

## **Meat content and carcass composition as related to sex and *RYR1* genotype in pigs from six genetic groups\***

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**In fatteners of six genetic groups the slaughter traits were studied based on carcass weight standardized to 85 kg hot weight. The highest mean lean meat content of carcass was found in fatteners from Line 890 – 59.18%, followed by [(L×Y)×D] – 57.08, [(L×Y)×(D×P)] – 56.73, L×Y - 56.57%, L – 56.18 and L×D – 56.00%. The effect was confirmed of genetic group and sex on lean meat content of carcass and related traits. Significant effects of interaction between genetic group and sex were noted for: weight of loin, weight of belly and weight of ham without external fat and skin, backfat thickness over shoulder and over back, and on sacrum point I. No CC genotype at the *RYR1* locus was noted among fatteners with highest lean meat content (Line 890).**

**KEY WORDS:** carcass / meat content / pigs / *RYR1* gene

Over the last years one may observe an intensive selection in pedigree herds of pigs towards improved slaughter traits. This tendency arises from the market's demand for porkers with a thin backfat and high muscle deposition. One of the methods of improving

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the muscle deposition in porkers from mass population is the introduction into commercial crossing of pig breeds known for a high growth rate and satisfactory slaughter properties. On the other hand, numerous authors indicate that improving the meat deposition in pigs is connected with the risk of decreasing meat quality [Grześkowiak 1995, 1996, Orzechowska 1997, Pospiech *et al.* 1998, Koćwin-Podsiadła *et al.* 1999, Daszkiewicz and Wajda 2002]. However, as obviously not all breeds (including those imported) contribute to a decrease of pork quality [Różycki 1998], it is necessary to select the parental material for crossing in such a way as to eliminate the possible pork defects.

The present study aimed at comparing porkers of selected genetic groups as regards the muscle deposition and morphological composition of carcasses with reference to sex and the presence of gene *RYRI*<sup>T</sup>.

### Material and methods

The material consisted of 486 porkers of six genetic groups (m – castrated males, f – females):

Landrace: L – 51 m, 44 f;

Landrace × Duroc: L×D – 69 m, 65 f;

Landrace × Yorkshire: L×Y – 34 m, 34 f;

[(Landrace × Yorkshire) × Duroc]: [(L×Y)×D] – 50 m, 34 f;

[(Landrace × Yorkshire) × (Duroc × Pietrain)]: [(L×Y)×(D×P)] – 28 m, 22 f;

Line 890\* (Line 990 × Pietrain): 25 m, 30 f.

The animals (with the exception of Line 890) came from the Jagodne farm, while the parental generation was imported from Denmark. Porkers of Line 890 were obtained from the Experimental Farm, Pawłowice, and were maintained at the Experimental Animal Nutrition Farm, Gorzyń. The material examined was comparable as regards slaughter conditions and post-slaughter treatment. The animals were slaughtered (after 2-4 h rest) at the meat plant Sokołów Podlaski, electrically stunned (250V, 2.5 s.) and bled in a laying position.

The evaluation of the muscle deposition and basic carcass quality traits was performed according to the method used at Polish Pig Testing Stations [Różycki 1996]. The slaughter value traits were analyzed after standardization to 85 kg of hot carcass weight.

The animals' genotype, as regards the presence of gene *RYRI*, was identified according to the PCR/RFLP method, after Kurył and Korwin-Kossakowska [1993]. Blood for the DNA analyses was obtained during slaughter.

The results were elaborated using a two-factor analysis of variance in a non-orthogonal arrangement and on the basis of the following model:

$$Y_{ij} = \mu + a_i + b_j + (ab)_{ij} + e_{ij}$$

where:

- $Y_{ij}$  – vector of the trait analyzed;
- $\mu$  – overall mean;
- $a_i$  – effect of genetic group;
- $b_j$  – effect of sex;
- $(ab)_{ij}$  – interaction genetic group  $\times$  sex;
- $e_{ij}$  – random error.

The mean values were compared by the NIR test, using STATISTICA PL 5.0.

### Results and discussion

Among the L, L $\times$ Y, L $\times$ D and [(L $\times$ Y) $\times$ D] porkers, there were found no animals bearing the gene *RYRI<sup>T</sup>*. In [(L $\times$ Y) $\times$ (D $\times$ P)] porkers found were 31 homozygotes free of this gene (62% of the total number of animals tested) and 17 heterozygotes (38%). In the Line 890 heterozygous were 38 (69%) and homozygous (stress-susceptible) 17 (31%) of pigs.

