The relation of *GH1, GHR* and *DGAT1* polymorphisms with estimated breeding values for milk production traits of German Holstein sires

E. Hradecká[1], J. Čítek[1], L. Panicke[2], V. Řehout[1], L. Hanusová[1]

[1]Agricultural Faculty, South Bohemian University in České Budějovice, Czech Republic
[2]FBN Dummerstorf, Germany

ABSTRACT: We analysed the relations of estimated breeding values (EBV) of 315 German Holstein sires to their genotypes in growth hormone gene (*GH1*), growth hormone receptor gene (*GHR*) and acylCoA-diacylglycerol acyltransferase 1 (*DGAT1*). The strong relation of *DGAT1 K232A* to the estimated breeding values for milk production traits has been confirmed, when allele $DGAT1^K$ was connected with higher milk fat yield, milk fat and milk protein content, while allele $DGAT1^A$ increased milk yield and milk protein yield. The effect of *DGAT1* genotype explained from 4.70% of variability of EBVs for fat yield to 31.90% of variability of EBVs for fat content. The evaluation of *GH1* 127 Leu/Val and *GHR* 257 SNP polymorphisms did not reveal an association of their polymorphism with EBVs for milk production traits, except the EBVs of GHR^G/GHR^G homozygotes for fat yield, which were significantly lower. The effect of *GH1* or *GHR* genotype explained only a negligible portion of variability of EBVs ($R^2 < 1.00\%$ in most cases).

Keywords: bovine; *GH1*; *GHR*; *DGAT1*; milk production; breeding value; Holstein

Animal breeding is based on population genetics as most of the economically important traits have polygenetic nature. Molecular genetics provides valuable information which could contribute to the knowledge of genes underlying quantitative production traits (Czarnik et al., 2007; Matějíček et al., 2007). However, the effect of many polymorphous variants of candidate genes or potential genetic markers is not properly known yet.

Growth hormone (*GH*) directly or indirectly affects numerous aspects of animal lactation, growth and reproduction. It plays an important role during nutrient partitioning. A significant role of *GH* during lactation is demonstrated by the 10–15% increase in milk yield which occurs in dairy cows treated with recombinant bovine *GH* (Bauman, 1999). The best-known polymorphism of *GH1* is the leucine to valine substitution at position 127 in exon 5. Lucy et al. (1993) reported the different frequencies of $GH1^L$ and $GH1^V$ alleles in major dairy breeds, and the correlation of gene variants with estimates of milk production in cows.

Growth hormone exerts its influence on growth and metabolism by interaction with growth hormone receptor on the surface of the target cells. The changes in the functional regions of *GHR* can affect its binding capacity and signalling pathway, and therefore alter the activity of *GH* in the target tissues (Argetsinger and Carter-Su, 1996). Several polymorphisms of bovine *GHR* were described by Aggrey et al. (1999) or Ge et al. (2000) but their association with meat production traits was insignificant.

The locus of acylCoA-diacylglycerol acyltransferase1 (*DGAT1*) was identified as that underlying

---

Supported by the Ministry of Education, Youth and Sports of the Czech Republic (Project No. MSM 6007665806).

the quantitative trait locus for milk production parameters in the centromeric region of bovine chromosome 14 (Coppieters et al., 1998). Grisart et al. (2002) described four polymorphisms, among them an *ApA* (Adenine *p* Adenine) to *GpC* (Guanine *p* Cytosine) dinucleotide substitution in exon 8, causing a lysine to alanine amino acid substitution (*K232A*). They found an extremely significant effect of this mutation on daughter yield deviations (DYDs) for milk yield, protein yield, fat yield, protein and fat content, which was lately confirmed by Spelman et al. (2002) or Čítek et al. (2007).

The aim of our paper was to analyse the relation of growth hormone gene (*GH1*), growth hormone receptor gene (*GHR*) and acylCoA-diacylglycerol acyltransferase1 (*DGAT1*) gene polymorphisms with breeding values of German Holstein sires for milk production traits.

