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Review

Selected candidate genes affecting milk fatty acids

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Cow´s milk consisted of relatively high quantity of saturated fatty acids (about 70 %), which are considered less beneficial health. The content of more desirable fatty acids is about 25 % (monounsaturated) and 5 % (polyunsaturated). The aim of this research was to find ways how to increase the content of mono- and polyunsaturated fatty acids in milk fat. One of the ways how to alter the content of fatty acids is the monitoring of candidate genes and their polymorphism. Therefore, the manuscript deals with selected candidate genes, particularly *DGAT1*, *SCD1* and *FASN*, which are associated with fatty acid biosynthesis. The results suggest that observing of this issue could be helpful for improving the quality of milk fat.

Keywords: cow, milk fat, heritability, *DGAT1*, *SCD1*, *FASN*

1 Introduction

The majority of economically important traits in livestock are complex, have continuously distributed phenotypes, and are influenced by multiple genes or quantitative trait loci (QTL) dispersed across the genome, and by an array of different environmental factors. Quantitative traits like milk yield production including the milk fat composition is influenced by DNA segments called QTL (Ibeagha-Awemu et al., 2008).

Biosynthesis of cow´s milk fat is a complex process regulated by multiple genes, which is one of the several metabolic pathways in milk production metabolism (Bionaz and Loor, 2008). Milk fatty acids can be produced by two ways – uptake from blood or *de novo* synthesis in the epithelial cells of the mammary gland (Neville and Picciano, 1997). Short-chain fatty acids and most of the medium-chain fatty acids that are predominantly synthesized *de novo*, have a medium to high heritability. Long-chain fatty acids are derived from blood lipids, which originate principally from the diet and endogenous lipids, and are characterized by low to medium heritability (Soyeurt et al., 2007; Stoop et al., 2008; Mele et al., 2009). Table 1 shows the descriptive statistics and heritability of selected fatty acids according to Krag et al. (2013). Each fatty acid is presented by its mean ($\overline{x}$), standard deviation (s_x) and genomic heritability estimate (h_g^2), respectively. The estimates of the h_g^2 are based on a univariate model.

Table 1 Content (g 100 g^{-1} fat) and heritability of selected fatty acids

Fatty acids	$\overline{x}$	s_x	h_g^2
Lauric acid (C12:0)	3.57	0.65	0.27
Myristic acid (C14:0)	11.29	1.30	0.25
Palmitic acid (C16:0)	28.95	3.25	0.14
Linoleic acid (C18:2 *c*9,*c*12)	1.69	0.30	0.17
α-linolenic acid – ALA (C18:3 *c*9,*c*12,*c*15)	0.49	0.10	0.30
Conjugated linoleic acids – CLA (C18:2 *c*9,*t*11)	0.63	0.16	0.19

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Identification of genomic regions, and preferably individual genes, responsible for genetic variation in milk fat composition will enhance the understanding of biological pathways involved in fatty acid synthesis and may point towards opportunities for changing milk fat composition via selective breeding (Bouwman et al., 2011). Candidate gene studies have shown that polymorphisms in diacylglycerol O-acyltransferase 1 (*DGAT1* K232A) (Grisart et al., 2002) and stearoyl-CoA desaturase 1 (*SCD1* A293V) (Taniguchi et al., 2004) have effects on milk fat composition (Mele et al., 2007; Moioli et al., 2007a; Schennink et al., 2007; Schennink et al., 2008; Kgwatalala et al., 2009; Conte et al., 2010).

1.1 DGAT1

DGAT1 catalyzes the terminal part in the synthesis of triacylglycerols, thereby contributing to control the rate of triacylglycerols synthesis in adipose cells – adipocytes (Ibeagha-Awemu et al., 2008). According to Grisart et al. (2002), among several polymorphisms in *DGAT1* substitution occurs at AA dinucleotide GC to exon 8 (coding sequence), resulting in a substitution of lysine to alanine (K232A). Remarkable attribute of mutation K232A is that variant lysine increases the fat yield (kg) and the percentage of fat and protein, while reducing the quantity of milk protein and variant alanine increases the quantity of milk protein content (Grisart et al., 2002; Spelman et al., 2002; Thaller et al., 2003). Schennink et al. (2007) reported a correlation among polymorphism of *DGAT1* K232A and the composition of milk fat. In this case, lysine allele associated with upper proportion of saturated fatty acids and C16:0 and minor proportion of C14:0, unsaturated oleic acid (C18:1 *c*9) and CLA.

1.2 SCD1

SCD1 is an enzyme of the endoplasmic reticulum, which contains iron in its structure. This enzyme is responsible for cellular biosynthesis of saturated to monounsaturated fatty acids (Ntambi and Miyazaki, 2004). *SCD1* gene is located on 26 BTA. Single nucleotide polymorphism (SNPs) in exon 5 causes the substitution (A293V) of valine to alanine (Taniguchi et al., 2004). Allele alanine is associated with a higher proportion of monounsaturated fatty acids and is hypothetically considered as candidate gene for milk fat quality (Moioli et al., 2007b). Studies suggest (Mele et al., 2007; Schennink et al., Conte et al., 2010) that allele alanine has a key role also in the synthesis of CLA.

