THE EFFECT OF RYR1 GENOTYPE IN TERMINAL BOARS ON CARCASS VALUE OF HYBRID PIGS SLAUGHTERED AT DIFFERENT SLAUGHTER WEIGHTS

Trčka P.[1], Čechová M.[2], Hadaš Z.[2], Sládek L.[2], Václavková E.[3]

[1]Food Market Control Department, Ministry of Agriculture of the Czech Republic,Praha
[2]Mendel University in Brno, Czech Republic
[3]VÚŽV Uhříněves, Czech Republic

Abstract

A total of 596 hybrid pigs, crossbreeds (Czech Large White x Czech Landrace) x Pietrain from production testing were used in our study. Stress negative (NN) sows F1 and 9 different Pietrain boars with even proportion of RYR1 genotype (3x NN, 3x Nn, 3x nn) were included in the experiment. After slaughtering, the carcasses were divided into 4 weight groups with 10-kg intervals from 65 to 105 kg. The effect of genotype of RYR1 gene in boars on the thickness of back fat, meatiness and length of carcass has been demonstrated based on variance analysis. Back fat was deepest in all weight groups in the progeny of boars with heterozygote genotype. In contrast, the lowest values were obtained in the progeny of boars with recessive homozygote genotype (nn) ($P < 0.001$). The lowest values of meatiness were recorded in the progeny of boars with genotype Nn compared to the progeny of boars with genotype nn, the difference being statistically significant ($P < 0.001$). No significant difference was found in meatiness between the progeny of NN and nn boars. The highest values of the carcass length were found in all groups in the progeny of boars with heterozygote genotype (Nn). The differences in this parameter between this genotype and the other two (NN and nn) were significant.

Key Words: pig, Pietrain, RYR1, carcass value

Nowadays an intensive pig breeding results in a substantial increase of performance in purebred pigs. This is largely due to the use of modern methods of breeding performance prediction (BLUP-AM) but also due to the use of molecular genetic methods by which the genotype of individual animals can be determined more accurately. Subsequently, targeted employment of breeding animals with proper performance and determined genotype at certain level of the hybridization programme can be implemented.

This is being currently used in ryanodine receptor (RYR1) gene determined by the PCR-RFLP method. Mutation of RYR1 gene and its association with the syndrome of malignant hyperthermia was described by (Fujii et al. 1991). This genotype has been determined in all breeding animals included in the hybridization programme in maternal position, and dominant homozygote animals, i.e. those with NN genotype have exclusively been used in order to minimize the occurrence of quality variation PSE. This gene has also been identified in boars of parental breeds in which problems with the occurrence of the porcine stress syndrome (PSS) has been observed such as the Pietrain breed. Thus the offer of boars with a defined genotype has been enlarged and breeders can choose animals with stress negative genotype NN, Nn or stress positive genotype nn. As stated in previous papers (Fisher et al. 2000, Gispert et al. 2000, Fábrega et al. 2004), worse meat quality and higher occurrence of quality variation PSE was observed in slaughter pigs with n allele. Nevertheless, the effect of the above gene on the carcass value of pigs has not been as much studied as the effect on meat quality. The latter problem has been studied by Oliver et al. (1993) who reported that halothane positive animals had lower thickness of back fat and more lean meat in carcasses. The development of PCR-RFLP methods enabled easy assessment of carcass value for individual genotypes. Stadler et al. (2007) mentioned that the highest meatiness was obtained in animals with nn genotype and the lowest meatiness was obtained in animals with NN genotype. Animals with heterozygote genotype usually obtain mean values of meatiness. Simpson et al. (1989) reported that animals with nn genotype had shorter carcasses compared with the other two genotypes. In contrast, animals with NN genotype had the longest carcasses.

The objective of this study is to assess the effect of RYR1 genotype of Pietrain boars, used for the production of final slaughter hybrids, on the carcass value of their progeny slaughtered at different weight.

Materials and Methods

Experimental animals

The experiment included 596 fattening pigs of hybrid combination (Czech large White x Czech Landrace) x Pietrain. A total of 9 boars, 3 of each genotype of the RYR1 gene (NN, Nn, nn) were used in the experiment.

