The analysis of carcass value in pigs of different genotypes

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ABSTRACT: In an experiment the analysis of some traits of carcass value in pigs of Czech Large White and Landrace breeds differentiated according to the genotype of *C-MYC* and *MYF4* genes was carried out. PCR-RFLP method was used for gene determination. In CLW pigs three genotypes of *C-MYC* gene were found out with a frequency of allele *A* 0.714 and *B* 0.286, in L pigs the *BB* genotype was not detected. In CLW pigs the respective frequencies of allele *A* and *B* of *MYF4* gene were 0.660 and 0.340, in L breed 0.917 and 0.083. There was a statistically significant difference in the levels of MLLT area ($P \leq 0.05$) between the genotypes *AA*, *AB* and *BB* of *C-MYC* gene in CLW pigs. In this breed statistically significant differences ($P \leq 0.05$) were detected between the genotypes *AA* and *AB* in these traits: MLLT area, percentage of main lean cuts and weight of main lean cuts in favour of genotype *BB* of *MYF4* gene. We did not find any significant differences in the measured levels of carcass value traits between different genotypes of *MYF4* gene in L breed.

Keywords: pig; breed; carcass value; genotype; *C-MYC; MYF4*

The ability of exact determination of genotype of individual pigs in a chosen locus brings about a possibility of studying possible associations between determined genotype and expected production traits. Different stations in the world deal with this issue. In many cases genetic researches are aimed at detection of loci (position, a part of chromosome) that have a statistically significant effect on some of the parameters of efficiency (Dvořák, 1999). The results of their research are mentioned by Kahánková *et al.* (1996), Fiedler *et al.* (1999), Cieslak *et al.* (2000).

In addition to relations to reproductive traits a lot of authors specialize in analyses of results of carcass value traits. Aspiration of scientific workstations is an exploitation of determined results in subsequent selection work in individual pig populations.

Besides the most frequently studied gene *RYR1* there is an effort to use other genes for determination of possible relation with carcass value of pigs. One of them is *MYF4* gene, a member of *MyoD* family, which is responsible for differentiation of proliferous myoblasts and its genetic variability (which is probably related with the number of myofibrils) ranks it among candidate genes. Pietruzska *et al.* (2002) studied the relation of myogenin to meatiness. In a set of 118 tested pigs they identified 98 animals with *AA* genotype and 20 pigs with *AB* genotype. In the set no animal with *BB* genotype was detected. Meatiness of slaughter pigs with *AA* genotype reached 53% and it was by 2.3% higher in comparison with *AB* heterozygotes. Kaniak and Jasek (1999) reported significantly higher meatiness of *AA* homozygotes in comparison with *AB* heterozygotes and slight dominance of *AA* homozygotes over pigs with *BB* genotype. Kahánková and Dvořák (1998) stated that animals with recessive allele *B* showed lower meatiness in comparison with *AA* homozygotes. Kolaříková *et al.* (2002) studied the influence of myogenin gene polymorphism on meat efficiency in Czech Large White pigs. They found out no significant differences in muscle depth in pigs with *BB* genotype in comparison with pigs with *AA* and *AB* genotype. They did not determine any relation with backfat thickness.

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C-MYC gene is another promising candidate gene for possible association with carcass value. Based on the *C-MYC* gene study Cieslak *et al.* (2000) found that polymorphism of this gene had an influence on meat efficiency of pigs. In Polish pig breeds they found a higher level of chosen carcass traits in pigs with genotype *AA*. Reiner *et al.* (1999) found a direct relation between *C-MYC* genotypes and carcass value.

MATERIAL AND METHODS

Czech Large White (CLW) and Landrace pigs (L) were fattened at a progeny testing station and they were tested in accordance with Czech State Standard ČSN 46 6164 (in the weight from 30 to 100 kg – feeding *ad libitum* with feed mixture Gent).

After slaughter the carcass was weighed in each tested animal and the percentage of lean meat was determined by a two-point method (ZP Zwei-Punkt-Verfahren) with electromechanical apparatus IS-D-04.

An equation by Pulkrábek *et al*. (2000) was used to calculate the percentage of lean meat.

A detailed carcass dissection was carried out (ČSN 46 6164) and the weight (to the nearest 0.1 kg) of main lean cuts (leg, chop, neck, shoulder) was determined, backfat thickness was measured at three places and averages and the area of MLLT (*musculus longisimus lumborum et thoracis*) were calculated.

Samples of blood were taken from the *vena cava cranialis* and transported to the laboratory of Genetic Department of Mendel University of Agriculture and Forestry in Brno.

The PCR-RFLP methods (Soumillion *et al*., 1997) were used to detect the genotypes of gene *MYF4*. The gene *C-MYC*, which is usually digested with *Hpa*II (Reiner *et al*., 1999), was cut with isoschizomer *Msp*I in our experiment.