1.3 FASN

Fatty acid synthase (*FASN*) is a candidate gene for adipocytes in fat and in milk fat. Morris et al. (2007) demonstrated that SNPs in the gene *FASN* is associated with differences in the composition of fatty acids in adipose tissue and in milk fat on pasture-fed cattle. *FASN* is a multi-enzyme system involved in the *de novo* synthesis. *De novo* fatty acid synthesis requires the *FASN* for the elongation of fatty acids and other compounds. One of them is the acetate, which is activated by acyl-CoA synthetase short-chain family member 2 (*ACSS2*). For *de novo* synthesis was *ACSS2* identified as a candidate gene associated with caproic, caprylic and capric acids (C6:0, C8:0 and C10:0). Morris et al. (2007) performed linkage analysis of fatty acids of cow´s milk at 19 BTA, and detecting a QTL for C8:0, C10:0, C12:0, C14:0, C18:1 *c*9 and C18:2 *c*9, *c*12.

2 Conclusions

Fatty acids composition is affected by many factors, which enable to alter milk fat. Studies have revealed that the genetic effect is more effective in saturated fatty acids, while unsaturated fatty acids are more influenced by non-genetic effects like nutrition. *DGAT1* gene affects rather quantity of milk fat, whereas *SCD1* quality of milk fat. *FASN* influences the synthesis of saturated and unsaturated fatty acids.

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References

BIONAZ, M. and LOOR, J.J. (2008) Gene network driving bovine milk fat synthesis during the lactation cycle. *BMC Genomics*, vol. 9, pp. 366–387. doi: http://dx.doi.org/10.1186/1471-2164-9-366

BOUWMAN, A.C. et al. (2011) Genome-wide association of milk fatty acids in Dutch dairy cattle. *BMC Genetics*, vol. 43, pp. 1–12.

CONTE, G. et al. (2010) Diacylglycerol acyltransferase 1, stearoyl-CoA desaturase 1., and sterol regulatory element binding protein 1 gene polymorphisms and milk fatty acid composition in Italian Brown cattle. *J Dairy Sci*, vol. 93, pp. 753–763.

GRISART, B. et al. (2002) Positional candidate cloning of a QTL in dairy cattle: Identification of a missense mutation in the bovine *DGAT1* gene with major effect on milk yield and composition. *Genome Res*, vol. 12, pp. 222–231.

IBEAGHA-AWEMU, E.M., KGWATALALA, P. and ZHAO, X. (2008) A critical analysis of production-associated DNA polymorphisms in the genes of cattle, goat, sheep, and pig. *Mamm Genome*, vol. 19, pp. 591–617.

KGWATALALA, P.M. et al. (2009) Stearoyl-CoA desaturase 13´UTR SNPs and their influence on milk fatty acid composition of Canadian Holstein cows. *J Anim Breed Genet*, vol. 126, pp. 394–403.

KRAG, K. et al. (2013) Genetic parameters for milk fatty acids in Danish Holstein cattle based on SNP markers using a Bayesian approach. *BMC Genetics*, vol. 14, pp. 1–10.

MELE M. et al. (2007) Stearoyl-coenzym A desaturase gene polymorphism and milk fatty acid composition in Italian Holsteins. *J Dairy Sci*, vol. 90, pp. 4458–4465.

MELE, M. et al. (2009) Genetic parameters for conjugated linoleic acid, selected milk fatty acids, and milk fatty acid unsaturation of Italian Holstein-Friesian cows. *J Dairy Sci*, vol. 92, pp. 392–400.

MOIOLI, B. et al. (2007b) Short communication: Effect of stearoyl-coenzym A desaturase polymorphism on fatty acid composition of milk. *J Dairy Sci*, vol. 90, pp. 3553–3558.

MOIOLI, B., D´ANDREA, M. and PILLA, F. (2007a) Candidate genes affecting sheep and goat milk quality. *Small Rum Res*, vol. 68, pp. 179–192.

MORRIS, C.A. et al. (2007) Fatty acid Synthase effects on bovine adipose fat and milk fat. *Mamm Genome*, vol. 18, pp. 64–74.

NEVILLE, M.C. and PICCIANO, M.F. (1997) Regulation of milk lipid secretion and composition. *Ann Rev Nutr*, vol. 17, pp. 159–184.

NTAMBI, J.M. and MIYAZAKI, M. (2004) Regulation of stearoyl-CoA desaturases and role in metabolism. *Prog Lip Res*, vol. 43, pp. 91-104.

SCHENNINK, A. et al. (2007) *DGAT1* underlies large genetic variation in milk-fat composition of dairy cows. *Anim Genet*, vol. 38, pp. 467–473.

SCHENNINK, A. et al. (2008): Milk fatty acid unsaturation: genetic parameters and effects of *SCD1* and *DGAT1*. *J Dairy Sci*, vol. 91, pp. 2135–2143.

SOYEURT, H. et al. (2007) Estimation of heritability and genetic correlations for the major fatty acids in bovine milk. *J Dairy Sci*, vol. 90, pp. 4435-4442.

SPELMAN, R.J. (2002) Characterization of the *DGAT1* gene in New Zealand dairy population. *J Dairy Sci*, vol. 85, pp. 3514–3517.

STOOP, W.M. et al. (2008) Genetic parameters for major milk fatty acids and milk production traits of Dutch Holstein-Friesians. *J Dairy Sci*, vol. 91, pp. 385–394.

TANIGUCHI, M. et al. (2004) Genotype of stearoyl-CoA desaturase is associated with fatty acid composititon in Japanese Black cattle. *Mamm Genome*, vol. 15, pp. 142–148.

THALLER, G. et al. (2003) Effetcs of *DGAT1* variants on milk production traits in German cattle breeds. *J Anim Sci*, vol. 81, pp. 1911–1918.