The analysis of variance conducted demonstrated a significant ( $P \leq 0.001$  and  $P \leq 0.01$ ) effect of both the genetic group and sex on the meat content of carcass and on most of the morphological composition traits analyzed (Tab. 1). Neither the genetic group nor sex showed a significant effect on loin eye area. An effect of interaction genetic group  $\times$  sex was also observed on weight of ham without fat and skin, and backfat thickness over the shoulder, over the last rib and on the back at sacrum point I.

The analyzed population of pigs showed a mean meat per cent of carcass amounting to  $56.75 \pm 2.59$ . This result, about 6 per cent points higher than the mean for the mass pig population in Poland, is comparable with the meat deposition observed in the EU member states [Lisiak and Borzuta 2003]. The mean meat content of pig carcasses in the EU in 2002 ranged from 56% in Finland and The Netherlands to about 60% in Belgium and Denmark [Koćwin-Podsiadła *et al.* 2003].

The meat content of carcass observed in the present study for Line 890 porkers (59.18%) was higher than that recorded for [(L $\times$ Y) $\times$ D] – 57.08%, [(L $\times$ Y) $\times$ (D $\times$ P)] – 56.73%, L $\times$ Y – 56.57%, L – 56.18%, and L $\times$ D – 56.00%. One should emphasize that in the Line 890 pigs, *i.e.* those showing the highest meat content of carcass there were no animals free from the stress susceptibility gene – *RYRI<sup>T</sup>*. The results cited by Koćwin-Podsiadła *et al.* [1993], Sellier and Monin [1994] and Sellier [1998] indicate that the carcasses of *RYRI<sup>T</sup>RYRI<sup>T</sup>* homozygotes contain 2-5% more meat than carcasses of homozygotes *RYRI<sup>C</sup>RYRI<sup>C</sup>*. Moreover, Line 890 porkers, compared with the remaining genetic groups, showed a significantly higher weight of meat in primary cuts, weight of ham without skin and fat and a lower fat thickness expressed as a mean of five measurements. Also the mean values of linear measurements of fat thickness showed the lowest carcass adiposity in Line 890. The high meat content of carcass in

Table 1. Means and their standard deviations (SD) for morphometric and composition of various ungulate groups and mean of sections

