) of bases was digested with an enzyme *Hae*III fragment region, but the 3 'UTR (357 bp) was treated with the enzyme *Nhe*I.

The obtained results were subjected to statistical analysis. An analysis of the relationship between individual genotypes and selected features of cow's habit, cross heights, chest circumference, muscles and body weight of the analysed animals was performed. The statistical analysis of the results was carried out using the Statistica®12 program. The mean values were compared using the Duncan test.

RESULTS

The frequencies of individual genotypes and alleles for the polymorphisms studied are presented in Table 1. The analysis of the obtained results indicates that the homozygous genotypes *CC* (1892 T>C) and *AA* (3359 A>C) were most frequent and the highest frequency alleles (MAF) were the alleles *C* and *A.*

Table 1. The genotype and allele frequencies of the studied

Genotype	Number of cows	Genotype frequencies		Allele frequencies	
PPARGC1A/HaeIII	157	*CC*	0.762	*C*	0.881
1892 T>C	59	*CT*	0.238	*T*	0.119
PPARGC1A/NheI	152	*AA*	0738	*A*	0.850
3359 A>C	46	*AC*	0.223	*C*	0.150
	8	*CC*	0.039		

Table 2 presented the results of body weight and selected zoom parameters of cows of the salers meat breed. Analysis of the relationship between the *PPARGC1A*/*Hae*III genotypes and body weight of the Salers cows showed similar relationships as in the case of *PPARGC1A*/*Nhe*I polymorphism. Genotype *CC* (1892 T>C) and *AA* (3359 A>C) conditioned the highest body mass of the analysed animals. Other features, such as c- blocking of the cows, muscularity, cross-heights and chest circumference, were the most favourable for heterozygous *CT* individuals with respect to the *PPARGC1A*/*Hae*III polymorphism. When analysing the relationships between *PPARGC1A*/*Nhe*I homozygous *CC* individuals obtained polymorphism and cows- like features, the highest scores (23.5 points). The musculature of the test animals was the best in the case genotype animals *AC*. Individuals with the *CC* genotype regarding the analysed feature were not significantly affected (the *AA* genotype was conditioned by the smallest score). Also, the genotype *CC* animals were characterised by measuring the height of the smallest cross circumferentially and d in the chest. Cows with *AA* and *AC* genotypes obtained slightly higher values of the described zoom measurements.

Table 2. Analysis of the relationship between polymorphism *PPARGC1A/HaeIII* and *PPARGC1A/NheI* and the meat performance traits of the salers breed

Genotype	Number of cows	Body weight [kg]	Conformation trait [point]	Muscularity [point]	Height of lower back [cm]	Chest girth [cm]
PPARGC1A/HaeIII						
CC	157	589.3 ± 35.9	22.1 ± 2.7	15.1 ± 2.1	146.0 ± 3.5	202.9 ± 3.9
CT	59	572.7 ± 6.4	22.5 ± 2.5	15.1 ± 2.2	146.2 ± 3.1	203.8 ± 3.9
PPARGC1A/NheI						
AA	152	586.4 ± 38.3	21.9 ± 2.7	15.0 ± 2.2	146.1 ± 3.3	203.2 ± 3.9
AC	46	585.0 ± 20.6	22.8 ± 2.4	15.5 ± 1.9	146.1 ± 3.8	203.2 ± 4.3
CC	8	0 ± 0	23.5 ± 1.7	15.3 ± 1.7	145.5 ± 3.0	201.5 ± 2.6

DISCUSSION

The analysed polymorphisms in the *PPARGC1A* gene were also investigated by other authors. For the 1892T>C polymorphism, the frequency of the most common allele ranged from 0.84 in the German Holstein cattle herd (Weikard et al. 2005) to 0.56 in the cattle herd and Holstein-Friesian from the Iranian area (Pasendideh et al. 2015). In the case polymorphism 3359, A>C demonstrated the most common allele frequencies of 0.88 in a herd of cattle Jersey (Kowalewska-Łuczak et al. 2010) and 0.56 in the herd German Holstein (Weikard et al. 2005).

