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ASSOCIATION OF POLYMORPHISM OF CHOSEN GENES WITH PRODUCTION TRAITS IN DAIRY CATTLE

ZWIĄZEK POLIMORFIZMU WYBRANYCH GENÓW Z CECHAMI PRODUKCYJNYMI KRÓW MLECZNYCH

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Streszczenie. Polimorfizm genów *DGAT1*, *ABCG2*, *SCD1* i *PPARGC1A* istotnie wpływa na wydajność mleka, tłuszczu i białka oraz skład chemiczny mleka. W zależności od rodzaju polimorfizmu powodują one zwiększenie bądź zmniejszenie wydajności mleka oraz tłuszczu i białka, a także ich zawartości w mleku. Na podstawie licznych badań można stwierdzić, iż słuszne jest genotypowanie zwierząt pod kątem polimorfizmu wybranych genów i wykorzystywanie tych informacji w programach hodowlanych w celu selekcji wspomaganą markerami, co pozwoli na rozwój populacji o najbardziej pożądanym cechach produkcyjnych.

Key words: polymorphism, cattle, production traits.

Słowa kluczowe: polimorfizm, bydło, cechy produkcyjne.

INTRODUCTION

A revolutionary breakthrough in breeding was the recognition of the dairy cattle genome, which gave the opportunity to identify individual genes and their influence, among others on production traits. Malinowski and Kłosowska (2000) emphasize that the efficiency and chemical composition of cow's milk and performance depend on many factors, but the most important of them are genetic factors.

The DNA of each individual consists of about 2.8 billion nucleotides, so the identification of individual fragments and the order of nucleotides is extremely difficult. In studies of the dairy population, comparing the genomes of each parent, the difference between individual nucleotides was noticed. It was shown that there were various nucleotides in the same genomic site. This phenomenon is called the one-nucleotide substitution polymorphism, colloquially SNP (Single Nucleotide Polymorphism). This is the basis for identifying variants of particular genes. As a result of DNA sequencing, approximately 600 SNPs of various genes associated or affecting the production level of dairy cows were detected (Gurgul et al. 2015).

The knowledge of genomic breeding values is particularly important for a dairy cattle farmer, as it allows the development of population with the most desirable characteristics. Krychowski and Piechowska (2015) note that the breeding value can be determined in the early stages of animal life. In addition, the sharpness of selection can be increased, and the cost of genomic evaluation is low. Having learned the breeding value of a given individual, one can decide about its role in the breeding program.

The purpose of this paper is to present the knowledge about modern gene selection, which allows the development of the population with the most desirable traits and its control, thus affecting the achievement of breeding progress. The main purpose of the paper is to present the polymorphism of selected genes and their relation to the production characteristics of dairy cattle.

DGAT1 gene

Grisart et al. (2004) claim that many quantitative trait loci (QTL) experiments led to the detection of QTL in cattle in chromosome 14, which had a significant impact on fat content in milk. The DGAT1 gene conditioning this feature according to Lopaschuk et al. (2010) occurs in all organs, however, the highest expression levels of this gene are found in white adipose tissue, skeletal muscle, heart and small intestine. Apart from the synthesis of TAG, DGAT1 affects the regulation of fatty acid metabolism. The DGAT1 gene encodes diacylglycerol acetyltransferase 1. Szyda and Komisarek (2007) explain that triglycerides (triacylglycerols) are the major fraction (over 98%) of milk fat compounds.

Szyda and Komisarek (2007) argue that one of the DGAT1 mutations is K232A, which relies on the two-nucleotide substitution of AA → GC within the exon 8. This results in a non-conservative replacement of lysine by alanine at the 232 position of the encoded polypeptide. The effect of this polymorphism is presented by Strzałkowska et al. (2005) on the example of the Holstein-Friesian cows of the Polish black-and-white variety. Strzałkowska et al. (2005) conclude that the average allele substitution effect allowed to achieve from 2 to 3 kg of protein and 6 kg of fat for 120–130 kg of milk. Two alleles (AA and GC) and three genotypes were identified. It was found that DGAT1 does not significantly affect the daily milk yield of cows, however, it has been shown that cows with the GC/GC genotype are characterized by a tendency to achieve more milk during the day. The milk from the Holstein-Friesian cows with the AA/GC genotype was characterized by a much higher content of fat and total protein in comparison with cows with the GC/GC genotype. From the research of Nowacka-Woszuik et al. (2008) it results that KK` bulls have a higher breeding value for fat and milk protein traits, and lower for milk and protein yields than AA and KA bulls. Gautier et al. (2007) also undertook an analysis of the effects of K232A and VNTR polymorphisms in three breeds of French dairy cattle. Studies have shown that different VNTR alleles determine the different fat content in milk of cows in the studied cattle. It was shown that bulls of the KK genotype have a higher breeding value of fat and protein content in milk, however, they are characterized by lower milk and protein yield in relation to AA and KA genotypes. The highest protein content in milk seems to be associated with the lowest milk yield, resulting in the lowest protein yield.

