THE EFFECT OF INTERACTION BETWEEN PKM2 AND GLUT4 GENOTYPES FOR PORK MEAT QUALITY

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Introduction

The meat quality and its technological usefulness is closely connected with the rate and extend of changes in muscle tissue after slaughter. Pyruvate kinase catalyzes the reversible conversion of phosphoenol pyruvate to pyruvate. It occurs in four isozymic forms M1, M2, L, and R, which express tissue specifically (Immamura *et al.*, 1986). M2 form is placed in the muscle, heart, and brain; and by L and R in hepatocytes and erythrocytes, respectively (Takegawa *et al.*,1984). The M1 and M2 isozymes are produced from a single PK-M gene, located in 7(q12-q23) pig chromosome (Noguchi *et al.*, 1986, Fontanesi *et al.*, 2003).

GLUT4 is an isoform present exclusively in muscle and adipose cells and plays a key role in cellular glucose uptake stimulated by insulin in these cells, and thereby is called insulin responsive GLUT (Abe et al 1997). There is some evidences concerning the effect of GLUT4 gene on some meat quality traits (Grindflek *et al.* 2002).

The aim of this study was to analyse the effect of interaction between PKM2 and GLUT4 genotypes for meat quality traits of stress resistant fatteners.

Materials and Methods

The studies covered 243 pigs, of which 95 were of the Landrace breed, 66 Landrace x Yorkshire and 82 (Landrace x Yorkshire) x Duroc crossbreeds. All animals were free from gene *RYR1*^T. The animals were slaughtered using electric stunner (INARCO line, STORK) and bleeding lying down 2-4 h after transportation, during autumn and winter season. The quality of meat was evaluated after slaughter on the *musculus Longissimus lumborum* (*LL*) (after last rib), on the basis of the following parameters: pH of the muscle tissue measured directly in the LL muscle 35 min, 2h, 3h, 24h, 48h, 96h and 144h and in water homogenate at 45 min *post mortem*, electric conductivity (EC) measured with LF-Star conductometer (Matthaüs) 35 min, 2h, 3h and 24 h *post mortem*, colour lightness (L*, Minolta CR310), rate of ATP breakdown expressed by R₁ = IMP/ATP indicator at 45 min *post mortem* (Honikel & Fischer 1977), water holding capacity (WHC) (Grau-Hamm 1952 as modified by Pohja & Ninivaara 1957), drip loss at 48h, 96h and 144h (Prange *et al.* 1977), technological yield in the curing and thermal processing (TY). The samples cut from the *LL muscle* at 45 min *post mortem* were analysed for the glycolytic potential (GP) and content of glycogen and lactate using enzymatic methods. The GP was calculated according to Monin & Sellier (1985). The chemical composition of muscle tissue was also analysed.

Genotypes of PKM2 gene were identified by the PCR/SSCP method according to Fontanesi *et al.* (2003) and genotypes of GLUT4 gene by PCR/RFLP method according to Grindflek *et al.* (2002). The data were statistically analysed using two-way anova (PKM2, GLUT4).

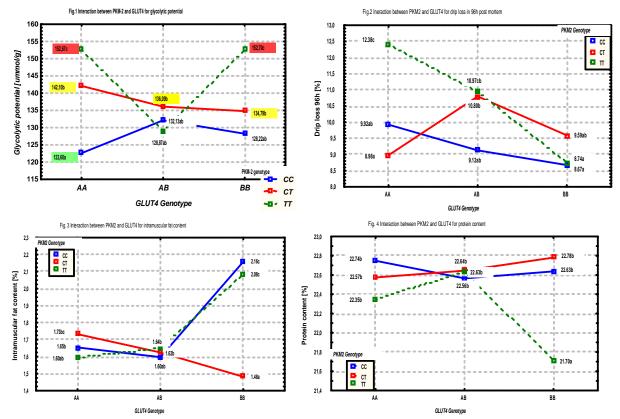
Results and Discussion

The analysis of variance showed that interaction between PKM2 and GLUT4 genotypes was statistically significant ($P \le 0.05$) for glycolytic potential, glycogen level, drip loss at 96 h post mortem and also for intramuscular fat and total protein content.

The GLUT4 gene polymorphism differentiated GP of fatteners being TT homozygotes at PKM2 locus (Fig. 1). It should observed that group of animals with TT/AA and TT/BB genotype at locus PKM2 and GLUT4 respectively had the same GP level, whereas TT/AA group by significant higher drip loss (3,64%), higher total protein content (0,65%) and about 0,5% lower intramuscular fat was characterised in comparison to TT/BB group (Fig. 1-4).

It should be stressed that among TT homozygotes of PKM2 gene animals being simultaneously AB heterozygotes of GLUT4 gene by the lowest GP and relatively high drip loss from LL muscle tissue were characterised.

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Conclusions

The interaction between GLUT4 and PKM2 genotypes indicate on the existing of two groups of fatteners with the same glycolytic potential level but strongly differentiated by drip loss and basic chemical composition of LL muscle.

The obtained interest preliminary results suggest that problem of genetic conditioning the GP variability should be analysed.

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