Porcine genotype was determined by DNA analysis of the following method described by (Otsu et al. 1992). Slaughter pigs were divided into three groups based on boars' genotype. F1 sows were used to form all groups in which the genotype NN is expected based on breeding practices. After delivery, all piglets were marked with numbers by notching, and classification into groups according to boar's genotype was carried out using coloured ear tags.

Measurement methods

After slaughtering, the carcasses were weighted within 30 min with accuracy of tenth of kg using the equipment FOM (FAT-O-MEAT'er SFK – Technology DK 2730 Herlen, Denmark) and the percentage proportion of muscles in carcasses (meatiness) was determined. The measurement included inside fat thickness and depth of the muscle *Musculus longissimus lumborum et thoracis* (MLLT) at the measurement site. Measurements and assessments were carried out in accordance with the Regulation 194/2004 Coll.

Another parameter under assessment was the carcass length, which is defined as the shortest connection between the cranial edge of pelvic physis and articulation of the first rib with the first thoracic vertebra.

Slaughter pigs were included into four weight categories based on carcass weight:

The first group – less than 75 kg
The second group – 75 to 85 kg
The third group – 85 to 95 kg
The fourth group – 95 kg and more

Statistical analyses

Means and standard errors of the obtained phenotype groups were calculated for each of the investigated group of animals using the Proc MEANS analysis.

The following analyses were carried out using the basic linear model (Proc GLM). The following linear model has been used for the parameters of carcass value (depth of MLLT muscle, fat, meatiness, and carcass length):

$$y_{ijklm} = \mu + g_i + b_{ij} + w_{ik} + s_l + e_{ijklm}$$

where y_{ijklm} is the value of measured parameter of m^{th} head of l^{th} sex from k^{th} weight group of j^{th} boar with i^{th} RYR1 genotype; μ is a total mean of a parameter, g_i is the effect of i^{th} RYR1 genotype, b_{ij} is the effect of j^{th} boar with i^{th} RYR1 genotype, w_{ik} is the effect of k^{th} weight group of progeny from boars with i^{th} RYR1 genotype, s_l is the effect of l^{th} sex of the slaughter animal, and e_{ijklm} is the residual effect.

Variance analysis was performed based on the above linear model for all parameters. The use of Type IV of the sum of the least squares appeared as most suitable. Significance of differences among individual factors in the linear model was tested using F test. LSmeans values were calculated for 12 groups (3RYR1 genotypes x 4 weight categories). The differences between the LSmeans were tested by the multiple t test. Statistical software SAS® 9.1 was used for all the calculations.

Results

Table 1 shows the mean phenotype values of all investigated parameters of carcass value in slaughtered pigs. The whole set of investigated animals was divided into four different weight groups. Each weight group was further divided based on the RYR1 genotype of the boars used into three subgroups.

Concerning the parameter "depth of MLLT muscle", the lowest values were measures in three weight groups of the progeny of heterozygote boars (Nn). However, no significant effect of genotype was recorded in this parameter in contrast to other parameters under investigation.

In all weight groups, the highest back fat was found in the progeny of boars with heterozygote genotype. In contrast, the lowest values were found in the progeny of boars with recessive homozygote genotype (nn).

Opposite results were obtained in meatiness when the lowest values were found in the progeny of Nn boars. No significant differences were found between meatiness in the progeny of NN and nn boars; significant difference was only found in the weight group 85-95 kg, when significantly higher meatiness was recorded in the progeny of recessive homozygote boars.

In the parameter "carcass length", the highest values were obtained in the progeny of Nn boars. While in the weight group < 75 kg the carcass length in the progeny of nn boars with was shorter by 1.3 cm compared with NN genotype, in other two weight groups, the values were nearly equal, and in the in the group 95-105 kg the values were higher by 0.27 cm.