Polymorphisms in the *PPARGC1A* gene studied in this study have been studied in relation to various cattle performance traits. The effect of these polymorphisms on milk yield, fat and protein yield in milk was demonstrated (Weikard et al. 2005; Khatib et al. 2007; Komisarek and Dorynek 2009; Boleckova et al. 2012; Pasandideh et al. 2015). However, in the work of Komisarek and Dorynek (2009) and Komisarek and Walendowska (2012) the relations between genotypes of 1892T>C polymorphism and estimated breeding values for

reproductive traits in Polish HF bulls and reproductive traits of Polish HF cows (respectively) were investigated. Other polymorphisms mapped in the *PPARGC1A* gene were analysed about cattle growth parameters by Li et al. (2014). This work demonstrates the association of marked genotypes with features such as body weight and average daily weight gain.

Intensive selection of growth traits is implemented in various beef cattle breeding programs. Due to the growing market requirements for high-quality meat, more and more attention from the breeders is gaining features related to the conformation of the animal body. Body evaluation results are used as selection criteria for inferring the quality of carcases (Shiotsuki et al. 2009). Choroszy et al. (2012) emphasise the importance of breeding programs developed for meat breeds, which assume the selection of the most valuable animals for reproduction. These animals should be characterised by appropriate features relevant to their development, i.e. due to body weight, well-developed skeleton, broad chest, a height at the withers suitable for a given breed, and a significant feature generally referred to as meatiness. The importance of these traits in beef cattle breeding was described in their studies (Adamczyk et al. 2004). It should also be emphasised that the priority in the breeding of beef cattle are proper zoometric parameters, which are responsible for the slaughter value and affecting the proper course of delivery.

CONCLUSIONS

Analysis of the relationship between the *PPARGC1A*/*Hae*III genotypes and body weight of the salers cows showed similar relationships as in the case of *PPARGC1A*/*Nhe*I polymorphism. Genotype homozygous *CC* and *AA* Both polymorphisms conditioned highest body mass analysed animals. Other traits such as cows' habit, muscularity, cross height and chest circumference were most favourable for heterozygous *CT* individuals concerning the *PPARGC1A/Hae*III polymorphism. When analysing the relationship between *PPARGC1A*/*Nhe*I polymorphism and cows-like traits, the best genetic parameters were found in *CC* genotypes. The musculature of the tested animals was the most favourable for animals with the *AC* genotype. In the study, there were no statistically significant differences between the individual genotypes of the tested cattle and the considered features, but thanks to this analysis it was possible to show certain tendencies to achieve lower or higher values of a given trait by an individual with a particular genotype. In conclusion, it can be concluded that the results of the above study can be used in the selection of beef cattle.

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ZALEŻNOŚCI MIĘDZY POLIMORFIZMEM GENU *PPARGC1A* A CECHAMI POKROJU KRÓW RASY SALERS

Streszczenie. W pracy analizowano dwa polimorfizmy SNP zlokalizowane w intronie 9 (1892T>C) oraz w regionie 3'UTR (3359A>C) genu *PPARGC1A* (GenBank accession number AY321517). Badania prowadzono w stadzie bydła mięsnego rasy salers. Identyfikacja genotypów poszczególnych osobników prowadzona była przy użyciu PCR-RFLP. Genotypy *CC* i *AA* generowały największą masę ciała analizowanych zwierząt. Inne cechy, takie jak pokrój krów, umięśnienie, wysokość w krzyżu oraz obwód klatki piersiowej, najkorzystniejsze były w przypadku osobników heterozygotycznych *CT*, w odniesieniu do polimorfizmu *PPARGC1A*/*Hae*III. Z analizy zależności między polimorfizmem *PPARGC1A/Nhe*I a cechami pokroju krów wynika, że najbardziej korzystny był genotyp *CC*. Otrzymane wyniki nie zostały potwierdzone statystycznie.

Słowa kluczowe: krowy rasy salers, cechy pokroju, masa ciała.