Time	Cervus elaphus										Total (mean±SD)	Cervus group % n=3
	L					S						
	Length (mm)	L3-0 (mm)	L2-0 (mm)	L1-0 (mm)	L0-0 (mm)	Line length (mm)	Weight (g)	Volume (mm <sup>3</sup> )	Area (mm <sup>2</sup> )	Perim. (mm)		
Lawrenceans (n=6)	36.10 <sup>a</sup> ±1.31	36.00 <sup>a</sup> ±1.31	36.57 <sup>a</sup> ±1.31	37.00 <sup>a</sup> ±1.31	37.00 <sup>a</sup> ±1.31	39.10 <sup>a</sup> ±1.31	15.00 <sup>a</sup> ±1.31	36.11 <sup>a</sup> ±1.31	37.00 <sup>a</sup> ±1.31	37.00 <sup>a</sup> ±1.31	36.75 <sup>a</sup> ±1.31	0.15
Weight of Prounce period summit	37.15 <sup>a</sup> ±0.10	37.15 <sup>a</sup> ±0.10	37.15 <sup>a</sup> ±0.10	37.15 <sup>a</sup> ±0.10	37.15 <sup>a</sup> ±0.10	37.15 <sup>a</sup> ±0.10	19.70 <sup>a</sup> ±0.10	37.16 <sup>a</sup> ±0.10	37.17 <sup>a</sup> ±0.10	37.17 <sup>a</sup> ±0.10	37.09 <sup>a</sup> ±0.10	1.16
Weight of Prounce alluvial flint	6.10 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	6.08 <sup>a</sup> ±0.51	1.11
Weight of Prounce alluvial flint	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	8.51 <sup>a</sup> ±0.51	1.34
Weight of body (kg)	6.90 <sup>a</sup> ±0.61	6.57 <sup>a</sup> ±0.57	6.17 <sup>a</sup> ±0.57	6.17 <sup>a</sup> ±0.57	6.17 <sup>a</sup> ±0.57	6.17 <sup>a</sup> ±0.57	18.57 <sup>a</sup> ±0.57	6.57 <sup>a</sup> ±0.57	6.17 <sup>a</sup> ±0.57	6.17 <sup>a</sup> ±0.57	6.09 <sup>a</sup> ±0.57	1.67
Body fluctuation over alluvial (kg)	7.00 <sup>a</sup> ±0.21	7.10 <sup>a</sup> ±0.21	7.20 <sup>a</sup> ±0.21	7.30 <sup>a</sup> ±0.21	7.40 <sup>a</sup> ±0.21	7.50 <sup>a</sup> ±0.21	10.00 <sup>a</sup> ±0.21	7.10 <sup>a</sup> ±0.21	7.20 <sup>a</sup> ±0.21	7.30 <sup>a</sup> ±0.21	7.00 <sup>a</sup> ±0.21	8.09
Body fluctuation on hill (kg)	7.10 <sup>a</sup> ±0.31	7.20 <sup>a</sup> ±0.31	7.30 <sup>a</sup> ±0.31	7.40 <sup>a</sup> ±0.31	7.50 <sup>a</sup> ±0.31	7.60 <sup>a</sup> ±0.31	10.00 <sup>a</sup> ±0.31	7.20 <sup>a</sup> ±0.31	7.30 <sup>a</sup> ±0.31	7.40 <sup>a</sup> ±0.31	7.10 <sup>a</sup> ±0.31	3.3
Body fluctuation on L. level (kg)	7.20 <sup>a</sup> ±0.41	7.30 <sup>a</sup> ±0.41	7.40 <sup>a</sup> ±0.41	7.50 <sup>a</sup> ±0.41	7.60 <sup>a</sup> ±0.41	7.70 <sup>a</sup> ±0.41	10.00 <sup>a</sup> ±0.41	7.30 <sup>a</sup> ±0.41	7.40 <sup>a</sup> ±0.41	7.50 <sup>a</sup> ±0.41	7.20 <sup>a</sup> ±0.41	5.56
Body fluctuation on H. level (kg)	7.30 <sup>a</sup> ±0.51	7.40 <sup>a</sup> ±0.51	7.50 <sup>a</sup> ±0.51	7.60 <sup>a</sup> ±0.51	7.70 <sup>a</sup> ±0.51	7.80 <sup>a</sup> ±0.51	10.00 <sup>a</sup> ±0.51	7.40 <sup>a</sup> ±0.51	7.50 <sup>a</sup> ±0.51	7.60 <sup>a</sup> ±0.51	7.30 <sup>a</sup> ±0.51	3.3
Body fluctuation on H. level (kg)	7.40 <sup>a</sup> ±0.61	7.50 <sup>a</sup> ±0.61	7.60 <sup>a</sup> ±0.61	7.70 <sup>a</sup> ±0.61	7.80 <sup>a</sup> ±0.61	7.90 <sup>a</sup> ±0.61	10.00 <sup>a</sup> ±0.61	7.50 <sup>a</sup> ±0.61	7.60 <sup>a</sup> ±0.61	7.70 <sup>a</sup> ±0.61	7.40 <sup>a</sup> ±0.61	1.04
Body fluctuation on H. level (kg)	7.50 <sup>a</sup> ±0.71	7.60 <sup>a</sup> ±0.71	7.70 <sup>a</sup> ±0.71	7.80 <sup>a</sup> ±0.71	7.90 <sup>a</sup> ±0.71	8.00 <sup>a</sup> ±0.71	10.00 <sup>a</sup> ±0.71	7.60 <sup>a</sup> ±0.71	7.70 <sup>a</sup> ±0.71	7.80 <sup>a</sup> ±0.71	7.50 <sup>a</sup> ±0.71	0.8
Average body fluctuation Prounce summit (kg)	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	7.00 <sup>a</sup> ±0.16	1.07
Lawrenceans (n=6)	53.51 <sup>a</sup> ±5.16	50.91 <sup>a</sup> ±5.16	53.66 <sup>a</sup> ±5.16	53.50 <sup>a</sup> ±5.16	53.50 <sup>a</sup> ±5.16	53.50 <sup>a</sup> ±5.16	53.50 <sup>a</sup> ±5.16	53.50 <sup>a</sup> ±5.16	53.50 <sup>a</sup> ±5.16	53.50 <sup>a</sup> ±5.16	53.09 <sup>a</sup> ±5.16	1.71
Weight length of cervus kg (kg)	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	8.15 <sup>a</sup> ±1.94	1.11

SD - non significant; \*\* - different significance; P < 0.01  
Values are given by regional factor of the significance is P < 0.01

porkers of Line 890 arises from the high muscle deposition in ham and not from the loin weight, as shown by the smallest length of the middle part of the carcass recorded in this group of animals. Blicharski and Ostrowski [1999], examining the carcass quality of Polish Large White, (PLW), Pietrain, and PLW × Pietrain porkers observed the highest meat content of carcass and the best ham filling (expressed as the share of meat in ham) in purebred Pietrain porkers. However, one must remember that although crossing with Pietrain boars leads to a significant improvement of the slaughter value of the progeny it creates a risk of a decrease in the meat quality, due to the exceptional susceptibility of this breed to stress.