The results of variance analysis

Table 2 shows the results of variance analysis for individual parameters of carcass value. The effect of the weight group proved to be the most important factor having impact on all the parameters under study on significance level 0.001. Highly significant effect of RYR1 genotype in boars on the differences in back fat thickness and meatiness (0.001 level), and on differences in carcass length (0.01 level) was reported. Boars with different RYR1 genotype showed significant effect on MLLT muscle depth (0.01level) and carcass length (0.001level). Sex of the fattening pigs was an important factor concerning thickness of back fat and meatiness (0.001level).

The values of the Least squares means for the progeny of boars with different RYR1 genotype

The values of the least squares means ± standard error for RYR1 genotype, calculated using a respective linear model, and demonstration of probability associated with multiple t test for comparison among progeny of boars with these genotypes are showed in Table 3. The values are given for all the investigated parameters and weight groups.

Table 1. Mean values ± standard errors of mean for carcass traits in the progeny of boars with different RYR1 genotype

Weight class	*RYR1* genotype of boar	n	Weight (kg)	Depth of *MLLT* (mm)	Backfat thickness (mm)	Meatieness (%)	Carcass length (cm)
Less than 75 kg	NN	53	70.22±4.383	59.15±8.688	12.94±3.290	57.99±2.191	78.72±3.597
	Nn	41	69.77±3.882	58.66±8.472	13.71±3.084	57.40±2.104	79.71±4.185
	nn	24	70.99±2.748	60.75±7.314	13.04±2.032	58.15±1.646	77.42±3.658
	Total in group	118	70.22±3.920	59.31±8.318	13.23±3.000	57.82±2.068	78.80±3.880
75 - 85 kg	NN	81	80.00±2.673	64.21±9.557	15.14±3.810	57.08±2.659	79.74±3.173
	Nn	67	80.81±2.955	62.63±7.783	16.03±4.221	56.01±3.404	80.84±4.294
	nn	46	80.69±2.946	59.09±5.124	14.59±2.482	56.79±2.035	79.78±2.913
	Total in group	194	80.44±2.848	62.45±8.289	15.31±3.723	56.64±2.843	80.13±3.567
85 - 95 kg	NN	68	88.89±2.925	63.44±7.739	16.66±3.991	55.84±3.016	81.40±2.876
	Nn	77	89.67±2.977	65.94±9.104	17.90±4.103	55.29±3.002	82.58±2.980
	nn	57	89.09±2.822	62.88±5.441	14.68±2.694	57.23±2.322	81.37±3.249
	Total in group	202	89.24±2.922	64.23±7.835	16.57±3.922	56.02±2.928	81.84±3.066
95 kg and more	NN	27	99.47±3.852	65.63±5.205	17.89±2.806	55.28±1.879	83.11±3.105
	Nn	31	100.64±3.952	66.74±8.752	19.06±3.820	54.60±2.670	83.61±3.413
	nn	24	99.06±2.861	64.29±5.974	17.63±2.961	55.28±2.483	83.38±3.943
	Total in group	82	99.79±3.652	65.66±6.943	18.26±3.292	55.02±2.374	83.38±3.445
	Total	596	84.06±9.790	62.87±8.214	15.73±3.919	56.44±2.802	80.89±3.754

In the carcass weight parameter, no significant differences were found in any weight group among individual subgroups of progeny of boars with different genotypes. Concerning this parameter, all subgroups of individual groups appeared consistent, balanced and comparable, which was the objective of our study.

In the lightest weight group, practically no significant differences between individual subgroups of progeny of boars with different RYR1 genotype appeared. The only exception was the carcass length which was significantly longer (0.05 level) in animals originated from boars with heterozygote genotype compared with those originated from boars with recessive homozygote genotype.

In the weight group 75–85 kg, highly significant differences (0.001level) were found in the depth of MLLT muscle between the progeny of boars with NN and nn genotype, and significant differences (0.05level) between the progeny of Nn and nn boars.The highest values were obtained in animals with dominant homozygote genotype, and the lowest values in animals with recessive homozygote genotype. Significant difference (0.05 level) was observed in back fat thickness between the progeny of Nn and nn boars. Significant differences were also found in the proportion of muscles between the progeny of boars with NN and Nn genotype (0.01 level), and between progeny of boars with Nn and nn genotype (0.05 level).