MATERIAL AND METHODS

A total of 315 German Holstein sires born in 1998 to 2001 were genotyped for 127 Leu/Val polymorphism in *GH1,* 257 SNP (exon 10) in *GHR* loci, and *K232A* polymorphism in *DGAT1*. DNA was isolated from whole blood or from frozen sperm. Analyses were performed by PCR/RFLP techniques.

For *GH1*, the primer sequences were as in Mitra et al. (1995). An amplified fragment of DNA (223 bp) was digested by *Alu*I overnight and digested fragments were visualised on 3.5% agarose gel stained with ethidium bromide.

For *GHR*, the primer sequences were as in Di Stasio et al. (2005). An amplified fragment of DNA (342 bp) was digested by *Alu*I.

For *DGAT1*, the primer sequences were as in Winter et al. (2002). The *K232A* polymorphism was distinguished by a restriction fragment length polymorphism using the restriction endonuclease *Cfr*I.

We analysed the relation between the detected genotypes and estimated breeding values (EBV) for milk production traits, i.e. 305 days milk yield (kg), fat content (%), fat yield (kg), protein content (%) and protein yield (kg) and the relative breeding value for milk production (RBVM). Estimated breeding values were provided by Vereinigte Informationssysteme Tierhaltung, Verden, Germany (EBVs of 2007/05). Generally, the use of daughter yield deviations (DYD) is preferred to EBVs, because EBVs contain information from other relatives than the bull's daughters. However, the large number of daughters makes the difference between the DYD and EBV negligible (Viitala et al., 2003). As shown in Table 1, the reliabilities of EBVs were equable (on average 146 daughters per sire), which enables their direct comparison.

The analysis was based on this mixed model equation:

$$EBV = \mu + G_i + e_{ijk}$$

where:

EBV = the estimated breeding value for partial milk production parameter
μ = the overall mean
G_i = the fixed effect of *DGAT1*, *GH1* or *GHR* alleles and their combinations
e_{ijk} = the residual effect

We used the software STATISTICA (StatSoft, Inc., Tulsa, Oklahoma, USA) for evaluation, namely the ANOVA/MANOVA procedure with post-hoc comparison of means (LSD test; *P* value). The Hardy-Weinberg equilibrium was tested by the χ^2 test.

RESULTS

The genotype frequencies at all loci are shown in Table 2. Predicted genotypic frequencies were

Table 1. Basic statistics of estimated breeding values of analysed sires

EBV	$\bar{x}$	s_x	Minimum	Maximum
Milk yield (kg)	687.606	605.580	–825.000	2 446.000
Fat yield (kg)	22.283	22.674	–47.000	83.000
Protein yield (kg)	22.181	18.292	–30.000	74.000
Fat content (%)	–0.056	0.268	–0.650	0.720
Protein content (%)	–0.011	0.108	–0.330	0.460
RBV	104.771	12.540	70.000	138.000
Reliability	92.810	2.065	88.000	96.000

Table 2. Genotype and allelic frequencies of *DGAT1*, *GH1*, and *GHR* genes

GH1	$GH1^L/GH1^L$	$GH1^L/GH1^V$	$GH1^V/GH1^V$
Abs. frequency	288	27	0
Observed frequency	0.914	0.086	0.000
Estimated frequency	0.916	0.082	0.002
	$\chi^2 = 0.002^{ns}$		
Alleles	$GH1^L = 0.957$	$GH1^V = 0.043$	
GHR	GHR^A/GHR^A	GHR^G/GHR^A	GHR^G/GHR^G
Abs. frequency	288	23	4
Observed frequency	0.914	0.073	0.013
Estimated frequency	0.904	0.094	0.002
	$\chi^2 = 0.049^{ns}$		
Alleles	$GHR^A = 0.951$	$GHR^G = 0.049$	
DGAT1	$DGAT1^A/DGAT1^A$	$DGAT1^K/DGAT1^A$	$DGAT1^K/DGAT1^K$
Abs. frequency	145	126	44
Observed frequency	0.460	0.400	0.140
Estimated frequency	0.436	0.449	0.115
	$\chi^2 = 0.012^{ns}$		
Alleles	$DGAT1^A = 0.660$	$DGAT1^K = 0.340$	

NS = differences are not significant

similar to the observed ones ($\chi^2 = 0.002 - 0.049$) suggesting that genotype distributions were in the Hardy-Weinberg equilibrium.

