

Effect of the Thyroglobulin (TG) and Leptin gene polymorphisms on the milk production traits in Hungarian Simmental cows

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Introduction

Leptin is the hormone product of the obese gene synthesized and secreted predominantly by white adipocytes (Zang et al., 1994; Ji et al., 1998). Polymorphisms in the leptin gene have been associated with serum leptin concentration, feed intake, milk yield (Liefers et al., 2002) and body fatness (Buchanan et al., 2003; Nkrumah et al., 2004). Polymorphism in the 5'-untranslated region of TG gene – which product is the precursor of thyroid hormones that influence lipid metabolism - has been concluded to affect intramuscular fat content in cattle (Barendse, 1999). Subcutaneous fat thickness, fat percentage of tissues and milk fat in general are expected to be influenced by TG polymorphisms, since iodothyronines affect adipocyte differentiation, as well as thyroid hormone levels influence milk fat percentage (Folley and Malpress, 1948). Aim of this study was to estimate the effect of leptin and TG loci on milk production traits and to determine the distribution of the different genotypes and allele frequencies in the Hungarian Simmental population.

Materials and methods

300 blood samples were collected from different Hungarian Simmental herds. Leptin and TG genotypes were determined by PCR-RFLP (polymerase chain reaction-restriction fragment length polymorphism) assay. Milk production data have been registered throughout three consecutive lactations and statistical analyses have been carried out to find association between individual genotypes and milk production traits. Dataset was analysed with SPSS 15.0 for Windows software. The predicted effect of detected polymorphisms was explored by the method of multivariate analysis of variance. Milk production ability of genotype groups has been compared using the method of least squares difference.

Results

Table 1. Frequencies of different genotypes in the studied loci

loci	genotypes	frequencies	X ²	p
Leptin	CC	56.9% (61.3%)	20.484	0.0001***
	TC	42.8% (33.9%)		
	TT	0.3% (4.6%)		
TG	CC	54.3% (54%)	0.063	0.955
	TC	38.4% (39%)		
	TT	7.3% (7%)		

The expected values are presented in brackets (df=2)
(*: p<0.05; ***p<0.005)

Table 2. Least square means and standard errors of some milk production parameters in TG genotype groups

TG	LSD±SE		
	305d milk yield (kg)	305d milk protein (%)	Maximum daily milk (kg)
CC	6353.8±182a	3.41±0.03a	28.23±0.71a
TC	6279.6±187	3.43±0.03b	27.91±0.73b
TT	6194.6±236b	3.40±0.04	27.48±0.91b

(a, b: different characters indicate significant (p<0.05) difference between genotypes)

Table 3. Least square means and standard errors of some milk production parameters in leptin genotype groups

	LSD±SE		p
	CC	TC	
Maximum daily milk (kg)	28,27±0,7	28,12±0,7	0,646
305d milk yield (kg)	6369,4±180,8	6330,1±182,2	0,643
305d milk fat yield (kg)	244,4±7,9	239,4±7,9	0,172
305d milk fat (%)	3,85±0,07a	3,78±0,07b	0,036*
305d milk protein yield (kg)	216,9±5,9	216,5±6	0,874
305d milk protein (%)	3,42±0,03	3,43±0,03	0,429

(a, b: different characters indicate significant difference between genotypes)

Discussion

The calculated χ² values for the TG genotypes indicated Hardy-Weinberg equilibrium in the population. In case of leptin genotypes, differences between the observed and expected genotype frequency values were significant (Table 1). The only leptin TT genotype animal found was not included in the statistical analysis. Leptin CC animals showed significantly higher 305 days milk fat percentage than TC cows. At TG locus TC cows showed the highest milk protein and 305 days milk protein percentage values. TG CC animals showed significantly higher 305 days milk yield (kg) than TT cows. As for 305 days milk yield (kg), 305 days fat yield (kg), and maximum daily milk yield (kg) CC animals produced significantly higher values than other genotypes. Most quantitative traits (such as milk production) with high economic relevance are polygenic, therefore may be influenced by other multiple genes as well. The tendency of correlations of our results in leptin polymorphism correspond to the findings of Liefers et al. (2005). However, no association has been found previous to our results between TG locus and milk production traits in dairy cattle. Molecular tests provide facilities for the direct selection among variants, however the benefits of the different alleles depend on the economic reasons given in the breeding programs.

Acknowledgement

The project was supported by the Hungarian Scientific Research Fund and National Research and Development Programme.

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