Most differences were observed in weight category 85-95 kg. Significant difference (0.05level) was found in MLLT muscle depth between the progeny of Nn and nn boars of boars. In back fat thickness, highly significant difference was found in subgroup of progeny of NN and Nn boars (0.01 level), between progeny ofom boars NN and nn (0.01 level), and between progeny of Nn and nn boars (0.001 level). In the proportion of lean meat, highly significant differences were found in subgroups of progeny of NN and nn boars (0.01 level), and in subgroups of the progeny of Nn and nn boars (0.001 level). Significant difference in this weight group was also found in carcass length where the subgroup of the progeny of boars with heterozygote genotype differed from the other two subgroups (0.05 level).

No significant differences among subgroups were found for the investigated parameters of carcass value in the weight group 95 kg and more.

Discussion

The effect of weight group on selected parameters of carcass value

The results of our study confirm the basic assumption and conclusions of many authors (Gu et al. 1992, Cisneroset et al. 1996, Sládek et al. 2003, Correa et al. 2004, Latorre et al. 2004) that the increasing weight of slaughter animals results, due to the growth, in the increase of individual muscles, muscle parts and volume of the deposited fat.

Our results are in agreement with the conclusions published by Sládek et al. (2003) that at increasing slaughter weight, the depth of MLLT muscle is increasing either. This corresponds with the results reported by Gu et al. (1992) and Cisneros et al. (1996) who mentioned the effect of increased weight of carcasses on the increasing size of MLLT muscle.

Our investigation also confirmed the conclusions of several authors (Gu et al. 1992, Cisneros et al. 1996, Čandek-Potokar et al. 1998, Sládek et al. 2003, Latorre et al. 2004, Lee et al. 2006) that fattening for higher slaughter weight results in marked deposition of fat tissue and increased thickness of back fat. However, Cisneros et al. (1996) stated that other important factor was the growth rate of animals when more rapidly growing animals had higher thickness of fat at the same weight. Similar results was described by (Tvrdoň et al. 1998).

Of the above mentioned factors, the increasing thickness of back fat is much more important as it has an impact on the tendency to decrease meatiness in heavier weight categories of pigs. It logically follows from the equation used for determination of lean meat proportion in carcasses in the slaughter. The coefficient used in the Czech Republic, by which the thickness of back fat multiplies at the assessment of lean meat proportion, has an absolute value of 0.72930; while the coefficient by which the depth of MLLT muscle multiplies has an absolute value of only 0.12853 (Collection of Laws No. 194/2004). This assumption has been confirmed by comparison of the resulting meatiness of slaughter pigs in individual weight categories which markedly decreased at increased weight of carcasses as reported by (Sládek et al. 2003).

Table 1 also shows the apparent effect of weight on carcass length, which corresponds with the results published by (Gu et al. 1992, Cisneros et al. 1996, Čandek-Potokar et al. 1998, Latorre et al. 2004).

The effect of RYR1 genotype in boars on their progeny

Boars which differed in genotype of RYR1 gene were used in our experiment, whereas all sows were stress-stable of NN genotype. Therefore all pigs of NN boars were of NN genotype, and pigs of nn boars were of Nn genotype. The progeny of Nn boars were partly of NN genotype and partly of Nn genotype, nearly of the same frequency of the genotypes. The use of sows with the only genotype NN resulted in absence of stress-positive genotype nn in the progeny under investigation.

As described above, in some of the investigated parameters of carcass value, a significant effect of genotype of RYR1 gene could be observed. This was especially the case of the parameter “back fat thickness”, “meatiness”, and “carcass length”.