GH1

The genetic analysis showed a very low occurrence of allele V in German Holstein sires. The statistical analysis did not reveal a significant relationship between EBVs and *GH1* genotype, though the values tended to be higher in $GH1^L/GH1^V$ heterozygotes (Table 3). The effect of genotype/allele described only insignificant portions of variability, when the value of R^2 did not exceed 1%. In cases of EBVs for fat and protein content the variability within heterozygotes even exceeded total variability of the evaluated set. The frequency of heterozygous sires was too small and their variability too large to allow to draw a decisive conclusion.

GHR

A low frequency of GHR^G allele and only 4 GHR^G per GHR^G homozygous sires (Table 2) were detected. As shown in Table 4, the effect of *GHR* genotype on milk production EBVs was mostly insignificant, which is partly due to the extreme allelic frequencies and high variance within low-numbered class-

Table 3. Mean breeding values ± s_x for milk production traits according to *GH1* genotype

Genotype	Milk (kg)	Fat (kg)	Protein (kg)	Fat (%)	Protein (%)	RBVM
$GH1^L/GH1^L$	676.003 ± 593.173	21.771 ± 22.256	21.840 ± 17.859	–0.0564 ± 0.266	–0.011 ± 0.105	104.510 ± 12.211
$GH1^L/GH1^V$	811.370 ± 726.365	27.741 ± 26.600	25.815 ± 22.481	–0.0510 ± 0.297	–0.017 ± 0.132	107.556 ± 15.636
$P <$	0.267	0.191	0.281	0.923	0.763	0.228
R^2	0.001	0.002	0.001	–0.003	–0.003	0.001
$GH1^L$	682.065 ± 599.217	22.038 ± 22.458	22.018 ± 18.072	–0.056 ± 0.267	–0.011 ± 0.107	104.647 ± 12.375
$GH1^V$	811.370 ± 726.365	27.741 ± 26.600	25.815 ± 22.481	–0.051 ± 0.297	–0.017 ± 0.132	107.557 ± 15.636
$P <$	0.277	0.201	0.291	0.924	0.768	0.238
R^2	0.000	0.001	0.000	–0.002	–0.001	0.001

Table 4. Mean breeding values ± s_x for milk production traits according to *GHR* genotype

Genotype	Milk (kg)	Fat (kg)	Protein (kg)	Fat (%)	Protein (%)	RBVM
GHR^{A}/GHR^{A}	701.615 ± 599.452	22.403 ± 23.002	22.458 ± 18.064	–0.062 ± 0.262	–0.014 ± 0.104	104.927 ± 12.476
GHR^{G}/GHR^{A}	577.609 ± 657.801	25.826 ± 14.025	20.826 ± 20.198	0.046 ± 0.330	0.017 ± 0.149	104.696 ± 12.481
GHR^{G}/GHR^{G}	311.500 ± 730.528	–6.750 ± 22.984	10.000 ± 24.372	–0.220 ± 0.241	–0.008 ± 0.073	94.000 ± 16.432
$P <$	0.294	0.028	0.375	0.085	0.410	0.224
R^2	0.003	0.016	0.000	0.009	0.000	0.003
GHR^{A}	696.853 ± 601.172	22.534 ± 22.706	22.396 ± 18.119	–0.058 ± 0.265	–0.013 ± 0.106	104.918 ± 12.455
GHR^{G}	509.935 ± 661.861	17.419 ± 21.444	18.032 ± 21.004	–0.023 ± 0.325	0.011 ± 0.133	101.936 ± 13.815
$P <$	0.092	0.221	0.195	0.482	0.235	0.197
R^2	0.003	0.001	0.001	–0.001	0.001	0.001

es. A post-hoc comparison showed significantly lower EBVs of GHR^{G}/GHR^{G} homozygotes for fat yield ($P < 0.028$) also with a tendency to lower EBVs for fat content ($P < 0.085$). This relation was not confirmed when the effect of alleles was tested. The portion of EBV variability explained by the effect of genotype/allele did not exceed 1.00%.