In the present study a high meat content carcass resulting from the share of the most valuable cut (loin), was observed also for crossbreeds with a 50% share of the Duroc breed – [(L×Y)×D], which constitute the final product of commercial crossing. One should emphasize that 100% of [(L×Y)×D] porkers appeared free of the RYR1<sup>T</sup> gene, which has a detrimental effect on meat quality.

A significant effect of sex was observed on the meat content of carcass, weight of meat in primary cuts, weight of belly and ham without fat and skin and all the linear measurements of fat thickness. The gilts were characterized by a higher meat deposition and better indicators of carcass quality than castrates. Moreover, as could be expected, the gilts showed a smaller carcass adiposity as indicated by the weight of belly and fat thickness measurements. These results, referring to the higher muscle deposition and lower adiposity of carcasses from gilts as compared to castrates, confirm those published earlier by van der Wal *et al.* [1993], Larzul *et al.* [1997], Candek-Potokar *et al.* [2000] and Latore *et al.* [2004].

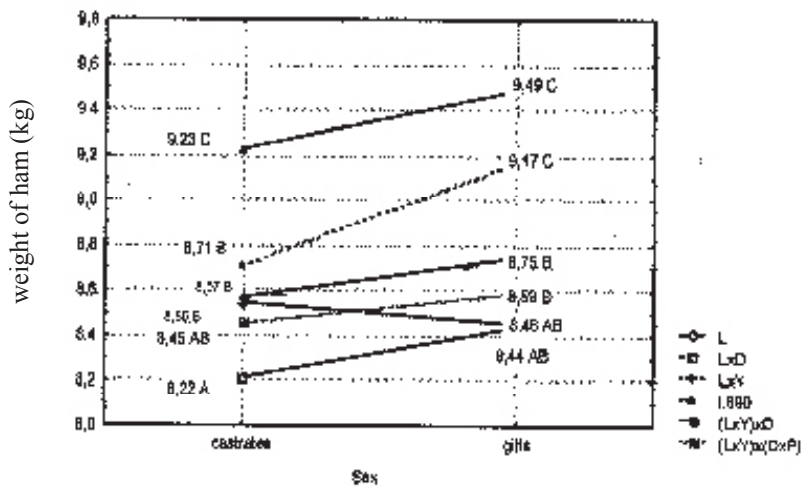


Fig. 1. Interactive effect of genetic group and sex for weight of ham without skin and fat.

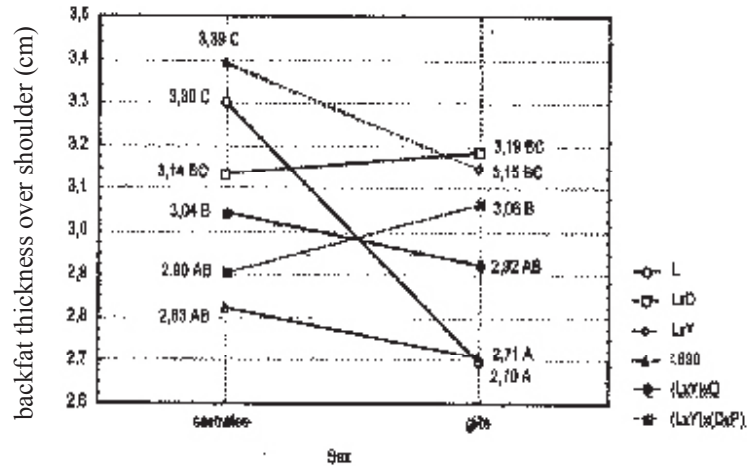


Fig. 2. Interactive effect of genetic group and sex for backfat thickness over shoulder.

