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# *SCD1* POLYMORPHISM AND BREEDING VALUE FOR MILK PRODUCTION TRAITS IN COWS

H. KULIG[1*], K. ŻUKOWSKI[2], I. KOWALEWSKA-ŁUCZAK[1] and P. ŁAKOMY[1]
*[1]West Pomeranian University of Technology in Szczecin, Department of Genetics and Animal Breeding, 70-311 Szczecin, Poland*
*[2]National Research Institute of Animal Production, Department of Animal Genetics and Animal Breeding, 32-083 Balice, Poland*

## Abstract

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The aim of this study was to estimate the associations between the *g.10153G>A* polymorphism and the breeding values for milk production traits (milk, fat and protein yield, fat and protein content) in Polish Holstein-Friesian cows. The frequencies of alleles and genotypes were determined in the examined herd. Statistically significant associations between the SNP and the breeding value for fat content and protein content were found. The results indicated that individuals with the allele *G* in the genotype might contribute to increase the value of these traits. However, further studies are needed to confirm these suggestions.

*Key words:* breeding value, cattle, SCD1

*List of abbreviations:* BVMY – breeding value for milk yield; BVFY – breeding value for fat yield; BVFC – breeding value for fat content; BVPY – breeding value for protein yield; BVPC – breeding value for protein content

## Introduction

Expression of genes encoding the enzymes that play a role in the synthesis and metabolism of fatty acids, including among others, stearoyl-CoA desaturase (SCD) was observed in the ruminant mammary gland. The SCD is the key enzyme responsible for the desaturation of fatty acids in the mammary gland and other tissues. The enzyme introduces a double *cis* bond between carbon 9 and 10, causing conversion of medium chain and long chain saturated fatty acids in their unsaturated counterparts thus contributing to maintaining the liquidity of milk. The products formed as a result of SCD activity are used as substrates for the synthesis of various lipids (Ntambi and Myazaki, 2004). Another consequence of the SCD activity is the synthesis of cis-9 and trans-11 CLA from the vaccenic acid (Taniguchi et al., 2004). SCD activity in the mammary gland is one of the factors which influence the ratio of unsaturated fatty acids in the bovine milk (Jacobs et al., 2011). Leptin and insulin are involved in the regulation of the SCD activity (Biddinger et al., 2006).

In the gene encoding bovine SCD isoform 1 (SCD1), mapped on bovine chromosome 26 (Campbell et al., 2001), 3 SNPs were identified within the 3'UTR (Jiang et al., 2008), and three SNPs in exon 5. In different breeds of cattle a significant association was observed between polymorphism *g.10329C>T* and the desaturation index, as well as composition of fatty acids in milk (Mele et al., 2007; Moioli et al., 2007; Schennink et al., 2008; Kgwatalala et al., 2009) and carcass (Taniguchi et al., 2004; Bartoñ et al., 2010; Li et al., 2011; Orrù et al., 2011). The SNPs in the 3'UTR were associated with the intramuscular fat thickness of Wagyu x Limousin cattle (Jiang et al., 2008). However, there is little data concerning other SCD1 polymorphisms in relation to pro-

*E-mail: hanna.kulig@zut.edu.pl

duction traits in cattle. The aim of the study was to evaluate the associations between *g.10153G>A* polymorphism and the breeding values for milk production traits in Polish Holstein-Friesian cows.

## Materials and Methods

The study covered a total of 975 Polish Holstein-Friesian (Black-and-White strain) cows belonging to one herd located in the in the western part of Poland. All the examined animals came from 305 sires. Cows were kept in similar environmental conditions and fed an identical standard diet.

Genomic DNA was extracted from blood using MasterPureTM Genomic DNA Purification Kit (Epicentre® Biotechnologies, Madison, USA) according to the manufacturer's instructions. The *g.10153G>A* SNP located within the fifth exon of the *SCD1* gene (GeneBank acc. no. AY241932) was analyzed (Taniguchi et al., 2004). The gene fragment of 204 bp in length, comprising the SNP, was amplified using a pair of primers with the following nucleotide sequences: 5'-GTG TCC TGT TGT TGT GCT TCA TCC TGC C-3' oraz 5'-AAT ATT CTC TCG GGG GTT GAT GGT CTT G-3' (Taniguchi et al., 2004). The PCR conditions were: 95ºC for 3 min., followed by 30 cycles of 94ºC - 45 s, 57ºC - 50 s, 72ºC – 60s; the final step was at 72ºC for 8 min. Amplicons were digested with *Nco*I restriction nuclease. The restriction fragments obtained were separated in 3% agarose gels with ethidium bromide and described using software for photodocumentation of electrophoretic separation and image storage (Vilber Lourmat).