DGAT1

The frequency of $DGAT1^{K}$ allele in the analysed data set reached 0.340. Table 5 summarizes the evaluation of polymorphism effect on milk production traits. The effect of *K232A* substitution on almost all analysed traits was significant ($P < 0.001$) with the exception of relative breeding value (RBV) for milk. Breeding values of $DGAT1^{A}/DGAT^{A}$ homozygotes compared to those of $DGAT1^{K}/DGAT^{K}$ were on average higher by 548 kg for milk yield and by 12.6 kg for protein yield, while they were lower by 15.4 kg for fat yield, by 0.45% for fat content and by 0.13% for protein content. The highest portion of variability was explained in EBVs for fat content (31.90% by genotype; 17.80% by allele).

Joint effect of *DGAT1-GH1*

Table 6 shows the results of the analysis of joint effect of *DGAT1-GH1* genotypes. Though its effect on EBVs was always evaluated as statistically highly significant, this was mainly due to *DGAT1* polymorphism. *GH1* caused no significant differences within the classes according to *DGAT1*, with the exception of EBV for protein content. The EBV of protein content of $DGAT1^{K}/DGAT1^{A}$-$GH1^{L}/GH1^{V}$ heterozygotes was higher by 0.066% than the EBV of $DGAT1^{K}/DGAT1^{A}$-$GH1^{L}/GH1^{L}$ sires ($P < 0.042$) and exceeded also the breeding values of $DGAT1^{K}$ per $DGAT1^{K}$-$GH1^{L}/GH1^{L}$ and $DGAT1^{K}/DGAT1^{K}$-$GH1^{L}/GH1^{V}$ genotypes (insignificantly).

DISCUSSION

GH1

The frequency of $GH1^{V}$ allele was low, which is generally reported in Holstein cattle (Lucy et al., 1993; Sorensen et al., 2002). As reported by Lucy

Table 5. Mean breeding values ± s_x for milk production traits according to *DGAT1* genotype

Genotype	Milk (kg)	Fat (kg)	Protein (kg)	Fat (%)	Protein (%)	RBVM
$DGAT1^{A}/DGAT1$	896.579 ± 549.536	17.566 ± 20.997	26.641 ± 17.465	–0.204 ± 0.182	–0.041 ± 0.115	106.483 ± 12.216
DGAT1^{K}/DGAT1	565.405 ± 590.275	23.992 ± 22.144	19.889 ± 18.019	0.017 ± 0.235	0.009 ± 0.115	103.818 ± 12.592
$DGAT1^{K}/DGAT1^{K}$	348.886 ± 587.681	32.932 ± 25.550	14.046 ± 18.106	0.225 ± 0.288	0.027 ± 0.090	101.864 ± 12.901
$P <$	0.000	0.000	0.000	0.000	0.000	0.055
R^2	0.110	0.047	0.055	0.319	0.063	0.012
$DGAT1^{A}$	796.262 ± 581.149	19.512 ± 22.656	24.596 ± 17.864	–0.137 ± 0.224	–0.026 ± 0.106	105.676 ± 12.363
$DGAT1^{K}$	479.369 ± 596.090	27.668 ± 23.891	17.486 ± 18.199	0.102 ± 0.275	0.017 ± 0.105	103.014 ± 12.696
$P <$	0.000	0.000	0.002	0.000	0.000	0.011
R^2	0.061	0.028	0.032	0.178	0.033	0.006