A statistical program Unistat (version 5.1) was used for mathematical and statistical evaluation of phenotypic levels of the studied traits.

RESULTS AND DISCUSSION

In the studied populations of pigs the frequencies of genotypes and alleles in chosen loci were evaluated. Results are shown in Tables 1 and 2. In *C-MYC* gene in breed CLW a higher frequency of dominant allele *A* (0.714) was detected compared to allele *B* (0.286). The frequency of *AA* genotypes 49.21% is similar to the frequency of heterozygotes *AB* 44.44%. The frequency of the third detected genotype is lower – 6.35%. In a set of the second tested breed (L) the *BB* genotype was not found, which had an influence on *A* allele frequency (0.909) compared to *B* allele (0.091) in this locus. The other two genotypes (*AA* and *AB*) had the frequency of 81.82% and 18.18%.

In both populations polymorphism of *MYF4* gene was detected.

In the group of CLW pigs the frequency of *A* allele was 0.660 and of *B* allele 0.340. Three genotypes *AA*, *AB* and *BB* with frequencies 46.67; 38.67 and 14.66 were detected. Kahánková (1998) reported quite similar frequencies of *A* and *B* allele (0.604 and 0.396) in the Czech Large White breed. Kolaříková *et al.* (2002) mentioned a lower occurrence of *AA*

Table 1. Frequency of genotypes and alleles of *C-MYC* gene in pigs of CLW and L breeds

Breed	A	Frequency of genotypes (%)			Frequency of alleles	
		AA	*AB*	*BB*	*A*	*B*
CLW	63	49.21	44.44	6.35	0.714	0.286
L	11	81.82	18.18	0	0.909	0.091

Table 2. Frequency of genotypes and alleles of *MYF4* gene in pigs of CLW and L breeds

Breed	*n*	Frequency of genotypes (%)			Frequency of alleles	
		AA	*AB*	*BB*	*A*	*B*
CLW	75	46.67	38.67	14.66	0.660	0.340
L	18	83.33	16.67	0	0.917	0.083

genotype, higher frequency of *BB* genotype and a similar frequency of *AB* genotype. It is interesting that the frequency of genotypes in *MYF4* locus is analogical as in *C-MYC* gene in Landrace breed. The *BB* genotype was not detected and the frequency of *AB* heterozygotes was 16.67% in this breed. It corresponds to a very high frequency of *A* allele 0.917 compared to *B* allele 0.083. These values are similar to the values reported by Bečková *et al.* (2002) in Norwegian Landrace breed even though they detected *BB* genotype in Landrace breed (but with a low frequency 2.5%). Kahánková (1998) detected *AA*, *Aa* and *aa* genotypes with the frequency of allele A 0.762 and recessive allele 0.238 in Landrace pigs.

Possible relations between determined genotypes and chosen traits of carcass value were evaluated.

Basic statistical characteristics of some traits of carcass value in the studied genotypes of *C-MYC* gene are shown in Tables 3 and 4.

In CLW pigs higher meatiness expressed by the percentage of main lean cuts and weight of main lean cuts was determined in pigs with *AA* genotype in *C-MYC* gene. It corresponds to the lowest thickness of subcutaneous fat in pigs with the recessive homozygous constitution in this locus. The largest MLLT area 4 771 mm^2 was measured in pigs with *AA* genotype. A statistically significant difference between *AA* and *BB* genotypes was found out in this trait on a significance level $P \leq 0.05$. Similar results were found out between *AB* and *BB* genotypes of this locus. Higher percentage of main lean cuts and weight of main lean cuts were determined in animals with *AA* genotype compared to pigs with *AB* genotype in *C-MYC* gene in Landrace breed (the *BB* genotype was not detected). It corresponds to lower backfat thickness in pigs with *AA* genotype of this gene. Existing differences in absolute values are not statistically significant in the tested set of animals. In the trait area of MLLT a higher phenotypic level was also detected in pigs with *AB* genotype in *C-MYC* gene. The findings in the same genotypes in both breeds were similar. These findings correspond to the results reported by Cieslak *et al.* (2000). They found out a higher level of carcass value in animals with *AA* genotype in *C-MYC* gene in Polish pig breeds. Reiner *et al.* (1999) stated that there was a direct relation between *C-MYC* genotypes and carcass value. In comparison with these results Resová (2001), who studied associations between *C-MYC* genes of pigs, found out that pigs with *AB*

Table 3. Basic statistical characteristics of particular traits according to determined genotypes of *C-MYC* gene in CLW pigs