Our results are in agreement with those published by Tor et al. (2001) who reported that higher thickness of back fat in the site of FOM measurement was observed in

pigs with dominant homozygote genotype (NN boars) compared with pigs with heterozygote genotype Nn (nn boars). Surprisingly enough, the pigs of boars with heterozygote genotype showed in all weight categories the highest thickness of back fat which markedly influenced meatiness which was in contrast the lowest. These results are not in accordance with the conclusions published by Stadler et al. (2007) that animals with heterozygote genotype obtain intermediate values of performance in the above parameters. Moreover, our results are not consistent with those reported by Fábrega et al. (2004) that no difference was found in the predicted proportion of lean meat in the progeny of boars with NN genotype and pigs of boars with nn genotype. In the progeny nn boars, the meatiness was in three out of four weight categories higher compared to the progeny of NN boars. These results are in accordance with the data from the literature where pigs with Nn genotype had higher meatiness that those with NN genotype (Sellier 1998, Aubry et al. 2000, Tor et al. 2001).

Our results are in agreement with data of Leach et al. (1996) and Tor et al. (2001) who did not find any difference in the length of carcass between animals with NN and Nn genotypes. However, we cannot confirm the results published by Simpson et al. (1989) that animals with nn genotype had shorter carcasses compared with the other two genotypes, and that animals with NN genotype had the longest carcasses. In our study, the highest values were obtained in pigs of boars with Nn genotype, and in two out of four weight categories; the difference was significant compared with the progeny o nn boars.

The depth of MLLT muscle was the only parameter of carcass value that was not affected by genotype of the RYR1 gene in the boars under study. This finding is in accordance with the data by (Leach et al. 1996). Yet, in this parameter significant differences among subgroups were found. Evaluation of the weight group 75-85 kg revealed that the highest depth of MLLT muscle was obtained in the progeny of NN boars. In contrast, the lowest depth of the MLLT muscle was observed in the progeny of nn boars. Intermediate results of this parameter were found in the progeny of Nn boars. The group of pigs originated from nn boars differed significantly from the other two groups. These results are in accordance with the data published by (Fábrega et al. 2004). However, Tor et al. (2001) obtained opposite results, i.e. that the depth of MLLT muscle was lower in the site of FOM measurement in pigs with NN genotype compared to pigs with Nn genotype. Based on our measurements, we cannot accept those results.

Table 2. Analysis of variance for carcass traits in the progeny of boars with different RYR1 genotype

Source of variation	DF	Significance probability associated with the F test for				
		Weight	Depth of *MLLT*	Backfat thickness	Meatieness	Carcass length
RYR1 genotype of boar	2	0.2406	0.1073	<0.0001	0.0002	0.0035
Boar within *RYR1* genotype	6	0.4964	0.0073	0.6656	0.5099	0.0003
Massic group within *RYR1* genotype	9	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
Sex of fatteners	1	0.7614	0.5942	<0.0001	<0.0001	0.0115
Model in total	18	<0.0001	<0.0001	<0.0001	<0.0001	<0.0001
Error	577					

Table 3. Least squares means ± standard error of the RYR1 genotypes for all analyzed traits in the progeny of boars with different RYR1 genotype

