Frequency And Effect Of Single Nucleotide Polymorphisms Of The *BTN1A1* And *STAT1* On Milk Production Traits In Czech Fleckvieh Cows

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Introduction

Modern breeding strategies in dairy cattle focus not only on increasing milk yield, but also on milk composition and quality. Information from SNP (single nucleotid polymorphism) linked to QTL can be used to improve selection for some production and non-production traits. The genes examined in this study were chosen because of their presumed effect on milk composition and their relationship with fat and protein metabolism. One of the genes chosen for this study was signal transducer and activator of transcription 1 (*STAT1*) which is responsible for milk protein synthesis as well as fat metabolism (Cobanoglu et al. (2006)). The second chosen gene was bovine milk protein butyrophilin 1 (*BTN1A1*) which plays an important role in secretion of milk lipids (Ogg et al. (2004)). The main goal of this study was to estimate allele frequencies of the SNP at the chosen genes and their relationship with milk production traits in the Czech Fleckvieh cattle. The second goal was based on the hypothesis that the effects of gene polymorphisms on investigated traits can differ in dual-purpose Czech Fleckvieh breed compared to dairy cattle breeds.

Material and methods

For the analyses the Czech Fleckvieh cows born from 2001 to 2008 were used. Three groups of cows with different breed proportions where involved. The first group included pure Czech Fleckvieh cows, the second group consisted the cows with 99 – 76% and the third group 75 – 50% of Czech Fleckvieh breed. All phenotypic data used for this study were obtained from the official progeny testing database of the Czech-Moravian Breeders' Corporation. The data set included 526 Czech Fleckvieh cows. The exact numbers of genotyped animals for both investigated genes are presented in the table 1. Estimated breeding values (BV) for milk traits used in analyses included breeding values for milk yield (BVMLK), fat percentage (BVFATP) and protein percentage (BVPROTP). The numbers of observations for investigated milk traits are presented in the table 2 for gene *BTN1A1* and in the table 3 for gene *STAT1*. Numbers of lactation per cow ranged from 1 to 3. The investigated animals originated from 4 herds which collaborate with the Institute of Animal Science, Prague. The DNA for analyses from 526 Czech Fleckvieh cows was extracted from blood samples. The polymorphism of genes *BTN1A1* and *STAT1* were distinguished by PCR

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and RFLP according to previously described methodology (Taylor et al. (1996); Cobanoglu et al. (2006)). Each methodology was optimized for current laboratory conditions.

The model used for the analyses included following fixed effects:
Y= herd+year+season+number of lactation+breed+effect of genotyp+age at calving+ residual

There were 4 herds, 8 years, 4 seasons, 3 lactations and 3 groups of breed. Age at first calving was included as regression.

Results and discussion

Genotype frequencies at the chosen genes are presented in the table 1. The frequencies presented here are similar to those presented in other studies of the same genes (Cobanoglu et al. (2006); Taylor et al. (1996)).

A significant effect of the polymorphism of gene *BTN1A1* on BVPROTP was found The *LA* genotype was associated with higher BV (statistically significant difference was observed between effect of genotypes *LL* and *LA*). No effect of this polymorphism on BV of milk yield and BV of fat percentage was found. Komisarek and Dorynek, (2003) did not find a significant effect of *BTN1A1* polymorphism on milk yield and composition in AI bulls, but they observed higher breeding values for milk fat content in bulls with the genotype *LL* compared to bulls with the genotype *LA*. The present study did not confirm the significant influence of *BTN1A1* on BVFATP, but there were significant differences between two groups of genotypes (*LL* and *LA*). Similar effects of BTN1A1 genotypes on milk, fat and protein yields were reported by Komisarek et al. (2006) in Jersey cows. The authors found higher milk, fat and protein yields for genotype *LL* compared to genotypes *LA* and *AA*.

A significant effect of the *STAT1* polymorphism on BVFATP and BVPROTP was found. In contrast, no significant effect on BVMLK was observed. In a study of Cobanoglu et al. (2006), significantly higher milk, fat and protein yields for genotypes *CC* and *CT* at *STAT1* in Holstein dairy cattle were demonstrated. In the present study involving Czech Fleckvieh cows significantly higher BV for protein percentage was found for genotype *TC* than for genotype *TT*. The same difference was observed for BVFATP where higher BV was found for genotype *TC* than for *TT*. We did not confirm significantly higher EBV for milk yield as in the study of Cobanoglu et al. (2006). This could be because of small number of observations at genotype *TT*. Estimated BV for genotypes *CC* and *CT* had similar trend as in the study of Cobanoglu et al. (2006).

Table 1: Frequency of BTN1A1 and STAT1 genotypes

Locus	Genotype	Frequency (n)
BTN1A1	*LL*	462
	LA	58
	AA	6
STAT1	*CC*	376
	CT	137
	TT	13

Table 2: Effect of *BTN1A1* on breeding values (BV) for milk yield, fat percentage and protein percentage in the Czech Fleckvieh cows

Production traits		*BTN1A1*			F – value	Significance
		LL n=1005	*LA* n=120	*AA* n=11		
BV Milk yield (kg)	$\mu+a_i$	219.95	311.48	250.19	2.44	
	$s_{\mu+ai}$	± 31.303	± 48.292	± 133.225		
BV Fat (%)	$\mu+a_i$	-0.01	0.02	-0.02	2.45	
	$s_{\mu+ai}$	±0.012	±0.018	±0.051		
BV Protein (%)	$\mu+a_i$	0.00	0.02	0.01	4.19	+
	$s_{\mu+ai}$	±0.007	±0.010	±0.030		

$^{+}P < 0.05$

Table 3: Effect of *STAT1* on breeding values (BV) for milk yield, fat percentage and protein percentage in the Czech Fleckvieh cows

Production traits		*STAT1*			F -value	Significance
		CC n=842	*TC* n=288	*TT* n=26		
BV Milk yield (kg)	$\mu+a_i$	227.53	226.53	301.97	0.39	
	$s_{\mu+ai}$	± 32.073	± 38.238	± 88.636		
BV Fat (%)	$\mu+a_i$	-0.01	0.01	-0.03	4.64	++
	$s_{\mu+ai}$	±0.012	±0.014	±0.034		
BV Protein (%)	$\mu+a_i$	0.00	0.01	-0.00	4.13	+
	$s_{\mu+ai}$	±0.007	±0.008	±0.020		

$^{+}P < 0.05$; $^{++}P < 0.01$;

Conclusion

A significant effect of BTN1A1 polymorphism on BVPROTP was found in this study. Cows with *LA* genotype had significantly higher BV for this trait. There was no effect of this polymorphism on BV for milk yield and fat percentage. The significant effect of the second investigated gene (*STAT1*) polymorphism was observed for BVFATP and BVPROTP. Higher BVFATP and BVPROTP were associated with genotype *TC* compared to genotype *TT*.

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