

THE EFFECT OF STRESS-SENSIBILITIES PIETRAIN BOARS ON CARCASS VALUES OF FINAL HYBRID PIGS

Čechová M., Hadaš Z, Sládek L.

Mendel University of Agriculture and Forestry, Brno, Czech Republic

Abstract

The aim of our study was to quantify the influence of the fathers' genotype in *RYRI* gene on the carcass of pigs. A total of 597 market pigs originating from crossbreeds (Czech Large White x Czech Landrace) x Pietrain, fattened under common conditions of large-capacity pig farm were slaughtered, weighted, measured and evaluated by FOM appliance. The slaughtered pigs were classified into groups of homozygous dominant genotype, heterozygous genotype and homozygous recessive genotype according to the father's genotype. The heaviest carcass and the highest muscling reached the pigs with *nn* genotype which had the thinnest layer of meat at the same time. The highest fat thickness and carcass length reached pigs with heterozygous genotype and the lowest value of pH₁. The differences between these qualitative characteristics were statistically significant among the groups. The obtained results suggest the possibility of using a suitable genotype of *RYRI* gene to produce high quality commercial pigs.

Key Words: Pig, Pietrain, *RYRI*, sex, carcass, meat quality

Prerequisite of a successful production of market pigs is a proper selection of the most suitable combination of commercial breeding as the quality of final hybrid pigs depends on the quality of the basic breeds entering the hybridization process. Hybridization programme should always use the advantages of individual breeds. One of the breeds used in C position in the hybridization programme is the Pietrain breed either in the form of purebred or hybrid boars. Nowadays the breeders have a possibility to choose individuals with intended genotype of *RYRI* gene. The use of Pietrain boars in hybridization programme and especially the effect of the genotype of *RYRI* gene on the quality of final hybrid pigs was studied by Fisher et al. (2000), Kortz et al. (2003), and Aziz (2004). However, the conclusions of the above authors are ambiguous.

Material and Methods

The experiment included 597 fattening pigs from hybridization (Czech Large White x Czech Landrace) x Pietrain. A total of 9 boars with the intended genotype of *RYRI* gene were mated, 3 of each genotype (*NN*, *Nn*, *nn*). Of the boars with *NN*, *Nn*, and *nn* 226, 220, and 151 progeny were assessed, respectively. Based on the mating plan and a subsequent marking of piglets, a precise origin of the progeny could be determined. The pigs were fattened at the same time under the conditions of a large-capacity pig farm and were fed the same feed compound.

After slaughtering, the carcasses were weighted and measurement and evaluations were carried out using the instrument FOM (FAT – O – MEAT'er SFK – Technology DK 2730 Herlen, Denmark) at which the percentage proportion of muscles in carcass weight (meatiness) had been determined.

The equation according to Pulkrábek et al. (2005) has been used for meatiness calculation. The assessment included also determination of meat and fat thickness. Further, the measurement of trunk length has been carried out as well as pH₁ measurement. Measurements and assessments were carried out in accordance with the Regulation 194/2004 Coll.

Results and Discussion

Basic statistical characteristics of selected traits of market value in individual groups according to *RYRI* genotype are shown in Table 1.

The highest meatiness was reported in pigs from boars with recessive homozygote genotype (56.8 %). In contrast, the lowest meatiness was found in the progeny from boars with heterozygote genotype, which was by 1.97 % lower compared to *nn*, and by 1.8 % lower compared to *NN*. The difference in the meatiness obtained between the groups *NN* : *Nn* and *Nn* : *nn* is highly significant ($p \leq 0.001$) but no significant difference was found between the groups *NN* : *nn* ($p \leq 0.05$). The same conclusions were recorded by Fisher et al. (2000) with the only difference that the lowest meatiness was found in animals with homozygote dominant genotype by 0.88 % lower compared to those with heterozygote genotype, and by 3.26 % lower compared to animals with recessive homozygote genotype. These results are in accordance with the data by Zhanga et al. (1992) stating that recessive allele (*n*) increases the meatiness of the carcass half but also with the statement of Azize (2004) that stress-susceptible animals produce more meatiness in carcass weight.