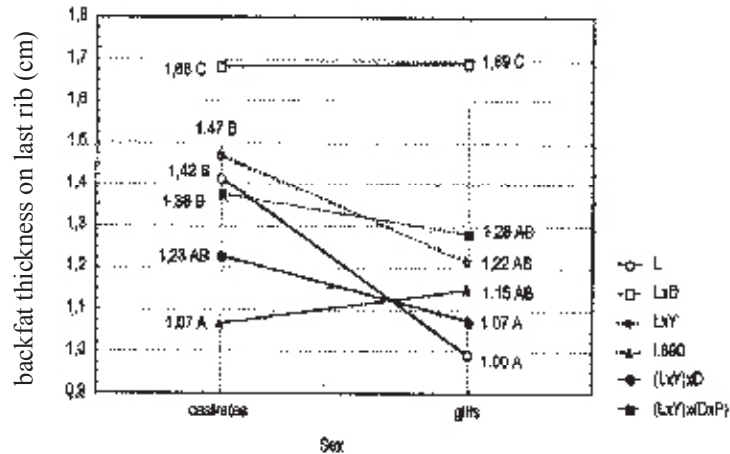


Fig. 3. Interactive effect of genetic group and sex for backfat thickness at last rib.

In the present work an effect of interaction genetic group x sex was observed on the weight of ham without fat and skin as well as fat thickness over shoulder, over the last rib and backfat thickness on sacrum point I (Tab. 1, Fig. 1-4).

Gilts from both Line 890 and LxY, as well as Line 890 castrated males, showed significantly higher (by about 1 kg) weight of ham without fat and skin (Fig. 1) than in remaining genetic groups.

The L pigs differed between sexes in the backfat thickness over the shoulder, at the

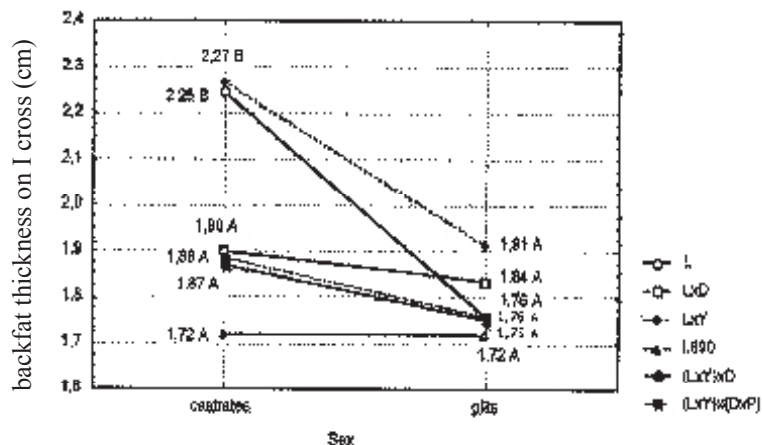


Fig. 4. Interactive effect of genetic group and sex for backfat thickness on sacrum I.

last rib and on sacrum point I, retaining however a correct tendency. L gilts showed a significantly lower adiposity than castrates (Fig. 2, 3 and 4). The LxD porkers (sexes pooled) differed clearly from the remaining groups in the backfat thickness measured at the last rib (Fig. 3). In the case of backfat thickness on sacrum point I differences between castrates and gilts were recorded in favour of the latter, similarly as in the L and LxY animals (0.49 and 0.36 cm, respectively) – Figure 4.

Summarizing, the results presented here show that the use of genetic pig groups imported from Denmark for crossing in commercial porker production in Poland is fully justified, as those animals demonstrate a high meat content of carcass (from 56 to 57.08%) and a high meat quality, confirmed by the absence of animals burdened by the stress susceptibility gene.

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## Mięsność i skład tuszy tuczników sześciu grup genetycznych w zależności od płci i obciążenia genem *RYR1<sup>T</sup>*

### Streszczenie

Celem pracy było określenie różnic zachodzących pod względem mięsności i składu morfologicznego tusz między tucznikami sześciu grup genetycznych, z uwzględnieniem płci i obciążenia genem *RYR1<sup>T</sup>*.

Cechy użytkowości analizowano na danych standaryzowanych na masę tuszy cieplej 85kg.

Największą mięsnością odznaczały się tuczniki linii 890 – 59,18%, wobec [(L×Y)×D] – 57,08%, [(L×Y)×(D×P)] – 56,73%, L×Y – 56,57%, Landrace – 56,18% oraz L×D – 56,00%. Potwierdzono istotny wpływ grupy genetycznej i płci na zawartość mięsa w tuszy i cech ją określających. Współdziałanie grupy genetycznej i płci odnotowano dla masy poledwicy, masy boczku, masy szynki zadniej bez słoniny i skóry, grubości słoniny nad łopatką i na grzbiecie oraz grubości słoniny na wysokości I krzyża.

W grupie o najwyższej mięsności (linia 890) nie stwierdzono zwierząt wolnych od genu wrażliwości na stres.