Similar observations regarding lower milk and protein yields were presented by Spelman et al. (2002), who analyzed milk production traits in Holstein-Friesian cattle, Jersey and Ayrshire, New Zealand. In addition Spelman et al. (2002) found that the KK genotype is associated with a higher milk fat yield. Citek et al. (2007) also note that the K allele is associated with a higher breeding value relative to the fat and milk fat content, while the A allele with milk and protein yields (Nowacka-Woszuk et al. 2008).

ABCG2 gene

The ABCG2 gene located on chromosome 6 encodes a protein that belongs to the superfamily of transporters containing the ATP binding domain. This protein protects cells and tissues from various xenobiotics and plays a key role in the intestines and liver. It also conditions the transport of large, hydrophobic molecules through the outer and intracellular membranes. These include both positively and negatively charged molecules, including those with toxic properties. The commonly occurring single nucleotide polymorphisms in ABCG2 may affect the absorption and distribution as well as changes in the efficacy and toxicity of drugs in large populations (Sarkadi et al. 2004).

An in-depth analysis of the gene sequence allowed Soltani-Ghombavani et al. (2016) to identify its polymorphism in 14th exon. In position 581 (from A to C) tyrosine was substituted by serine (Y581S) (Cohen-Zinder et al. 2005). The results showed that this polymorphism (Y581S) results in significant changes affecting the breeding value of dairy cattle. The AC genotype cows were characterized by a lower breeding value in terms of milk yield compared to individuals with the AA genotype. It should also be noted that they were also characterized by a much higher content of both fat and protein in milk. Analyzing the results, Soltani-Ghombavani et al. (2016) argue that the action of the A-allele has a negative effect on the fat and protein content in milk, however, it has a significant positive impact on the dairy yield of Israeli Holstein-Friesian cows and Norwegian Red cows. Interestingly, the effect of substitution of the A-allele was the increase in milk yield by as much as 278.1 kg, which is also confirmed by research carried out by Cohen-Zinder et al. (2005).

In the studies of Alim et al. (2013) individuals with CC genotype were characterized by the highest efficiency and protein content in 305-day lactations, higher by 2.65 kg and 0.04% respectively, compared to cows of AA genotype. Cows being heterozygotes of the AC genotype were characterized by intermediate values of these traits. The results show that the substitution of the allele at position g. 45599A> C-A reduces the protein yield by 1.27 kg and its content in milk by 0.019% in 305-day lactations. At the same time, this suggests that g.45599A> C-C increases protein yield and percentage of protein in milk. The results suggest that the identified polymorphism may become a potential genetic marker to increase the milk yield of Chinese Holstein-Friesian cows (Alim et al. 2013). Research by Mousavizadeh et al. (2013) also showed the influence of ABCG2 gene polymorphism. An increase in milk yield was noted while reducing fat and protein in milk.

SCD1 gene

The SCD1 gene is responsible for the metabolism of fatty acids in tissues and in the mammary gland. It encodes the stearoyl-CoA 1 desaturase (delta9-desaturase). Delta9-desaturase plays an important role in the endogenous synthesis of conjugated linoleic acid

in ruminants and the effect of this protein on the formation of cis double bond between 9 and 10 carbon, resulting in the conversion of medium and long-chain saturated acids into their corresponding unsaturated chains. According to Paton and Ntambi (2009), the SCD1 gene is expressed in many tissues, however, researchers emphasize that the highest expression of this gene was observed in adipose tissue and in the liver. The activity of delta9-desaturase in the mammary gland affects the profile of fatty acids in bovine milk. In the work of Kuczaja et al. (2013) the authors investigated the possibilities of increasing protein synthesis in the mammary gland of cows using nutritional treatments. The authors describe the effective use of amino acids for the synthesis of milk protein according to a linear and logarithmic model with a different percentage of coverage of amino acid needs.

