

THE INFLUENCE OF PRKAG3 GENE ON CARCASS COMPOSITION TRAITS OF STRESS RESISTANT FATTENERS

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Introduction

The detrimental effect of the Rendement Napole (RN) gene on pork meat quality attributes has been demonstrated by a number of researches (Le Roy *et al.*, 1990, 2000, Koćwin-Podsiadła 1995). The RN⁻ allele is also known to positively influence the lean meat content, backfat thickness and the weight of lean meat joints (Enfalt *et al.*, 1997, Le Roy *et al.*, 2000, Hamilton *et al.*, 2003). Previously, the phenotype of RN gene was estimated on the basis of Napole yield, then *in vivo* or *post mortem* measurements of muscle glycolytic potential (GP) (Fernandez *et al.*, 1990, Le Roy *et al.*, 1994, Lundstrom *et al.*, 1996). Milan *et al.*, (2000) identified the dominant RN⁻ mutation in the PRKAG3 gene. The objective of this experiment was assessment of the impact of PRKAG3 gene on carcass composition of stress resistant fatteners.

Materials and Methods

The investigations covered 384 stress resistant fatteners [Landrace-79, Landrace x Duroc – 125, Landrace x Yorkshire – 67, (Landrace x Yorkshire)x Duroc – 83, (Landrace x Yorkshire)x(Duroc x Pietrain)-30]. The animals were kept under the same environmental conditions and fed a full bath feed. The animals were slaughtered at approximately 110kg body weight 2-4 hours after transportation using electrical stunning method and recumbent bleeding out. Measurements of pork meatiness and its components were made using Danish apparatus ULTRA-FOM 100 produced by SFK Technology. The estimation of carcass composition was performed in accordance with methodology using in Polish Pig Testing Stations (Różycki 1996). All data concerning carcass composition traits were standardised on 85 kg of hot carcass weight. The RYR1 genotypes were established according to Fujii *et al.*, (1991). At 45 minutes *post mortem*, samples from LL muscle were collected in tubes with 0.5M PCA for subsequent determination of glycolytic potential (GP) according to formula proposed by Monin and Sellier (1985). The polymorphism of PRKAG3 gene was identified according to Milan *et al.*, (2000). The data were analysed using one-way analysis of variance in non-orthogonal scheme. The significance of differences between means was calculated using Duncan's test.

Results and Discussion

The analysis of variance demonstrated the influence of PRKAG3 gene only on the following carcass composition traits: backfat thickness measured over *Gluteus medius* muscle in 3 points (I-st, II-nd and III-rd cross), average backfat thickness, *Longissimus dorsi* muscle weight and belly weight (Table 1).

No statistically confirmed differences between AA and GG animals (RN⁻/RN⁻ and rn⁺/rn⁺) for analysed carcass composition traits was found in the present study. AG (RN⁻/rn⁺) animals compared with homozygous AA and GG fatteners (RN⁻/RN⁻ and rn⁺/rn⁺ respectively), had a thicker backfat measured over *Gluteus medius* muscle and average backfat. Differences were confirmed statistically between AA and AG genotypes (Table 1). Moeller *et al.*, (2003) showed that PRKAG3 gene had no effect on backfat thickness with the exception of last lumbar backfat depth. Other studies have reported, that the RN⁻ phenotype is associated with leaner carcasses and a decrease of backfat thickness (Le Roy *et al.*, 1996, 2000; Enfalt *et al.*, 1997; Hamilton *et al.*, 2003).

It was confirmed statistically that heterozygous AG (RN⁻/rn⁺) fatteners compared with homozygous AA and GG fatteners (RN⁻/RN⁻ and rn⁺/rn⁺ respectively), had the significantly lowest *Longissimus dorsi* muscle weight and highest belly weight (Table 1). In contrast, Le Roy *et al.*, (2000) reported significant increase in the weight of lean joints (ham and loin) and a decrease in belly weight in RN⁻ allele (RN⁻/rn⁺) carriers identified by GP distribution. Olsson *et al.*, (2003) also identified the RN⁻ phenotype on the basis of GP distribution, and a higher percentage share of *Longissimus dorsi* muscle in carriers of RN⁻ allele (RN⁻/rn⁺).

The diverging results relating to the PRKAG3 gene on carcass composition traits were probably due to animals with high glycolytic potential who have been identified by PCR-RFLP DNA test as GG (rn⁺/rn⁺) animals.

Table 1: Means and their standard deviations for carcass composition traits from different PRKAG3 genotypes.

Trait	PRKAG3			Average n=384	F-emp. p-value
	AA RN/RN ⁻ n=6	AG RN/rn ⁺ n=27	GG rn ⁺ /rn ⁺ n=351		
Lean meat content (%)	56,05 ±2,49	55,53 ±4,33	55,99 ±4,05	55,96 ±4,05	0,192 0,826
Backfat thickness over <i>gluteus medius</i> muscle (cm):					
I cross	1,61A ±0,24	2,18B ±0,40	1,91A ±0,37	1,93 ±0,38	9,498 0,000
II cross	1,25a ±0,19	1,55b ±0,36	1,41ab ±0,33	1,42 ±0,33	3,433 0,033
III cross	2,01A ±0,31	2,50B ±0,49	2,27AB ±0,43	2,28 ±0,44	5,172 0,006
Average backfat thickness (cm)	1,82A ±0,19	2,18B ±0,32	2,06AB ±0,28	2,03 ±0,29	6,414 0,002
<i>Longissimus dorsi</i> muscle weight (kg)	3,13B ±0,25	2,73A ±0,30	2,94AB ±0,33	2,92 ±0,33	6,562 0,002
Belly weight (kg)	6,28A ±0,57	7,07B ±0,75	6,56A ±0,58	6,60 ±0,61	10,693 0,000

Means marked different letters A, B differ statistically at $p \leq 0.01$; a, b differ statistically at $p \leq 0.05$

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