EVALUATION OF INTRAMUSCULAR FAT CONTENT IN CATTLE BY MOLECULAR AND IMAGING TECHNIQUES

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Abstract – The objective of this study was to estimate the effect of thyroglobulin (TG) locus on the marbling of meat in Hungarian cattle populations as well as confirmation of the obtained results by digital cross-sectional imaging technique, (X-ray computerised tomography, CT). The carcass fat and ribs joint fat were determined by manual dissection of carcasses and by CT-analysis of ribs joint (11-13th ribs). Genotypes were determined by PCR-RFLP (polymerase chain reaction-restriction fragment length polymorphism) assay, lipid content of *longissimus* muscle (LD) was measured gravimetrically by Soxhlet method and it was evaluated on CT scans, too. Statistical analyses have been carried out to find association between the individual genotypes and fat content. TT animals showed the highest fat percentage values in carcass and LD, difference between genotypes was significant ($p<0.05$). Similar results were obtained by CT technique.

Key Words – Beef cattle, TG, PCR-RFLP, CT

I. INTRODUCTION

Intramuscular fat content, also known as marbling of meat, represents a valuable beef quality trait. The effect of polymorphism in the 5'-untranslated region of TG gene –which product is the precursor of hormones that influence lipid metabolism- has been concluded to affect intramuscular fat content in cattle [1]. TG mainly affects the fat content of LD [2]. TG gene physically maps to the centromeric region of bovine chromosome 14 [3]. Digital cross sectional imaging techniques (X-ray Computerised- and Magnetic Resonance tomography) are perfectly suitable methods for in vivo estimation of body and/or carcass composition in animals after slaughter (without complete dissection) [4]. The objective of this study was to estimate the effect of TG locus on the marbling of meat in Hungarian beef cattle populations. Since use of TG polymorphism in selection to improve beef quality traits is available in Hungary, it has been decided to confirm the obtained results by CT technique as well.

II. MATERIALS AND METHODS

120 bulls of different genotypes (Charolais x Angus crossbred, Hungarian Simmental and Hungarian Holstein), were selected, kept in identical conditions and fed the same diet until reaching the age of 16-18 month. Animals were slaughtered at approximately similar live weight, under commercial conditions using Hungarian standard procedure. Blood samples have been collected during exsanguinations and were stored at -20°C until DNA extraction. Genomic DNA was isolated from whole blood [5]. TG polymorphism was detected by PCR-RFLP assay using the method described by Barendse [1] and TT, TC, or CC genotype determined. Slaughter weight, hot and cold carcass weight and EUROP classification scores were recorded prior to slaughter and on the slaughter line. After 24 hours chilling, right carcasses have been jointed and dissected: lean meat, fat and bone were separated. Rib samples have been taken from LD cut between the 11-13th rib. CT-analysis of rib samples were performed by Siemens Somatom Emotion 6 equipment according to the method described by Holló et al. [6]. Scans were evaluated by MIP image processing software. The intramuscular fat level of LD in the whole ribs joint was evaluated based on standard CT thresholds for fat on Hounsfield scale (interval 0-200). After removing surface fat, lipid content of LD was determined gravimetrically by Soxhlet method, using petroleum ether as solvent.

Dataset was analyzed with the SPSS 15.0 for Windows software. Multivariate analysis of variance (general linear model, GLM) was applied to determine differences in beef characteristics; breed and genotype were included as fixed effects and fat percentage of LD as dependent variable.

III. RESULTS AND DISCUSSION

Least square mean values of carcass fat, ribs joint fat as well as intramuscular fat content of different genotypes obtained by CT examinations and Soxhlet–method are presented in Table 1.

TT animals showed the highest fat percentage values and a decreasing tendency was observed from genotype TT to CC. Contrasting TT genotype vs. TC and CC, the difference proved to be significant.

The presented fat content values for the bulls with different TG genotypes are lower than those obtained by Thaller et al. [2] in German Holstein and Charolais breeds and are moderately lower than our previous results obtained in Hungarian beef cattle [7].

Table 1. Least square means (LSM) and standard errors for fat content of different genotypes in different Hungarian cattle breeds

TG genot. n=120	Fat % in carcass (manual dissection	Fat % ribs joint (%) (CT technique)	IM fat % (Soxhlet-method)	IM fat % (CT technique)
	LSM±SEM			
CC (n=79)	8.37±0.5^a	10.90±0.5^a	2.42±0.2^a	0.98±0.1^a
TC (n=38)	8.76±0.8^a	11.48±0.9^a	2.70±0.4^a	1.03±0.2^a
TT (n=3)	19.4±1.1^b	22.23±1.2^b	8.93±0.9^b	3.05±0.8^b

$^{a-b}$ means with different letters indicate significant differences between genotypes ($p<0.05$)

IV. CONCLUSION

Molecular tests can 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. A possible marker assisted selection (MAS) approach -such as selecting for TT genotypes at the TG locus- might be performed, if higher intramuscular fat content is desirable.

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