Next, a statistical analysis of associations between genotypes and the breeding value for milk yield – BVMY (kg), fat yield – BVFY (kg), fat content – BVFC (%), protein yield – BVPY (kg) and protein content – BVPC (%) was carried out. The breeding values data came from official electronic documentation of the herd. The data evaluation was carried out by the National Research Institute of Animal Production in Balice (Poland). An association analysis was carried out using MIXED procedure implemented in SAS (SAS v. 9.3). The following linear model was applied:

$$y_i = \mu + b_i + \varepsilon_i,$$

where: $y_i$ – predicted breeding value of a cow; $\mu$ – overall mean; $b_i$ – the effect of genotype (i= -1, 0, 1); $\varepsilon_i$ – error.

Differences between the means were compared by the Duncan's multiple range tests.

## Results

The amplicons digested with *Nco*I revealed uncut 204-bp fragments (allele *G*) and cut fragments of 165 and 39 bp (allele *A*). The frequencies of genotypes and alleles in a herd were as follows: *AA* – 0.42, *GA* – 0.52, *GG* – 0.06, *A* – 0.68, *G* – 0.32.

Means of breeding values for milk productions traits in relation to the *g.10153G>A* polymorphism are presented in the Table 1. There was a significant association between genotypes and breeding value for fat content ($P \leq 0.01$) and protein content in milk ($P \leq 0.01$). Cows with *GG* genotype were characterized by higher values of these traits when compared with the *AA* cows. The differences amounting to 0.06% in case of breeding value for fat content and 0.04% in case of breeding value for protein content. Statistically significant effect for fat yield ($P \leq 0.01$) was also observed, but no significant differences in the values of this trait between cows with different genotypes were found at $P \leq 0.05$.

No significant associations were found between the genotypes and the breeding values for milk and protein yields in this study. However, it was found that the *GA* genotype cows were characterized by the highest breeding values for these traits.

**Table 1**
**Means with standard errors of estimated breeding values for milk production traits in cows of different *g.10153G>A* genotypes**

| Trait | Genotype | | | Significance |
|---|---|---|---|---|
| | *GG* (n = 58) | *GA* (n = 506) | *AA* (n = 411) | |
| BVMY | 231.60 ± 49.79 | 312.48 ± 16.86 | 291.67 ± 18.70 | 0.27 |
| BVFY | 10.20 ± 1.65 | 10.98 ± 0.56 | 8.19 ± 0.62 | ≤ 0.00 |
| FAFC | 0.01 ± 0.02$^{a}$ | -0.03 ± 0.01$^{ab}$ | -0.05 ± 0.01$^{b}$ | 0.01 |
| FAPY | 10.28 ± 1.50 | 10.90 ± 0.51 | 9.39 ± 0.56 | 0.14 |
| FAPC | 0.04 ± 0.01$^{a}$ | 0.01 ± 0.00$^{b}$ | 0.00 ± 0.00$^{b}$ | ≤ 0.00 |

Means in rows marked with different superscripts differ significantly at $P \leq 0.05$.

## Discussion

Identification of the *loci* which have larger effect on production traits of dairy cattle may help explain the variability in the analyzed traits and provide additional information that could be incorporated into the programs of traditional selection of breeding material. So, association studies are being continued (Ciecierska et al., 2013; Kadlecova et al., 2014). As a result of a number of studies, QTLs for milk traits were mapped on each bovine autosome, whereas most of them were found on the 6 and 14 (Ogorevc et al., 2009). The *SCD1* gene has been mapped on the bovine chromosome 26 in the vicinity of QTL for fat yield (Gautier et al., 2006). It can be assumed that the analyzed *g.10153G>A* SNP is located in close proximity to another polymorphism significantly related to fat yield, or another so far undetected polymorphism that affects other milk traits.

