Session 29.

E-mail: istvan.anton@atk.hu

Effect of the Leptin gene polymorphism on the intramuscular fat deposition in Hungarian Angus cattle

I. Anton[1], K. Kovács[1], G. Holló[2], V. Farkas[3] and A. Zsolnai[1]

[1]Research Institute for Animal Breeding and Nutrition, Gesztenyés u. 1., 2053 Herceghalom, Hungary
[2]University of Kaposvár, Guba S. u. 40, 7400 Kaposvár, Hungary
[3]University of Pannonia, Georgikon Faculty of Agriculture, Deák F. u. 16., 8360 Keszthely, Hungary

Introduction

Intramuscular fat content, also known as marbling of meat, represents a valuable beef quality trait. Leptin is the hormone product of the obese gene synthesized and secreted predominantly by white adipocytes This protein is supposed to be involved in the regulation of body weight by transmission of a lipostatic signal from adipocytes to the leptin receptor in hypothalamus resulting in appetite suppression and increased thermogenesis (Zang et al., 1994; Ji et al., 1998). The leptin gene has been mapped to bovine chromosome 4 (Stone et al., 1996). Poly-morphisms 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). The objective of this study was to estimate the effect of leptin gene polymorphism on the marbling of meat in a Hungarian Angus population. Since the results for the possible use of the mentioned polymorphism in selection to improve beef quality traits are few in number and rather contradictory, it has been decided to carry out studies in the existing Hungarian Angus population with the aim to provide additional data to this particular subject.

Materials and methods

173 blood samples were collected from randomly selected Red Angus bulls. Leptin genotypes were determined by PCR-RFLP (polymerase chain reaction-restriction fragment length polymorphism) assay. Primer design for the leptin polymorphism (C/T substitution at position 528 according to GeneBank accession no. AB070368) was based on the 5' nuclease assay described by Nkrumah et al. (2004). Bulls were kept and fed in identical conditions. Following slaughter, lipid content of musculus longissimus dorsi (LD) and musculus semitendinosus (ST) were determined gravimetrically by the Soxhlet method. Beef quality trait data were collected and statistical analyses have been carried out to find association between the individual genotypes and intramuscular fat deposition. Dataset was analysed with SPSS 15.0 for Windows software. The effect of the polymorphism was explored by the method of multivariate analysis of variance. Fat deposition capacity of genotype groups has been compared using the method of least squares differences.

Results

Table 1. Frequencies of different genotypes in the leptin locus

locus	genotypes	frequencies	X2	p
Leptin	CC TC TT	56.1% (56.25%) 38.2% (37.5%) 5.8% (6.25%)	0.081	0.960

The expected values are presented in brackets (df=2)

Table 2. Least square means and standard errors, variance, additive effect and dominance for fat content of LD and ST of different genotypes in Angus bulls

locus	genotypes		fat % LD	fat % ST
Leptin n=173	CC (n=97)	LSM±SE	14.43 ± 0.90	8.88 ± 0.51a
	TC (n=66)		14.41 ± 0.95	8.62 ± 0.53a
	TT (n=10)		15.45 ± 1.25	12.52 ± 0.92b
	Variance % #		0	0.1
	additive effect		0.51	1.82 *
	dominance		0.53	2.08 *

a, b: different characters indicate significant ($p<0.05$) difference between genotypes
#percentage of variance due to the studied loci in the total phenotypic variance
* confidence level of the predicted factors ($P<0.05$)

Discussion

The calculated χ^2 values for the leptin genotypes indicated Hardy-Weinberg equilibrium in the population. Differences between the observed and expected genotype frequency values were not significant (Table 1).
TT bulls showed the highest fat percentage values in the *musculus longissimus dorsi (LD)* and *musculus semitendinosus (ST)*. In case of *ST* the difference between CC and TT genotypes was significant ($p<0.05$) (Table 2.). The tendency of correlations of our results in leptin polymorphism correspond to the findings of Nkrumah et al. (2004). Most quantitative traits with high economic relevance are polygenic, therefore may be influenced by other multiple genes as well. Molecular tests provide facilities for the direct selection among variants, however the benefits of different alleles depend on the economic reasons given in the breeding programs.

Acknowledgement

The project was supported by the Hungarian Scientific Research Fund (Project 78174).

References

- Buchanan F.C., Fitzsimmons C.J., Van Kessel A.G., Thue T.D., Winkelman-Sim C. and Schmutz S.M. (2003): Association of a missense mutation in the bovine leptin gene with carcass fat content and leptin mRNA levels. Genet. Sel. Evol. 34, 105-116.
- Ji S., Willis G.M., Scott R.R., Spurlock M.E. (1998): Partial cloning and expression of the bovine leptin gene. Anim. Biotechnol., 9, 1-4.
- Liefers S.C., te Pas M.F.W., Veerkamp R.F. and van der Lende T. (2002): Associations between leptin gene polymorphism and production, liveweight, energy balance, feed intake and fertility in Holstein heifers. J. Dairy Sci., 85, 1633- 1638.
- Nkrumah J.D., Li C., Yu J., Basarab J.A., Guercio S., Meng Y., Murdoch B., Hansen C. and Moore S. S. (2004): Association of a single nucleotide polymorphism in the bovine leptin gene with feed intake, growth, feed efficiency, feeding behavior and carcass merit. J. Anim. Sci., 84, 211-219.
- Stone, R. T., Kappes, S. M., Beattie, C. W., (1996): The bovine homologue of the obese gene maps to chromosome 4. Mamm. Genome, 7, 399-400.
- Zhang Y., Proenca R., Maffei M., Barone M., Leopold L. and Friedman J.M. (1994): Positional cloning of the mouse obesity gene and its human homologue. Nature, 372, 425-432.