Table 6. Mean breeding values ± s_x for milk production traits according to joint genotypes of *DGAT1* and *GH1*

Genotype		Milk (kg)	Fat (kg)	Protein (kg)	Fat (%)	Protein (%)	RBVM
$DGAT1^A/DGAT1^A$ $GH1^L/GH1^L$	$n = 130$	$873.131^{AbC} \pm 517.517$	$17.062^{aBc} \pm 19.729$	$26.369^{AB} \pm 16.362$	$-0.199^{ABCD} \pm 0.182$	$-0.036^{ABC} \pm 0.097$	106.269 ± 11.393
$DGAT1^A/DGAT1^A$ $GH1^L/GH1^V$	$n = 15$	$1\,099.800^{DEF} \pm 767.476$	$21.933^{d} \pm 30.415$	$29.000^{C} \pm 25.768$	$-0.245^{EFGH} \pm 0.183$	$-0.089^{DEF} \pm 0.103$	108.33 ± 18.302
$DGAT1^K/DGAT1^A$ $GH1^L/GH1^L$	$n = 116$	$575.388^{ADg} \pm 596.682$	$23.397^{aef} \pm 22.407$	$19.672^{A} \pm 17.950$	$0.006^{AEIJ} \pm 0.234$	$0.004^{ADg} \pm 0.113$	103.603 ± 12.556
$DGAT1^K/DGAT1^A$ $GH1^L/GH1^V$	$n = 11$	$499.182^{bE} \pm 522.912$	28.546 ± 12.091	23.364 ± 18.885	$0.098^{BF} \pm 0.260$	$0.070^{BEg} \pm 0.111$	106.545 ± 12.770
$DGAT1^K/DGAT1^K$ $GH1^L/GH1^L$	$n = 41$	$327.854^{CFg} \pm 595.655$	$32.512^{Be} \pm 25.495$	$13.342^{BC} \pm 18.472$	$0.230^{CGI} \pm 0.280$	$0.027^{CF} \pm 0.092$	101.390 ± 13.323
$DGAT1^K/DGAT1^K$ $GH1^L/GH1^V$	$n = 2$	457.000 ± 446.891	$55.500^{cdf} \pm 16.263$	19.000 ± 4.243	$0.420^{DHJ} \pm 0.042$	0.045 ± 0.120	108.000 ± 4.243
$P <$		0.000	0.001	0.001	0.000	0.000	0.192
R^2		0.110	0.051	0.051	0.331	0.077	0.008

^{abc}means with the same letter within one column differ significantly ($P < 0.05$)

^{ABC}means with the same letter within one column differ significantly ($P < 0.01$)

et al. (1993), dairy breeds with larger mature size (Holstein) are supposed to have the highest frequency of $GH1^L$, which also correlates with higher milk production. As shown by Čítek et al. (2005), the spread of both alleles in the German Holstein population was affected indirectly by selection for milk production in the past, resulting in a higher occurrence of allele $GH1^L$.

Though the relation between the allele $GH1^L$ and the level of milk production was documented (Bauman, 1999; Panicke et al., 2001), it is not always expressed when analysing the association between the genotypes and estimated breeding values. Lucy et al. (1993) found similar estimated transmitting abilities (ETA) in Holstein bulls of different *GH1* genotypes, while the milk production was significantly higher in $GH1^L/GH1^L$ compared to $GH1^L/GH1^V$ Holstein cows. Schlee et al. (1994) found no significant difference between milk breeding values in Simmental bulls, but the effects on milk fat and protein content approached significance with a higher percentage in $GH1^L/GH1^V$ heterozygotes. In Polish Friesian bulls and heifers Grochowska et al. (2001) reported significant differences between genotypes, when $GH1^L/GH1^V$ heterozygotes revealed the highest values for milk and protein yields, while $GH1^L/GH1^L$ homozygotes were superior in fat yield.

