THE INFLUENCE OF THE GENES MYOG AND MYF6 ON SELECTED INDICATORS OF THE FATTENING CAPACITY AND THE CARCASS VALUES OF PIGS*

H. Kratochvílová, R. Stupka, J. Čítek, M. Šprysl, M. Okrouhlá, V. Dvořáková

Czech University of Life Sciences, Faculty of Agrobiology, Food and Natural Resources, Department of Animal Husbandry, Prague, Czech Republic

The genes MYOG play the key role in the development and differentiation of muscular cells during the growth of an embryo. For this reason they are considered to be candidate genes for the indicators of the quality of the meat of pigs. The objective of this study was to determinate the influence of the genes MYOG and MYF6 on selected indicators of the quality of the meat of pigs. For monitoring these indicators, 70 pigs (interbreeding combination ((LW_S x D) x (LW_M x L) were tested. Among the genotypes of the gene MYOG, no serious statistical differences were identified with regard to indicators of the fattening capacity and the quality of meat. Within the genes MYF6, serious statistical differences relating to average daily weight gain were identified ($P \leq 0.05$) within the genotypes AA and AB. As for live weight, serious statistical differences were identified ($P \leq 0.05$) within the same genotypes. Among the genotypes of the genes MYOG and MYF6 no serious statistical differences were identified with regard to weight and the proportion of main meat parts.

MYOG; MYF6; polymorphism; carcass value; meat production traits; pig

INTRODUCTION

The genes MYOG and MYF6 belong to the MYOD group. This group includes 4 genes: MYOD1 (MYF3), MYOG (MYF4), MYF5 and MYF6 (MRF4-herculine). These genes control the development and differentiation of muscular cells during the development of an embryo (Olson, 1990). Every gene has its specific influence in the course of myogenesis.

The genes MYF5 and MYOD1 (MYF3) play the principal role in the phase of the proliferation of myoblasts, while the genes MYOG (MYF4, myogenine) and MYF6 (MRF4) are connected with the differentiation and the maturing of myofibrils (Wyszyńska-Koko, Kurył, 2004).

The value of the gene MYF6 in the post-natal phase is ten times higher than that of other genes of the group MYOD (Bober et al., 1991). The fragment of the gene MYF6 that includes exon 1, exon 2 and intron was amplified by means of primers designed in accordance with to human DNA, mouse RNA and genome DNA (Vykoukalová et al., 2003). Wyszyńska-Koko et al. (2006) identified two polymorphisms (within respective promoter and exon 1). Vykoukalová et al. (2003) had already identified 3 mononucleotide polymorphisms within introne1.

Myogenine (MYOG) plays the key role in the differentiation of muscles and controls the beginning of the fusion of myoblast and the origination of myofibers (Soumillion et al., 1997). Ernst et al. (1993) identified by means of endonucleasis MspI three fragments of this gene (4, 9 – 4, 2-kb were indicated as polymorphic fragments, and 2,3-kb was indicated as a mono-morphic one). Soumillion et al. (1997) tested polymorphism MspI in 3 locations of the MYOG gene of pigs. These locations were on the promoter, second intron and the 3' end of the gene. He tested 105 pigs that were not related to each other and were selected from 7 breeds (Meishan, Pietrain, Duroc, Hampshire, Great Yorkshire, Dutch Landrace and wild pigs). The best location for the study of relationships between PCR and RFLP and the variability of the characteristics of meat within individual breeds of pigs, was identified on the 3' end of the gene.

MATERIAL AND METHODS

In the course of monitoring the influence of the polymorphic variants of the genes MYOG and MYF6 on indicators of the fattening capacity and the quality of the meat, 70 pigs of the interbred combination (LW_S x D) x (LW_M x L) were tested at the test station in Ploskov/Lány. The feed of the pigs was in accordance with to the standards for nutrients (Šimeček et al., 2000) in 3 phases with continual transfer.

After reaching a live weight of about 123 kg, the animals were slaughtered. During the course of this experiment, the following indicators were monitored:

- average daily weight gain (g/day),
- live weight (kg),
- weight of the right side of the carcass (kg),
- backfat thickness measured above the last breast vertebra (mm),
- weight and the proportion of the main meat parts (loin, ham, shoulder, neck) (kg, %),

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– fat content and the proportion of main meat parts (kg, %),
– weight and proportion of loin (kg, %),
– weight and proportion of ham (kg, %),
– weight and proportion of neck (kg, %),
– weight and proportion of shoulder (kg, %),
– weight and proportion of belly (kg, %),
– lean meat content – ZP method (%).

Blood samples were taken in the slaughterhouse in test tubes with K2EDTA. DNA was isolated by means of JET Quick (Blood and Cell Culture) DNA SpinKit – GENOM-ED – and stored at a temperature of 20 degrees below zero. The analysis as such was performed by means of the PCR/RFLP method. The polymorphism of the gene MYOG in the 3´ end was identified by means of the method described by Soumillion et al. (1997) on 70 pigs. The polymorphism of the gene MYF6 at intron 1 was identified by means of the method designed by Vykoukalová et al. (2003) on 62 pigs.

