Joint effects of *CSN3* and *LGB* genes on breeding values of milk production parameters in Czech Fleckvieh

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Abstract

The aim of this study was to estimate the joint effects of *CSN3* and *LGB* loci on breeding values of milk production parameters. *CSN3* (kappa-casein) and *LGB* (beta-lactoglobulin) genotypes of 120 Czech Fleckvieh sires were detected using the PCR-RFLP method. Breeding values of sires were obtained from the Official Database of Progeny Testing. Ten genotype combinations were detected. Genotypes *ABAB* (25.0 %), *ABAA* (13.3 %) and *ABBB* (13.3 %) were the most frequent. Significant effects of genotype combinations on breeding values for fat and protein content were found. The highest breeding values for milk (+621 kg) and protein (+15.8 kg) yields were associated with genotype combination *ABAA*, while the highest breeding values for content parameters (+0.15 % for protein content and +0.55 % for fat content) were associated with genotype combination *BBAB*. In comparison with the results of our previous studies focusing on separate testing of *CSN3* and *LGB* loci, the results of the current study refer to the advantage of comparing the effects of all genotype combinations. This finding brings a clearer view on loci effects and helps to simplify decisions useful for breeding.

Introduction

Kappa-casein (*CSN3*) and beta-lactoglobulin (*LGB*) loci affect the milk production parameters and quality of milk protein.

The kappa-casein gene is situated on bovine chromosome 6 and encodes milk protein important for the structure and stability of casein micelles (Alexander et al., 1988). The most common alleles are *A*, *B* and *E*. Allele *A* is associated with higher milk yield but lower protein content, while allele *B* is linked with higher protein content (Neubauerová, 2001) and higher milk quality (Strzalkowska et al., 2002) but lower milk yield (Boettcher et al., 2004; Caroli et al., 2004). The negative effect of allele *E* on milk protein quality was reported by Ikonen et al. (1997).

The beta-lactoglobulin (*LGB*) gene is situated on bovine chromosome 11 and encodes the main protein of whey (Eggen and Fries, 1995). Common alleles are *A, B, C* and *D*, with alleles *A* and *B* being the most frequent (Panicke et al., 1996). The *LGB* locus affects mainly milk composition and milk quality and especially *B* allele was recognized as superior for milk quality in European cattle breeds (Strzalkowska et al., 2002). Allele *A* is associated rather with yield parameters (Neubauerová, 2001).

The objective of this study was to determine genotype frequencies of *CSN3* and *LGB* genes and find the joint effect of their genotypes on milk production parameters expressed by the breeding values of sires. The results will help to explain the role of the joint effect of *CSN3* and *LGB* genotypes in the Czech Fleckvieh breed.

Material and methods

Genotypes of kappa-casein (*CSN3*) and beta-lactoglobulin (*LGB*) loci were detected in 120 Czech Fleckvieh sires using a Polymerase Chain Reaction and Restriction Fragment Length Polymorphism method (PCR-RFLP) and electrophoresis on agarose gel. DNA was obtained from the semen of sires (Ashwell et al., 1996). Detection of *CSN3* alleles *A*, *B* and *E* was carried out according to Lien and Rogne (1993). *LGB* alleles *A* and *B* were identified according to Agrawala et al. (1992).Breeding values of observed sires were obtained from the Official Database of Progeny Testing.

First the frequencies of *CSN3* and *LGB* genotypes were calculated. In the second step, statistical analysis was carried out by means of the programme package SAS using GLM and the following model equation:

$$y_{ijklm} = \mu + G_i + b_1R_j + b_2P_k + G_i(O_l) + e_{ijklm}$$

where y was the breeding value of the sire, μ was the average of observed breeding values, G was the joint effect of *CSN3* and *LGB* genotypes, bR was the linear regression on the year of sire birth, bP was the linear regression on the share of the Czech Fleckvieh breed in sires, G(O) was the effect of grandsire with the nested effect of *CSN3* and *LGB*, and e was the set of residual effects.