As far as the carcass length is concerned, the longest carcass was observed in animals from boars with heterozygous genotype (81.72 cm), and the shortest carcass was found in pigs from boars with dominant homozygous genotype (80.42 cm). The group of pigs from boars with recessive homozygous genotype reached the length of 80.65 cm. Very highly statistically significant difference was found between the group $NN : Nn$ and highly statistically significant between the group $Nn : nn$. The results are in agreement with Fisher et al. (2000), when the longest carcass was found in animals with the genotype Nn and the shortest in animals with the genotype NN ; the differences being statistically significant. However, the results do not correspond with the results of Leach et al. (1996) who did not find any difference between the group NN and Nn . The results are not in accordance with the findings of Zhanga et al. (1992) either, that the recessive allele decreases the length of carcass.

The highest carcass weight was found in the group of market hybrids from the boars with homozygote recessive genotype (nn) compared to groups with heterozygote genotype Nn (0.47 %) and homozygote dominant genotype NN (3.75 %).

Highly significant difference ($p \leq 0.01$) was found between the groups $NN : Nn$ and $NN : nn$. Similar results

were obtained by Leach et al.(1996) when the highest carcass weight was found in the group of nn genotype compared to NN and Nn genotypes, with statistically significant difference ($p \leq 0,05$). Kortz et al. (2003) reported that the highest carcass weight was obtained in individuals with heterozygote genotype (80.7 kg), and the lowest weight was recorded in animals with homozygote recessive genotype (79.07 kg).

Evaluation of fat thickness showed the lowest values in the group of progeny from boars with recessive homozygous genotype (15 mm), but surprisingly enough the same value for the group of progeny from boars with dominant homozygous genotype. The highest value of fat thickness was found in animals from boars with heterozygous genotype (17 mm). Highly significant differences in fat thickness were found between the groups $NN : Nn$ and $Nn : nn$. These results are not in accordance with the data obtained by Fisher et al. (2000) when the highest fat thickness was reported in animals with genotype NN (17.4 mm) compared to those with genotype nn (16.4 mm); the difference being significant. The lowest fat thickness in recessive homozygous genotypes is also reported by Monin et al. (1999).

Table 1. Basic statistical characteristics of selected traits of market value in individual groups according to RYR1 genotype

Trait	Genotype	Mean	St.d.	Min.	Max.	t - test
Meatness (%)	NN	56.7	2.76	47.6	61.9	a) +++
	Nn	55.7	3.05	46.7	61.1	b) -
	nn	56.8	2.40	47.7	62.3	c) +++
Carcass length (cm)	NN	80.42	3.45	70.0	89.0	a) +++
	Nn	81.72	3.95	70.0	91.0	b) -
	nn	80.65	3.75	71.0	89.0	c) ++
Carcass weight (kg)	NN	82.7	9.76	60.1	112.7	a) ++
	Nn	85.4	11.18	60.1	116.4	b) ++
	nn	85.8	9.71	65.1	119.7	c) -
Fat thickness (mm)	NN	15.0	3.94	8.0	26.0	a) +++
	Nn	17.0	4.24	9.0	30.0	b) -
	nn	15.0	3.05	98.0	28.0	c) +++
pH1	NN	6.30	0.27	5.72	6.94	a) +++
	Nn	6.22	0.26	5.31	6.93	b) -
	nn	6.30	0.30	5.60	6.90	c) ++

a) $NN : Nn$ b) $NN : nn$ c) $Nn : nn$

$p \leq 0.05$, $p \leq 0.01$, $p \leq 0.001$

Of meat qualitative characteristics, the differences among pH1 values have been assessed. Surprisingly, the same values were found in animals with both dominant and recessive homozygous genotype (6.30); the lowest values being found in animals with heterozygous genotype (6.22). Very highly statistically significant difference was found between *NN* and *Nn* genotypes, and highly significant difference between *Nn* and *nn*. These results are not in agreement with the findings of Fisher et al. (1996), Monin et al. (1999), and Kortz et al. (2003) who reported that the highest pH1 value could be found in animals with *NN* genotype, and the lowest values in those with *nn* genotype. Although low pH1 is not apparent from the mean values, the minimum values reveal that the groups *Nn* and *nn* contain pale, soft, exudative pork (PSE) which is according to Kovářová et al. (2006) characterized by pH1 \leq 5.6, and pork inclining to PSE is characterized by pH1 5.6 – 5.8.

In the group of recessive homozygous genotype, 0.7 % of pork with PSE traits, and 7.28 % of pork inclining to PSE were observed. In the group of heterozygous genotype, the corresponding values were 0.91 % and 4.55 %, respectively. In the group of dominant homozygous genotype, 2.65 % of pork inclining to PSE was found.

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