The results of the tests were evaluated by statistical and mathematical methods, the SAS programme, and the procedures MEANS, UNIVARIATE, GLM (SAS, 2001). The differences among the individual monitored features were tested by variance analysis. For the evaluation of the influence of a genotype the following model was applied:

$$Y_{ijk} = \mu + G_i + P_j + H_k + e_{ijk}$$

When: μ – the average of the population
G_i – the stable effect of the genotype MYOG (AA, AB, BB) or MYF6 (AA, AB, BB)
P_j – the stable effect of sex
H_k – the stable effect of weight
e_{ijk} – residual error

RESULTS AND DISCUSSION

The frequency of the genes MYOG and MYF6 within the monitored group is included in Table 1.

In both genes the allele A prevailed. This was also demonstrated by Verner et al. (2007).

The number and frequency of the genotypes of both genes within the monitored group of animals is included in Table 2.

In the gene MYOG the genotype AA (48 individuals) prevailed. The number of the genotypes BB (only 6 individuals) was the least. Kłosowska et al. (2004) stated that the genotype BB of the gene MYOG predominates in the hybrids. The genotype AA was not represented at all. Kapełanski et al. (2005) state that genotype AB predominates in the hybrids PLW x PL and (PLW x PL) x PI, while the number of AB genotypes is the least.

In the gene MYF6 the most frequent genotype was AB (23 individuals). The number of BB genotypes (only 18 individuals) was the least. The same sequence of genotypes is presented by Verner et al. (2007) within the Landrace and Large White breeds.

Table 3 evaluates the influence of the genotypes on the selected indicators of the fattening capacity and the quality of meat.

No serious statistical differences were identified with regard to indicators of the fattening capacity and the quality of meat within the genotypes of the gene MYOG. Krzęcio et al. (2007) found serious statistical differences ($P \leq 0.05$) with regard to the height of the backfat thickness between genotypes AB and BB. Individuals with genotype BB showed greater backfat thickness than those with genotype AB. A serious statistical difference ($P \leq 0.01$) in the height of the backfat thickness was also identified by Cieślak et al. (2002). The backfat thickness of animals with genotype BB was greater than that of the

Table 1. Frequency of the alleles of the genes MYOG and MYF6 within the monitored group

	MYOG		MYF6	
Allele	A	B	A	B
Frequency	0.80	0.20	0.53	0.48

Table 2. Number and frequency of individual genotypes within the monitored group

	MYOG			MYF6		
Genotype	AA	AB	BB	AA	AB	BB
Number	48	16	6	21	23	18
Frequency	0.68	0.23	0.09	0.34	0.37	0.29

Table 3. Influence of the genotypes of the genes MYOG and MYF6 on the selected indicators of the breeding ratio and the quality of meat

Trait	MYOG			MYF6		
	AA	AB	BB	AA	AB	BB
Average daily weight gain (g/day)	893.0	937.0	884.0	893.0*	895.0*	925.0
Live weight (kg)	107.0	111.4	106.5	107.5	106.9*	109.2*
Weight of the right side of the carcass (kg)	42.8	44.0	41.9	42.7	42.5	43.3
Backfat thickness (mm)	19.6	20.8	20.0	19.1	19.3	21.2
Lean meat content – ZP method (%)	59.2	59.3	58.8	59.9	59.0	59.1

* ($P \leq 0.05$)

Table 4. Influence of the genotypes on the indicators of the weight of selected parts

Trait	MYOG			MYF6		
	AA	AB	BB	AA	AB	BB
Weight of main meat parts (kg)	22.8	23.7	23.2	23.2	22.9	23.1
Proportion of main meat parts (%)	53.4	53.8	55.4	54.3	53.9	53.3
Fat content of main meat parts (kg)	5.6	5.7	5.0	5.3	5.6	5.7
Proportion of main meat parts (%)	13.2	12.9	12.0	12.4	13.1	13.2
Weight of neck (kg)	2.9	3.1	3.2	3.1	2.9	3.1
Proportion of neck (%)	6.8	7.1	7.5	7.2	6.8	7.1
Weight of shoulder (kg)	4.3	4.5	4.2	4.3	4.3	4.4
Proportion of shoulder (%)	10.1	10.1	10.1	10.2	10.1	10.2
Weight of loin (kg)	5.8	6.1	6.0	6.0	5.8	5.8
Proportion of loin (%)	13.5	14.0	14.4	14.0	13.7	13.3
Weight of ham (kg)	9.8	10.0	9.8	9.8	9.9	9.8
Proportion of ham (%)	23.0	22.7	23.4	23.0	23.2	22.7
Weight of belly (kg)	7.6	7.8	7.4	7.5	7.6	7.5
Proportion of belly (%)	17.7	17.6	17.7	17.6	17.9	17.4

animals with genotype AB. In both studies no genotype AA was identified.

