Polymorphism Of *CYP11B1* Gene And Its Relation To Milk Production Traits In Czech Fleckvieh Cattle

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Introduction

Knowledge of particular genes, their polymorphisms and effects can help in understanding molecular pathways that lead to health problems or different production in cattle. That could be important for selection as well as for prevention of diseases. Candidate genes for economically important traits are chosen because of previous linkage studies in cattle as well as for biological functions in cattle and other species.

Steroid 11β-hydroxylase (*CYP11B1*; cytochrome P450, subfamily XI B, polypeptide 1) gene encodes a steroid 11-beta-hydroxylase that converts 11-deoxycortisol to cortisol and 11-deoxycorticosterone to corticosterone. Cortisol is one of the principal hormones involved in lipogenesis and lipolysis. There was found a miRNA target site in bovine *CYP11B1* that is expressed in the mammary gland. This is a possible involvement in the regulation of gene expression (Ogoverc et al. (2009)). Prolactin regulatory element-binding (PREB) protein is a transcription factor not only for prolactin but it also regulates the expression of *CYP11B1* (Imachi et al. (2008)). The *CYP11B1* gene is positioned on bovine chromosome 14 near marker *ILSTS039*. This marker is associated with milk traits (Looft et al. (2001); Kuhn et al. (2004)). This makes the *CYP11B1* gene a functional and positional candidate gene for milk production traits as are milk yield and milk components yield.

Material and methods

Population and Phenotypes

There were examined a total of 1080 lactations in 475 Czech Fleckvieh cows in this study. The cows were sampled from 4 herds and from 80 sires. Lactation data were from years 2001-2008. Data on cow number, sire, year of calving, breed, milk production traits and breeding values were extracted from the official progeny testing database of the Czech-Moravian Breeders' Corporation. For this study, the cows were divided to three groups according to the genetic share of Czech Fleckvieh breed in the pedigree. In the first group were thoroughbred Czech Fleckvieh cows, in the second group were cows with 76-99%, and in the third group were cows with 50-75% of Czech Fleckvieh.

SNP Genotyping

The DNA was extracted from blood for genotyping. The method PCR-RFLP previously shown by Kaupe et al. (2007) was used for genotyping. This method detects alanin (Ala) and valin (Val) polymorphism (V30A) in *CYP11B1* gene product.

Statistical analyses

Deviation of genotype frequencies from Hardy-Weinberg equilibrium was tested by χ^2-test.

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We made the statistical analysis for milk yield (MY), fat yield (FY), fat percentage (FP), protein yield (PY), and protein percentage (PP) as well as for cows' breeding values for milk yield (MYBV), fat percentage (FPBV), and protein percentage (PPBV). For statistical analysis we used following linear model with fixed effects:

$$y_{ijklmn} = \mu + HYS_{ijk} + B_l + N_m + G_n + \beta_x + e_{ijklmn}$$

where y is the trait observed; μ is the population mean; HYS is the combined effect of herd, year and season of first calving; B is the effect of breed group; N is the effect of number of laction (the first lactation; the second lactation; the third and further lactation); G is the effect of genotype *CYP11B1* (Ala/Ala, Ala/Val, or Val/Val); β is the regression on age at first calving of cow and e is the residual effect. The analyses were implemented using the GLM procedure in SAS 9.2 (SAS Institute Inc.)
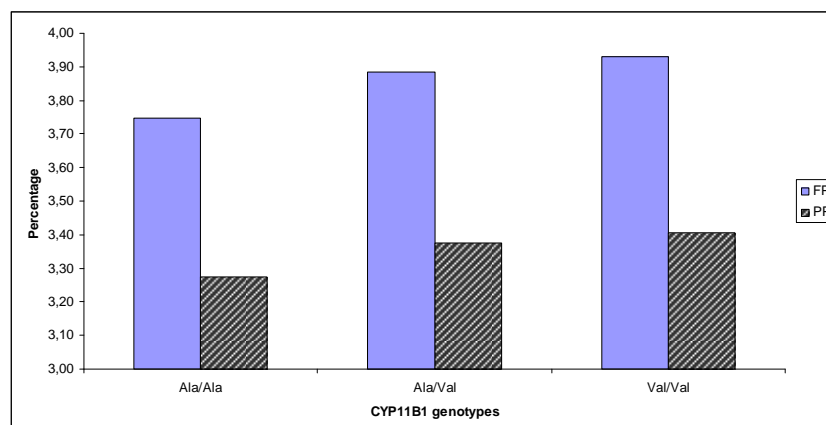
Results and discussion