Results and discussion

Ten genotype combinations of *CSN3* and *LGB* genes were found in the observed sires (Table 1). The most frequent genotype combination was *ABAB* (25.0 %). The frequency of combination *BBBB*, which is reported to increase breeding values for protein and fat contents (Kučerová et al., 2006), was detected only in 4.2 %. On the other hand, the frequency of combination *AAAA*, which is reported to increase breeding values for milk and protein yields (Kaminski et al., 2002), was found in 8.3 %.

Table 1. Genotype frequencies in the observed sires

CSN3+LGB genotypes	n	Frequency (%)
AAAA	10	8.3
AAAB	13	10.8
AABB	5	4.2
ABAA	16	13.3
ABAB	30	25
ABBB	16	13.3
BBAA	8	6.7
BBAB	13	10.8
BBBB	5	4.2
BEBB	4	3.4

Significant associations between genotype combinations *CSN3* and *LGB* and breeding values for fat and protein contents were found (Table 2). The highest breeding values for milk and protein yields were associated with genotype combination *ABAA*, while Kaminski et al. (2002) reported the highest breeding values for milk and protein yields in relation to genotype combination

AAAA. A similar tendency was found in genotype combination *BBBB*, but this genotype was carried only by 5 sires, which is insufficient for drawing reliable conclusions. On the other hand, the highest breeding values for content parameters were associated with the similar genotype combination *BBAB*. Compared to our findings, Kaminski et al. (2002) found the highest breeding values for content parameters associated with genotype combinations *ABAB* and *ABBB*. Contrary to our results, Neubauerová (2001) did not find any significant association between *CSN3* and *LGB* genotypes and breeding values of milk production parameters.

Table 2. The relation between genotype combinations of *CSN3* and *LGB* genes and breeding values of milk production parameters

CSN3+LGB genotypes	n	Average breeding values for				
		Milk yield (kg)	Protein yield (kg)	Protein content (%)	Fat yield (kg)	Fat content (%)
AAAA	10	+313	+15.2	-0.08[ab]	+14.1	+0.04[ab]
AAAB	13	+400	+16.7	-0.13[c]	-6.8	-0.41[cd]
AABB	5	+229	+12.1	-0.08[d]	+12.9	+0.08[e]
ABAA	16	+621	+15.8	-0.25	-36.3	-1.20[b]
ABAB	30	+24	+10.1	+0.03[ac]	+2.7	+0.04[d]
ABBB	16	+361	+14.5	-0.11	-22.0	-0.72[f]
BBAA	8	+427	+7.6	-0.27	-51.9	-1.34[a]
BBAB	13	-317	+4.7	+0.15[bd]	+14.9	+0.55[cf]
BBBB	5	+533	+15.1	-0.27	-63.9	-1.67[e]
BEBB	4	+144	+8.7	-0.06	-27.4	-0.66

[a], [b], [c], [d], [e] or [f] means the significant difference $P < 0.05$ between two *CSN3+LGB* genotypes marked with the identical symbol within one parameter.

In comparison with the results of previous studies focusing on separate testing of *CSN3* and *LGB* genotypes, the results of the current study refer to the advantage of comparing the effects of all genotype combinations due to separating the animals with identical genotype of one locus (e.g. *BB*) according to different genotypes of the second locus (e.g., *BBAA*, *BBAB* and *BBBB*). This finding is consistent with the finding of Strzalkowska et al. (2002), brings a clearer view on loci effects and helps to simplify decisions useful for breeding.

Conclusion

Significant effects of *CSN3* and *LGB* genes on protein and fat contents were found. Only genotype *ABAB* improved all parameters. Other genotypes either increased yield but decreased content parameters or increased content but decreased yield parameters. The highest breeding values for milk and protein yields were associated with genotype combination *ABAA*, whereas the highest breeding values for content parameters were associated with genotype combination *BBAB*. Results of genotypes *BBBB*, *AABB* and *BEBB* cannot be taken into consideration for reliable conclusions due to the small number of animals carrying these combinations.

This study was supported by project MZE 0002701402.

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