Weight class	Trait	Least squares mean ± standard error of *RYR1* genotype of boar			Significance probability associated with the multiple t test		
		NN	Nn	nn	NN-Nn	NN-nn	Nn-nn
Less than 75 kg	Carcass Weight (kg)	70.22±0.445	69.84±0.506	70.97±0.669	0.5759	0.3471	0.1776
	Muscle depth (mm)	58.97±1.080	58.40±1.226	60.36±1.623	0.7302	0.4734	0.3357
	Backfat thickness (mm)	13.30±0.463	13.95±0.525	13.17±0.695	0.3456	0.8842	0.3709
	Lean meat content (%)	57.70±0.346	57.19±0.393	58.00±0.519	0.3226	0.6331	0.2117
	Carcass length (cm)	78.82±0.463	79.72±0.526	77.72±0.696	0.1949	0.1886	**0.0218**
75 - 85 kg	Carcass Weight (kg)	80.08±0.364	80.93±0.399	80.68±0.478	0.1146	0.3208	0.6830
	Muscle depth (mm)	64.62±0.881	62.23±0.967	59.00±1.158	0.0684	**0.0001**	**0.0328**
	Backfat thickness (mm)	15.31±0.378	16.06±0.414	14.40±0.496	0.1812	0.1442	**0.0104**
	Lean meat content (%)	57.03±0.282	55.94±0.309	56.92±0.371	**0.0095**	0.8112	**0.0436**
	Carcass length (cm)	79.77±0.378	80.66±0.415	79.79±0.497	0.1146	0.9751	0.1817
85 - 95 kg	Carcass Weight (kg)	88.88±0.392	89.69±0.371	89.10±0.431	0.1328	0.7062	0.2979
	Muscle depth (mm)	63.45±0.949	65.89±0.899	62.93±1.045	0.0625	0.7154	**0.0324**
	Backfat thickness (mm)	16.46±0.407	17.98±0.385	14.70±0.448	**0.0067**	**0.0039**	**<.0001**
	Lean meat content (%)	55.98±0.304	55.22±0.288	57.22±0.335	0.0684	**0.0063**	**<.0001**
	Carcass length (cm)	81.33±0.407	82.48±0.386	81.24±0.449	**0.0403**	0.8817	**0.0360**
95 kg and more	Carcass Weight (kg)	99.56±0.628	100.51±0.586	99.04±0.665	0.2666	0.5719	0.0966
	Muscle depth (mm)	66.31±1.522	67.15±1.420	64.46±1.612	0.6850	0.4025	0.2081
	Backfat thickness (mm)	17.61±0.652	18.66±0.608	17.04±0.690	0.2419	0.5460	0.0787
	Lean meat content (%)	55.61±0.487	54.94±0.454	55.73±0.516	0.3166	0.8661	0.2517
	Carcass length (cm)	82.93±0.653	83.73±0.609	83.21±0.692	0.3699	0.7627	0.5765
Total	Carcass Weight (kg)	84.68±0.234	85.24±0.235	84.95±0.285	0.0917	0.4737	0.4231
	Muscle depth (mm)	63.34±0.568	63.42±0.569	61.69±0.690	0.9169	0.0659	0.0534
	Backfat thickness (mm)	15.67±0.243	16.66±0.244	14.83±0.296	**0.0040**	**0.0287**	**<.0001**
	Lean meat content (%)	56.58±0.182	55.82±0.182	56.97±0.221	**0.0033**	0.1773	**<.0001**
	Carcass length (cm)	80.71±0.244	81.65±0.244	80.49±0.296	**0.0068**	0.5645	**0.0027**

Conclusion

Our investigation confirms the importance of a proper selection and suitable gene pool at the production of fattening pigs. Our results also suggest that the use of heterozygote boars in RYR1 gene will not always yield progeny with an intermediate performance. As expected, the progeny of boars with recessive homozygote genotype (nn) obtained better results in the parameters "thickness of back fat" and "meatiness". On the other hand, the progeny of boars with dominant homozygote and heterozygote genotype had better results in the parameter "depth of MLLT muscle". In the first and last weight groups, no significant differences were found between the genotypes under study, except for the parameter "carcass length". This can, however, be due to the lower number of animals in the marginal groups. In spite of that, great emphasis has to be placed on the selection of breeding animals and optimum slaughter weight.

References

Aubry A., Ligonesche B., Guéblez R., Gaudré D.,(2000): Comparison des porcs charcutiers NN et Nn pour les performances de croissance, carcasse et qualite à de viande, et l'aptitude à produire du jambon cuit. Journèes Rech. Porcine France, 32: 361-367

Cisneros F., Ellis M., McKeith F.K., McCaw J., Fernando R.L.,(1996): Influence of slaughter weight on growth and carcass characteristics, commercial cutting and curing yields, and meat duality of barrows and gilts from two genotypes. J. Anim. Sci.,74: 925–933

Correa J.A., Faucitano L., Laforest J.P., Rivest J., Marcoux M., Gariépy C.,(2006): Effects of slaughter weight on carcass composition and meat quality in pigs of two different growth rates. Meat Science Volume 72, Issue 1 , 91-99

Čandek-Potokar M., Žlender B., Lefaucheur L., Bonneau M.,(1998): Effects of age and/or weight at slaughter on longissimus dorsi muscle: biochemical traits and sensory quality in pigs. Meat Science, Vol. 48, No. 314, 287-300,