In the studied herd of Polish Holstein-Friesian cows, a higher frequency of allele *A* was observed, which is also confirmed by the results of other studies on this polymorphism, concerning breeds such as Chinese Holstein (Alim et al., 2012), Italian Holstein (Milanesi et al., 2008) and Japanese Black (Tanigushi et al., 2004). Moreover, the analyzed polymorphism was associated with the breeding value for protein and fat content in milk of cows. Animals with the *GG* genotype were characterized by a significantly higher value of these traits compared with the *AA* cows. In terms of protein content, similar results were obtained by Alim et al. (2012) when analyzing milk traits in Chinese Holstein cows. Moreover, authors associated this polymorphism with milk, protein and fat yield, while the highest values of these traits were observed in cows with the heterozygous genotype. The results of this study also show that the heterozygous individuals were characterized by the highest breeding value for milk, fat and protein yield, but the differences between genotypes were not statistically confirmed.

Associations between other *SCD1* gene polymorphisms and milk production traits were also analyzed in dairy cattle. Significant associations between the *g.10329C>T* polymorphism and milk and protein yield in Italian Holstein cows were demonstrated by Macciotta et al. (2008), and milk, fat and protein yield in Chinese Holstein cows by Alim et al. (2012). In another study, Komisarek and Dorynek (2009) found associations between this polymorphism and breeding values for fat content in Polish Holstein-Friesian bulls. However, it was not confirmed after false discovery rate correction (FDR).

## Conclusions

The presented results could be useful in the selection strategies aimed at improving milk production traits of cattle. If data on the *g.10153G>A* polymorphism in the *SCD1* gene are incorporated into breeding programs developed for Polish Holstein-Friesian cattle, it might contribute to improving the fat and protein content. Giving preference to breeding individuals with the allele *G* in the genotype might contribute to increase in the value of these traits. However, suggestions should be supported by further research carried out on other herds with a more equal distribution of the different genotypes.

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## References

**Alim, M. A., Y. P. Fan, X. P. Wu, Y. Xie, Y. Zhang, S. L. Zhang, D. X. Sun, Y. Zhang, Q. Zhang, L. Liu and G. Guo,** 2012. Genetic effects of stearoyl-coenzyme A desaturase (SCD) polymorphism on milk production traits in the Chinese dairy population. *Molecular Biology Reports*, **39**: 8733-8740.

**Bartoň, L., T. Kott, D. Bureš, D. Řehák, R. Zahrádková and B. Kottová,** 2010. The polymorphisms of stearoyl-CoA desaturase (SCD1) and sterol regulatory element binding protein-1 (SREBP-1) genes and their association with the fatty acid profile of muscle and subcutaneous fat in Fleckvieh bulls. *Meat Science*, **85**: 15-20.

**Biddinger, S. B., M. Miyazaki, J. Boucher, J. M. Ntambi and C. R. Kahn,** 2006. Leptin suppresses stearoyl-CoA desaturase 1 by mechanisms independent of insulin and sterol regulatory element-binding protein-1c. *Diabetes*, **55**: 2032-2041.

**Campbell, E. M. G., D. S. Gallagher, S. K. Davis, J. F. Taylor and S. B. Smith,** 2001. Rapid communication: Mapping of the bovine stearoyl-coenzyme A desaturase (*SCD*) gene to BTA26. *Journal of Animal Science*, **79**: 1954-1955.

**Ciecierska, D., A. Frost, W. Grzesiak, W. S. Proskura, A. Dybus and A. Olszewski,** 2013. The influence of fatty acid synthase polymorphism on milk production traits in Polish Holstein-Friesian cattle. *The Journal of Animal & Plant Sciences*, **23**: 376-379.

**Gautier, M., H. Hayes and A. Eggen,** 2003. A comprehensive radiation hybrid map of bovine Chromosome 26 (BTA26): comparative chromosomal organization between HSA10q and BTA26 and BTA28. *Mammalian Genome*, **14**: 711-721.

**Jacobs, A. A. A., J. van Baal, M. A. Smits, H. Z. H. Taweel, W. H. Hendriks, A. M. van Vuuren and J. Dijkstra,** 2011. Effects of feeding rapeseed oil, soybean oil, or linseed oil on stearoyl-CoA desaturase expression in the mammary gland of dairy cows. *Journal of Dairy Science*, **94**: 874-887.