The encoding SCD1 gene has been mapped in bovine chromosome 26 (Campbell et al. 2001). Within this site, several QTLs have been identified for fat yield and for several other milk traits. Some of the SNPs near SCD1 showed a significant association with the fatty acid composition in the fat tissue of the carcass and in milk (Taniguschi et al. 2004, Moiola et al. 2007). In studies carried out by Kulig et al. (2013), 975 Polish Holstein-Friesian cows were examined and the frequency of occurrence of genotypes and alleles of a single polymorphism g.10329C> T located in exon 5 of the SCD1 gene was determined. In the examined herd, all possible genotypes of the SCD1 gene were identified. The frequency of the analyzed genotypes and alleles was as follows: CC – 0.54, CT – 0.40, TT – 0.06, C – 0.74, T – 0.26. Statistical analysis revealed that this polymorphism was related to the breeding value for protein content in milk. This was also confirmed after Bonferroni's correction. The TT genotype cows were characterized by the highest breeding value. A significant effect of the polymorphism on fat content in milk was also demonstrated, however, after the Bonferroni correction, this trend was not maintained (Kulig et al. 2013). Cows with CT genotype were characterized by the highest milk yield, while those with TT genotype the lowest. Fat efficiency in representatives of all genotypes was similar, however, the highest fat yield was characteristic for cows with the CT genotype. The analysis of the frequency of the alleles of the polymorphism studied showed that the C allele occurs most frequently (0.315) in the population of Polish Holstein-Friesian cows. This is also confirmed by studies carried out on other breeds of cows such as: Italian Holstein, Canadian Holstein, Japanese Black, Valdostana and Fleckvieh (Taniguschi et al. 2004; Moiola et al. 2007; Macciotta et al. 2008) The relationship between polymorphisms of the SCD1 gene and fatty acid profile has also been analyzed in carcass fat. Polymorphism 10329C> T significantly influenced the composition of intramuscular fat fatty acids in Japanese black cows (Taniguschi et al. 2004; Matsushashi et al. 2011).

PPARGC1A gene

According to Weikard et al. (2005), the PPARGC1A gene has been mapped in chromosome 6. It consists of 16 exons, and its characteristic feature is the diverse expression in different types of tissues. It encodes the coactivator-1 alpha of the gamma receptor activated by peroxisome proliferators (PGC1- α). Its role is to activate various nuclear hormone receptors and transcription factors that regulate energy balance. It has also

been proven that PGC1- α is involved in the expression of genes related to oxidative metabolism, adipogenesis and gluconeogenesis (Puigserver and Spiegelman 2003). Ates et al. (2014) note that the impact of only two polymorphisms of the PPARGC1A gene on the production characteristics of dairy cattle was confirmed. One of these polymorphisms is c.1892T> C, which results from the substitution of threonine by cysteine in position. The second polymorphism of the PPARGC1A gene is c.3359A> C located in the 3'UTR region and results in alanine being substituted by cysteine at position 968. Weikard et al. (2005) suggests that the low turnout of the C allele at c.1892T> C affects the low fat content in milk in German Holstein cows. On the other hand, research carried out by Khatip et al. (2007) do not confirm the existence of such dependence in American Holstein breed cattle. Alim et al. (2012) in their studies proved that the level of protein in milk was higher in homozygous cows of the Holstein Chinese race with the genotype TT in position c.1892T> C. On the other hand, Komisarek and Walendowska (2012) did not report any relationship between the T allele and milk production traits. Similar results were obtained by Kowalewska-Łuczak et al. (2010) who did not report the effect of the polymorphisms of the PPARGC1A c.1892T> C and c.3359A> C gene on the production characteristics of the Jersey cows. In earlier studies, the CC frequency was the highest frequency in German Holstein breed cattle (0.68) (Weikard et al. 2005), Polish Holstein-Friesian (0.53), German Holstein-Friesian (0.56) (Komisarek and Dorynek 2009) and Chinese Holstein (0.49) (Alim et al. 2012). Khatib et al. (2007) found that the A-allele at position c.3359A> C influenced the increase of protein content in milk and decreased milk yield of cows. No relationship was found by the researchers between c.1892T> C polymorphism and milk production traits. Kowalewska-Łuczak et al. (2010) on the basis of research conducted on Jersey cows, did not notice any different effects of c.1892T> C and c.3359A> C polymorphisms on milk, fat and protein yields. Schennink et al. (2009) demonstrated the relationship between c.1892T> C and the composition of milk fat in Dutch holstein-Friesian cows.

SUMMARY

The purpose of each breeding program is to achieve higher efficiency in livestock production under anticipated environmental conditions. In the livestock breeding programs, the theory of inheritance of quantitative traits is used, according to which the functional traits are conditioned by the operation of many hypothetical genes. Currently, genome selection using SNP genetic markers is introduced in cattle breeding. Genomic selection, as a modern method of assessing the breeding value of cattle has many advantages. Thanks to it, there is a possibility of a new way of managing a herd of cows, including through the valuation of very young animals, it allows a better selection of mothers of bulls and embryo donors. Due to genomic selection, the breeding progress is much faster, which shortens the intergenerational gap and increases the sharpness of the selection. Particular attention should be paid to the fact that genomic selection allows the assessment of relatedness of the population and the detection of carriers of genetic defects. This is one of the reliable methods, performed directly on the subject.

Polymorphisms of *DGAT1*, *ABCG2*, *SCD1* and *PPARGC1A* genes significantly affect the milk, fat and protein yield and chemical composition of milk. Depending on the type of polymorphism, they increase or decrease the milk, fat and protein yield as well as fat and protein content in milk. Based on the research carried out by numerous authors, it can be concluded that genotyping animals for polymorphism of selected genes and using this information in breeding programs for selection supported by markers, which will allow the development of populations with the most desirable production characteristics is right.

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