Generally, the influence of *GH1* polymorphism on milk production traits is not conclusive and is rather breed-specific (Lucy et al., 1993; Sorensen et al., 2002). The association analysis is limited by the lack of homozygous $GH1^V/GH1^V$ animals, which disables a direct comparison of both homozygous variants. Similar breeding values of $GH1^L/GH1^L$ and $GH1^L/GH1^V$ animals may also be explained as the consequence of $GH1^L$ dominance over $GH1^V$ variant (Grochowska et al., 2001; Sorensen et al., 2002). Another reason could be the genetic background of the population where the bulls are tested/mated. The indirect recombination effect should also be taken into account. The differences between breeds suggest that there may exist further linked polymorphisms in regions that are involved in the gene regulation or other mutations in regions within or close to the gene that affect the expression of the gene by changing the binding affinity of transcription factors (Lucy et al., 1993; Schlee et al., 1994; Sorensen et al., 2002).

GHR

Similar allelic frequencies were described in Finnish Ayrshire, where Viitala et al. (2006) found 0.870 GHR^A and 0.130 GHR^G. Ge et al. (2000) detected a somewhat higher frequency of GHR^G allele (0.220) in Angus cattle, while Di Stasio et al. (2005) found almost equal allelic distribution in Piemontese (GHR^A = 0.490; GHR^G = 0.510).

The effect of 257 SNP was tested mostly in relation to meat production traits (Ge et al., 2000; Di Stasio et al., 2005). Viitala et al. (2006) tested the effects of four *GHR* exonic SNPs on milk production traits, but found no effect of 257 SNP on QTL variance. We found significantly lower EBVs for fat production in GHR^G/GHR^G homozygotes. Though, three of the four GHR^G/GHR^G homozygous bulls were simultaneously $DGAT^A/DGAT^A$ homozygotes, which probably affected the result of the analysis. The low frequency and high variability of GHR^G/GHR^G homozygotes disable to find any significant trend.

DGAT1

As reported by Grisart et al. (2002), following the evolutionary conservation of lysine residue, $DGAT1^K$ is more than likely the ancestral state while $DGAT1^A$ corresponds to a more recently evolved state. The occurrence of $DGAT1^K$ allele is indirectly influenced by selection and decreased while selecting for high milk yield. On the contrary, because milk fat has been preferred in cattle breeding since the 50s', its frequency may be higher in some populations. For example Weller et al. (2003) described that in Israeli Holsteins the frequency of $DGAT1^K$ decreased from 15 to 5% between 1981 and 1990 and since then it has increased to 10%. Spelman et al. (2002) noted very variable frequencies of $DGAT1^K$ in Holstein Friesian bulls based on the origin of the genetic material. From 0.60, it decreased with a higher portion of overseas genes (0.24 $DGAT1^K$ in 91–100% of overseas bulls) while it increased in the homebred (New Zealander) population, where it was similar to Jersey breed (0.88 $DGAT1^K$). This result implies the indirect selection of alleles through selection aimed at different breeding goals in Holstein Friesian and Jersey populations. A lower frequency of $DGAT1^K$ was found in Ayrshire (0.22 according to Spelman et al., 2002), Montbeliard, where $DGAT1^A$ is almost fixed (Gautier et al., 2007) or Czech Simmental sires (0.08, our unpublished data). According to our previous analysis (Čítek et al., 2007) done in two groups of sires of different age, the selection for breeding value for protein yield did not essentially affect the frequencies at the amino acid position 232 Lysine – Alanine of the locus of *DGAT1*, although the $DGAT1^A/DGAT1^A$

genotype was found to be significantly better in the main selection criterion. The reason may be seen in the moderate selection for fat yield coupled with selection for protein in the breeding programme, which could keep the frequencies stable; and also in the fact that the *DGAT1* itself does not directly influence the protein synthesis. However, it will be interesting to monitor the frequencies as a certain tendency in the allele $DGAT1^A$ in the sires of different age has been observed.