Fàbrega E.X. Manteca J.M. Gispert, D. Carrión, A. Velarde, J.L. Ruiz-de-la-Torre, A. Diestre.,(2004): A comparison of halothane homozygous negative and positive pietrain sire lines in relation to carcass and meat quality, and welfare traits. Meat Science 66 (2004) 777–787

Fisher, P., Mellet, F. D., Hofman, L. C.: Halothane genotype and pork quality. 1. carcass and meat duality characteristics of three halothane genotypes.*Meat Science*, 2000, 54: 97 – 105

Fujii J., Otsu K., Zorzato F., De Leon S., Khanna V.K., Weiler J.E., O'Brien P.J., MacLennan D.H.,(1991): Identification of a mutation in porcine ryanodine receptor associated with malignant hyperthermia. Science. 1991, Volume 253, Issue 5018, Pages 448-451

Gispert M., Faucitano L., Oliver M. A., Guardia M. D., Coll C., Siggens K., Harvey K., Diestre A. (2000): A survey of preslaughter conditions, halothane gene frequency and carcass and meat quality in five spanish pig commercial abattoirs. Meat Science 55: 97 – 106.

Gu Y., Schinckel A.P. and Martin T.G.,(1992): Growth, development, and carcass composition in five genotypes of swine. J. Anim. Sci. 70:1719.

Latorre M.A., Lázaro R., Valencia D.G., Medel P., Mateos G.G.,(2004): The effects of gender and slaughter weight on the growth performance, carcass traits, and meat quality characteristics of heavy pigs. J. Anim. Sci., 82: 526–533

Leach L.M., Ellis M., Sutton D.S., McKeith F.K., Wilson E.R.,(1996): The Growth performance, Carcass Characteristics, and Meat Quality of Halothane Carrier and Negative Pigs. J. Anim. Sci., 74: 934–943

Lee C.Y., Kwon O.C., Ha D.M., Shin H.W., Lee J.., Ha Y.J., Lee J.H., Ha S.H., Kim W. K., Kim K.W., Kim D.H.,(2006): Growth efficiency, carcass quality characteristics and profitability of finishing pigs slaughtered at 130 vs. 110 Kg. Journal of Animal Science and Technology, 48(4): 493-502

Oliver, M. A., Gispert, M., Diestre, A.,(1993): The effects of breed and halothane sensitivity on pig meat quality. Meat Science 35 (1993) 105-118

Otsu K., Phillips M.S., Khanna V.K., De Leon S., Maclennan D.H.,(1992): Refinement of diagnostic assays for a probable cause mutation for porcine and human malignant hyperthermia. Genomics 13 (3): 835-837

SAS (1999). SAS Version 8.0, SAS Institute Inc., Cary, NC.

Sellier P., (1998): Genetics of meat and carcass traits. In: Rothschild M. F., Ruvinsky A. (eds), The Genetics of the Pig. CAB International, New York.

Sládek L., Čechová M., Mikule V.,(2003): Carcass value of tested hybrid pig combination slaughtered in different slaughter weight. Acta Universitatis Agriculturae et Silviculturae Mendelianae Brunensis, 51 (LI), 2003, č. 5, s. 71 – 78

Stadler K., Conatser G.,(2007): Porcine Stress Syndrome and Its Effects on Maternal, Feedlot and Carcass Quantitative and Qualitative Traits. Dostupné dne 12.02.2007 na www http://www.utextension.utk.edu/publications/animals/default.asp www.utextension.utk.edu/publications/pbfiles/PB1606.pdf

Tor M., Estany J., Villalba D., Cubiló D., Tibau J., Soler J., Sanchez A., Noguera J. L.,(2001): A within-breed comparison of *RYR1* pig genotypes for performance, feeding behaviour, and carcass, meat and fat quality traits. J. Anim. Breed. Genet. 118, 417-427

Tvrdoň Z., Čechová M., Dřímalová K.,(1998): The analysis of influence of backfat thicknees on fertility in sows. Czech J. Anim. Sci., 43, 417.

This study was supported by the project No. QH 71284 which is financed by the Ministry of Agriculture Czech Republic**.**