Frequencies of Ala/Ala, Ala/Val and Val/Val genotypes in Czech Fleckvieh population were 0.07, 0.38 and 0.55. Genotype distribution of gene *CYP11B1* was in Hardy-Weinberg equilibrium ($P < 0.05$).
Association tests between Ala/Val polymorphism in *CYP11B1* gene in the Czech Fleckvieh population were significant for FP ($P < 0.05$) and PP ($P < 0.01$). The *CYP11B1^V* allele increased both FP and PP (Table 1, Figure 1). The same results were reported by Kaupe et al. (2007). Similar results were found for the association with breeding values (Table 2). On the other hand, gene variant with *CYP11B1^A* was significantly associated ($P < 0.001$) with higher MYBV (Figure 2).

Table 1: Estimates of effects on milk production traits associated with Ala/Val polymorphism in *CYP11B1* gene in Czech Fleckvieh cows

| Genotype	Ala/Ala	Ala/Val	Val/Val		
Trait	$\mu + a_i$	$\mu + a_i$	$\mu + a_i$	F value	Signif.
	$\pm s_{\mu+ai}$	$\pm s_{\mu+ai}$	$\pm s_{\mu+ai}$		
MY	7914.16	7758.30	7602.84	0.79	
	± 340.58	± 193.69	± 186.73		
FY	291.39	297.09	294.06	0.22	
	± 11.97	± 6.81	± 6.56		
FP	3.75	3.88	3.93	4.23	*
	± 0.07	± 0.04	± 0.04		
PY	257.34	259.75	256.02	0.32	
	± 10.34	± 5.88	± 5.67		
PP	3.27	3.37	3.40	4.97	**
	± 0.04	± 0.03	± 0.02		

* $P < 0.05$; **$P < 0.01$

Figure 1: Level of fat percentage (FP) and protein percentage (PP) for different genotypes of *CYP11B1* gene in Czech Fleckvieh cows

Table 2: Estimates of effects on breeding values of cows associated with Ala/Val polymorphism in *CYP11B1* gene in Czech Fleckvieh cows

Genotype	Ala/Ala	Ala/Val	Val/Val		
Trait	$\mu+a_i$ $\pm s_{\mu+ai}$	$\mu+a_i$ $\pm s_{\mu+ai}$	$\mu+a_i$ $\pm s_{\mu+ai}$	F value	Signif.
MYBV	321.20 ± 60.09	250.00 ± 34.65	153.87 ± 33.65	8.71	***
PPBV	0.00 ± 0.01	-0.01 ± 0.01	0.02 ± 0.01	6.43	**
FPBV	-0.03 ± 0.02	-0.02 ± 0.01	0.01 ± 0.01	4.30	*

* $P < 0.05$; **$P < 0.01$; ***$P < 0.001$
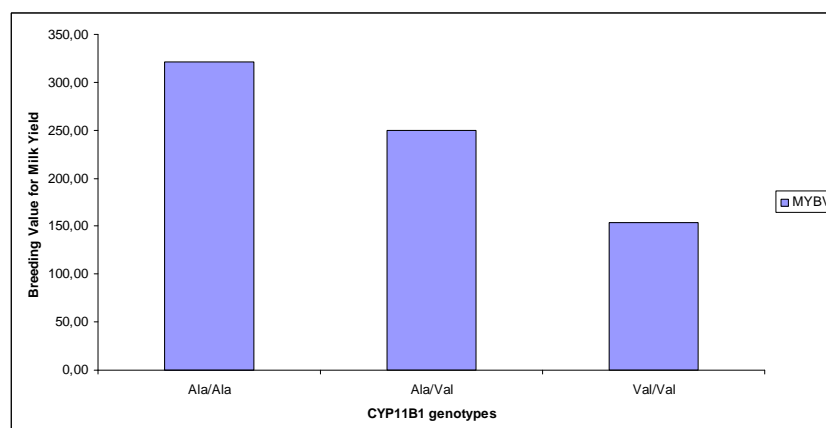
Figure 1: Level of breeding value for milk yield (MYBV) for different genotypes of *CYP11B1* gene in Czech Fleckvieh cows

Conclusion

Significant effect of the Ala/Val polymorphism in bovine *CYP11B1* gene was found on fat and protein contents as well as on breeding values for fat and protein contents, and milk yield in Czech Fleckvieh cows. The study revealed new important information with possible future use in Czech Fleckvieh breeding. Further analyses are necessary to confirm the findings before their application.

Acknowledgement

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