Our results correspond well with many other authors (Grisart et al., 2002; Weller et al., 2003; Kühn et al., 2004) who confirmed that $DGAT1^K$ allele was associated with decreased milk and protein yield while it increased fat yield, fat and protein content. As reported by Grisart et al. (2002), a simultaneous decrease in milk and protein yield and increase in fat yield are an interesting feature of $DGAT1^A$ to $DGAT1^K$ substitution as there exists a positive genetic correlation between these three yield traits. The response of $DGAT1^K/DGAT1^A$ heterozygotes could be characterized as intermediate, which confirms our previous findings (Čítek et al., 2007) and corresponds with the hypothesis of the effect of the locus being approximately codominant with intermediate heredity (Grisart et al., 2002).

CONCLUSIONS

The analyses confirmed *DGAT1* as a strong candidate for application in marker-assisted selection, though additional mutation could attribute to its effect. We did not prove a significant effect of *GH1* or *GHR* polymorphisms on EBVs for milk production traits with the exception of EBV for fat yield, which was lower in GHR^G/GHR^G homozygotes. We can expect an additional effect primarily in joint application with other markers. The effect would be not high as the extreme allelic frequencies were already achieved by past selection. However, the important role of growth hormone and growth hormone receptor in the lactation process is well known, thus their polymorphisms and interaction with other traits should be the subject of further research.

REFERENCES

Aggrey S.E., Yao J., Sabour M.P., Lin C.Y., Zadworny D., Hayes J.F., Kuhnlein U. (1999): Markers within the regulatory region of the growth hormone receptor gene and their association with milk-related traits in Holsteins. J. Hered., 90, 148–151.

Argetsinger L.S., Carter-Su C. (1996): Mechanism of signalling by growth hormone receptor. Physiol. Rev., 76, 1089–1107.

Bauman D.E. (1999): Bovine somatotropin and lactation: from basic science to commercial application. Domest. Anim. Endocrinol., 17, 101–116.

Coppieters W., Riquet J., Arranz J. J., Berzi P., Cambisano N., Grisart B., Karim L., Marcq F., Moreau L., Nezer C., Simon P., Vanmanshoven P., Wagenaar D., Georges M. (1998): A *QTL* with major effect on milk yield and composition maps to bovine chromosome 14. Mamm. Genome, 9, 540–544.

Czarnik U., Galiński M., Pareek Ch.S., Zabolewicz T., Wielgosy-Groth Z. (2007): Study of an association between SNP 775C>T within the bovine *ITBG2* gene and milk performance traits in Black and White cows. Czech J. Anim. Sci., 52, 1–6.

Čítek J., Řehout V., Bláhová B., Pávková J., Panicke L. (2005): The genetic divergence among cattle breeds on candidate loci. FBN Dummerstorf, Schriftenreihe, 15, 43–48.

Čítek J., Řehout V., Hradecká E., Večerek L., Panicke L. (2007): The breeding values of German Holstein sires and the *DGAT1* polymorphism. Arch. Tierz., 50, 136–146.

Di Stasio L., Destefanis G., Brugiapaglia A., Albera A., Rolando A. (2005): Polymorphism of the *GHR* gene in cattle and relationships with meat production and quality. Anim. Genet., 36, 138–140.

Gautier M., Capitan A., Fritz S., Eggen A., Boichard D., Druet T. (2007): Characterization of the *DGAT1 K232* and a variable number of tandem repeat polymorphisms in French dairy cattle. J. Dairy Sci., 90, 2980–2988.

Ge W., Davis M.E., Hines H.C., Irvin K.M. (2000): Rapid communication: Single nucleotide polymorphism detected in exon 10 of the bovine growth hormone receptor gene. J. Anim. Sci., 78, 2229–2230.

Grisart B., Coppieters W, Farnir F., Karim K., Ford C., Cambisano N., Mni M., Reid S., Spelman R., Georges M., Snell R. (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., 12, 222–231.