**Jiang, Z., J. J. Michal, D. J. Tobey, T. F. Daniels, D. C. Rule and M. D. MacNeil,** 2008. Significant associations of stearoyl-CoA desaturase (*SCD1*) gene with fat deposition and composition in skeletal muscle. *International Journal of Biological Sciences*, **4**: 345-351.

**Kadlecova, V., D. Nemeckova, K. Jecminkova and L. Stadnik,** 2014. The effects of polymorphism in the DGAT1 gene on energy balance and milk production traits in primiparous Holstein cows during the first six months of lactation. *Bulgarian Journal of Agricultural Science*, **20**: 203-209.

**Kgwatalala, P. M., E. M. Ibeagha-Awemu, A. F. Mustafa and X. Zhao,** 2009. Stearoyl-CoA desaturase 1 genotype and stage of lactation influences milk fatty acid composition of Canadian Holstein cows. *Animal Genetics*, **40**: 609-615.

**Komisarek, J. and Z. Dorynek,** 2009. Effect of *ABCG2*, *PPARGC1A*, *OLR1* and *SCD1* gene polymorphism on estimated breeding values for functional and production traits in Polish Holstein-Friesian bulls. *Journal of Applied Genetics*, **50**, 125-132.

**Li, C., N. Aldai, M. Vinsky, M. E. R. Dugan and T. A. McAllister,** 2011. Association analyses of single nucleotide polymorphisms in bovine stearoyl-CoA desaturase and fatty acid synthase genes with fatty acid composition in commercial crossbred beef steers. *Animal Genetics*, **43**: 93-97.

**Macciotta, N. P. P., M. Mele, G. Conte, A. Serra, B. Castiglioni, S. Chessa, A. Buccioni, G. Pagnacco and P. Secchiari,** 2008. Association between a polymorphism at the stearoyl CoA desaturase locus and milk production traits in Italian Holsteins. *Journal of Dairy Science*, **91**, 3184-3189.

**Mele, M., G. Conte, B. Castiglioni, S. Chessa, N. P. P. Macciotta, A. Serra, A. Buccioni, G. Pagnacco and P. Secchiari,** 2007. Stearoyl-Coenzyme A Desaturase gene polymorphism and milk fatty acid composition in Italian Holsteins. *Journal of Dairy Science*, **90**: 4458-4465.

**Milanesi, E., L. Nicoloso and P. Crepaldi,** 2008. Stearoyl CoA desaturase (SCD) gene polymorphisms in Italian cattle breeds. *Journal of Animal Breeding and Genetics*, **125**: 63-67.

**Moioli, B., G. Contarini, A. Avalli, G. Catillo, L. Orrù, G. De Matteis, G. Masoero and F. Napolitano,** 2007. Short Communication: Effect of Stearoyl-Coenzyme A Desaturase polymorphism on fatty acid composition of milk. *Journal of Dairy Science*, **90**: 3553-3558.

**Ntambi, J. M. and M. Miyazaki,** 2004. Regulation of stearoyl-CoA desaturases and role in metabolism. *Progress in Lipid Research*, **43**: 91-104.

**Ogorevc, J., T. Kunej, A. Razpet and P. Dovc**, 2009. Database of cattle candidate genes and genetic markers for milk production and mastitis. *Animal Genetics*, **40**: 832-851.

**Orrù, L., G. F. Cifuni, E. Piasentier, M. Corazzin, S. Bovolenta and B. Moioli,** 2011. Association analyses of single nucleotide polymorphisms in the *LEP* and *SCD1* genes on the fatty acid profile of muscle fat in Simmental bulls. *Meat Science*, **87**: 344-348.

**Schennink, A., J. M. L. Heck, H. Bovenhuis, M. H. P. W. Visker, H. J. F. Van Valenberg and J. A. M. Van Arendonk,** 2008. Milk fatty acid unsaturation: Genetic parameters and effects of stearoyl-CoA desaturase (SCD1) and acyl CoA:diacylglycerol acyltransferase 1 (DGAT1). *Journal of Dairy Science*, **91**: 2135-2143.

**Taniguchi, M., T. Utsugi, K. Oyama, H. Mannen, M. Kobayashi, Y. Tanabe, A. Ogino and S. Tsuji,** 2004. Genotype of stearoyl-CoA desaturase is associated with fatty acid composition in Japanese Black cattle. *Mammalian Genome*, **14**: 142-148.

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