Wyszyńska-Koko et al. (2006) presented serious statistical differences ($P \leq 0.01$) in the average daily weight gain among the genotypes AA and BB, BB and AB. The individuals with genotype AA showed a higher average daily weight gain than those with genotype BB. At the same time, the individuals with genotype BB showed higher average daily weight gain than those with genotype AB.

Within the gene MYF6 serious statistical differences were identified in daily weight gain between genotypes AA and AB. The average daily weight gain shown by individuals with genotype AB (895.0 g/day) was higher than that of those with genotype AA (893.0 g/day). Serious statistical differences in the live weight ($P \leq 0.05$) were determined between genotypes AB and BB. The individuals with genotype BB showed a higher live weight (109.2 kg) than those with genotype AB (106.9 kg). Verner et al. (2007) did not identify any serious statistical differences among the genotypes of the gene MYF6 with regards to average daily weight gain, weight before slaughtering, backfat thickness and lean meat content.

The influence of the genotypes on the indicators of the weight of selected parts and their proportion is shown in Table 4.

Within the genotypes of the genes MYOG and MYF6, no serious statistical differences relating to the indicators presented in Table 4 were identified.

Verner et al. (2007) demonstrate serious statistical differences ($P \leq 0.05$) between the genotypes AA and AB with regard to the weight of the right side of the carcass. The individuals with genotype AA showed a higher weight of the right side of the carcass than those with genotype AB. In addition, they identify serious statistical differences ($P \leq 0.01$) between genotypes AA and BB in the weight of the loin. Genotype AA again showed a higher weight.

Wyszyńska-Koko et al. (2006) identified serious statistical differences within individual genotypes of the gene MYOG with regard to the weight of the ham. Krzęcio et al. (2007) identified serious statistical differences ($P \leq 0.05$) between genotypes AB and BB of the gene MYOG with regard to the weight of the right side of the carcass. The weight of the belly of those animals with genotype BB was higher.

Verner et al. (2007) did not identify any serious statistical differences within the genotypes of the gene MYF6 with regard to the weight of the loin, ham and belly.

CONCLUSIONS

- In both genes the allele A predominated.
- In the gene MYOG, genotype AA (48 individuals) predominated. The number of genotype BB was the least (6 individuals).
- In the gene MYF6, genotype AB (23 individuals) predominated. On the contrary, the number of genotype BB was the least.
- In the course of monitoring the indicators of the fattening capacity and the quality of meat, no serious statistical indicators among the genotypes of the gene MYOG were identified.
- In the gene MYF6, serious statistical differences between genotypes AA and AB ($P \leq 0.05$) were identified with regard to average daily weight gain. The individuals with genotype AB showed a higher average daily weight gain (895.0 g/day) than those with genotype AA (893.0 g/day).
- With regard to live weight, serious statistical differences were identified between genotypes AB and BB. The individuals with genotype BB showed a higher live weight (109.2 kg) than those with genotype AB (106.9 kg).
- With regard to weight as such, the proportion of the main parts and selected parts of the carcass, no serious statistical differences were identified within the genotypes of the genes MYOG and MYF6.

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Vliv genů MYOG a MYF6 na vybrané ukazatele výkrmnosti a jatečné hodnoty prasat.

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Geny rodiny MYOD hrají klíčovou roli ve vývoji a diferenciaci svalových buněk během embryonálního vývoje. Z tohoto důvodu jsou považovány za kandidátní geny pro ukazatele masné užitkovosti prasat. Cílem této práce bylo stanovit vliv genů MYOG a MYF6, které patří do rodiny genů MYOD, na vybrané ukazatele masné užitkovosti prasat. Pro sledování ukazatelů výkrmnosti a jatečné hodnoty byl použit soubor 70 jatečných prasat kombinace křížení (BU x L) x (BO x D). U sledovaných ukazatelů výkrmnosti a jatečné hodnoty mezi genotypy genu MYOG nebyly zjištěny žádné statisticky významné rozdíly. U genu MYF6 byly zjištěny statisticky významné rozdíly ($P \leq 0,05$) u průměrného denního přírůstku mezi genotypy AA a AB. U živé hmotnosti byly stanoveny statisticky významné rozdíly ($P \leq 0,05$) mezi genotypy AB a BB. Mezi genotypy genů MYOG a MYF6 nebyly zjištěny žádné statisticky významné rozdíly u hmotnosti a podílu hlavních masitých částí a vybraných jatečných partií.

MYOG; MYF6; polymorfismus; jatečná hodnota; masná užitkovost; prase

Contact Address:

Ing. Hana K r a t o c h v í l o v á , Česká zemědělská univerzita v Praze, Fakulta agrobiologie, potravinových a přírodních zdrojů, Kamýcká 129, 165 21 Praha 6-Suchdol, Česká republika, tel.: +420 224 383 060, e-mail: kratochvilova@af.czu.cz