Grochowska R., Sorensen P., Zwierzchowski L., Snochowski M., Lovendahl P. (2001): Genetic variation in stimulated *GH* release and in *IGF-I* of young dairy cattle and their associations with the leucine/valine polymorphism in the *GH* gene. J. Anim. Sci., 79, 450–476.

Kühn C., Thaller G., Winter A., Bininda-Emonds O.R.P., Kaupe B., Erhardt G., Bennewitz J., Schwerin M., Fries

R. (2004): Evidence for multiple alleles at the *DGAT1* locus better explains a quantitative trait locus with major effect on milk fat content in cattle. Genetics, 167, 1873–1881.

Lucy M.C., Hauser S.D., Eppard P.J., Krivi G.G., Clark J.H., Bauman D.E., Collier R.J. (1993): Variants of somatotropin in cattle: gene frequencies in major dairy breeds and associated milk production. Domest. Anim. Endocrinol., 10, 325–333.

Matějíček A., Matějíčková J., Němcová E., Jandurová O.M., Štípková M., Bouška J., Frelich J. (2007): Joint effects of *CSN3* and *LGB* genotypes and their relation to breeding values of milk production parameters in Czech Fleckvieh. Czech J. Anim. Sci., 52, 83–87.

Mitra A., Schlee P., Balakrishman C.R., Pirchner F. (1995): Polymorphisms at growth-hormone and prolactin loci in Indian cattle and buffalo. J. Anim. Breed. Genet., 112, 71–74.

Panicke L., Čítek J., Schmidt M., Řehout V., Erhardt G., Staufenbiel R. (2001): Enzyme activities and milk performance by clusters of growth hormone gene (*GH*) and β-casein (β-cN) in German Holsteins. Czech J. Anim. Sci., 46, 202–208.

Schlee P., Graml R., Rottsmann O., Pirchner F. (1994): Influence of growth-hormone genotypes on breeding values of Simmental bulls. J. Anim. Breed. Genet., 111, 253–256.

Sorensen P., Grochowska R., Holm L., Henryoon M., Lovendahl P. (2002): Polymorphism in the bovine growth hormone gene affects endocrine release in dairy calves. J. Dairy Sci., 85, 1887–1893.

Spelman R.J., Ford A.C., McElhinney P., Gregory G.C., Snell R.G. (2002): Characterization of the *DGAT1* gene in the New Zealand dairy population. J. Dairy Sci., 85, 3514–3517.

Viitala S., Schulman N., de Koning D., Elo K., Kinos R., Virta A., Mäki-Tanila A., Vilkki J. (2003): Quantitative trait loci affecting milk production traits in Finnish Ayrshire dairy cattle. J. Dairy Sci., 86, 1828–1836.

Viitala S., Szyda J., Blott S., Schulman N., Lidauer M., Mäki-Tanila A., Georges M., Vilkki J. (2006): The role of the bovine growth hormone receptor and prolactin receptor genes in milk, fat and protein production in Finnish Ayrshire dairy cattle. Genetics, 173, 2151–2164.

Weller J.I., Golik M., Seroussi E., Ezra E., Ron M. (2003): Population-wide analysis of a *QTL* affecting milk-fat production in the Israeli Holstein population. J. Dairy Sci., 86, 2219–2227.

Winter A., Krämer W., Werner F.A.O., Kollers S., Kata S., Durstewitz G., Buitkamp J., Womack J.E., Thaller G., Fries R. (2002): Association of lysine232 alanine polymorphism in bovine gene encoding acylCoA: diacylglycerol acyltransferase (*DGAT1*) with variation at a quantitative trait locus for milk fat content. PNAS, 99, 9300–9305.

Received: 2007–09–13
Accepted after corrections: 2008–03–11

Corresponding Author

Ing. Eva Hradecká, Ph.D., Agricultural Faculty, University of South Bohemia in České Budějovice, Studentská 13,
370 05 České Budějovice, Czech Republic
Tel. +420 387 772 723, e-mail: hradecka@zf.jcu.cz