Trait	Genotype	*n*	Average	S_x	V_x	X_{min}	X_{max}
MLLT area (mm^2)	*AA*	31	4 706^a	524	11.13	3 710	5 880
	AB	28	4 719^b	484	10.27	3 700	6 020
	BB	4	4 110^{a,b}	323	7.87	3 830	4 460
Main lean cuts (%)	*AA*	31	52.23	3.23	6.19	47.54	58.65
	AB	28	51.81	2.73	5.26	45.95	57.32
	BB	4	51.41	1.78	3.47	49.61	53.11
Main lean cuts (kg)	*AA*	31	21.07	1.47	6.97	18.78	23.93
	AB	28	20.96	1.36	6.47	18.84	24.26
	BB	4	20.09	0.95	4.74	19.15	21.37
Backfat thickness (mm)	*AA*	31	20.7	3.5	16.83	15.0	28.0
	AB	28	19.6	4.3	21.70	10.7	27.0
	BB	4	19.3	3.2	16.73	14.7	22.3
Lean meat proportion (%)	*AA*	31	56.65	3.67	6.46	51.00	65.00
	AB	28	58.50	4.75	8.12	50.00	67.00
	BB	4	59.00	3.74	6.34	55.00	64.00

$^{a,b}P \leq 0.05$

Table 4. Basic statistical characteristics of particular traits according to determined genotypes of *C-MYC* gene in L pigs

Trait	Genotype	*n*	Average	S_x	V_x	X_{min}	X_{max}
MLLT area (mm^2)	*AA*	9	4 516	439	10	3 980	5 260
	AB	2	4 690	240	5	4 520	4 860
	BB	0	–	–	–	–	–
Main lean cuts (%)	*AA*	9	54.32	2.43	4	51.31	58.28
	AB	2	52.42	2.57	5	50.6	54.23
	BB	0	–	–	–	–	–
Main lean cuts (kg)	*AA*	9	21.11	1.05	5	19.81	22.73
	AB	2	20.24	1.29	6	19.33	21.15
	BB	0	–	–	–	–	–
Backfat thickness (mm)	*AA*	9	18.5	3.6	20	12.7	23.3
	AB	2	19.,5	0.,3	1	19.3	19.7
	BB	0	–	–	–	–	–
Lean meat proportion (%)	*AA*	9	59.89	5.16	9	54	69
	AB	2	57	1.41	2	56	58
	BB	0	–	–	–	–	–

Table 5. Basic statistical characteristics of particular traits according to determined genotypes of *MYF4* gene in CLW pigs

Trait	Genotype	*n*	Average	S_x	V_x	X_{min}	X_{max}
MLLT area (mm^2)	*AA*	35	4 622^{a}	478	10.34	3 720	5 660
	AB	29	4 616^{b}	524	11.36	3 640	5 520
	BB	11	5 132^{a,b}	548	10.68	4 520	6 020
Main lean cuts (%)	*AA*	35	51.80^{a}	2.72	5.25	45.95	56.74
	AB	29	51.57	2.49	4.82	47.88	57.32
	BB	11	53.81^{a}	3.44	6.39	48.59	58.65
Main lean cuts (kg)	*AA*	35	20.98^{a}	1.24	5.93	18.84	23.83
	AB	29	20.64^{b}	1.36	6.60	18.78	24.26
	BB	11	21.93^{a,b}	1.38	6.30	20.02	23.93
Backfat thickness (mm)	*AA*	35	21.0	3.5	16.78	10.7	28.0
	AB	29	20.1	3.5	17.47	13.7	26.7
	BB	11	19.4	4.9	25.45	12.0	27.0
Lean meat proportion (%)	*AA*	35	57.65	3.90	6.76	51.00	65.00
	AB	29	57.58	4.04	7.02	51.00	67.00
	BB	11	57.91	5.24	9.05	50.00	67.00

^{a,b} $P \leq 0.05$

Table 6. Basic statistical characteristics of particular traits according to determined genotypes of *MYF4* gene in L pigs

Trait	Genotype	*n*	Average	S_x	V_x	X_{min}	X_{max}
MLLT area (mm^2)	*AA*	15	4 441	444	10	3 610	5 160
	AB	3	4 920	374	8	4 520	5 260
	BB	0	–	–	–	–	–
Main lean cuts (%)	*AA*	15	53.33	2.03	4	49.48	57.61
	AB	3	54.52	3.84	7	50.6	58.28
	BB	0	–	–	–	–	–
Main lean cuts (kg)	*AA*	15	20.85	0.81	4	19.79	22.41
	AB	3	21.49	1.88	9	19.33	22.73
	BB	0	–	–	–	–	–
Backfat thickness (mm)	*AA*	15	19.0	2.5	13	13.7	23.3
	AB	3	16.9	3.6	22	12.7	19.3
	BB	0	–	–	–	–	–
Lean meat proportion (%)	*AA*	15	58.47	3.31	6	54	65
	AB	3	63	5.57	9	58	69
	BB	0	–	–	–	–	–

genotype had the highest percentage of lean meat and the lowest backfat thickness. She did not find a significant relation between the genotype of *C-MYC* gene and traits of pork production.

The analysis of possible relations between the genotypes of *MYF4* locus and studied traits was carried out in Czech Large White and Landrace pigs. The results of statistical evaluation are shown in Tables 5 and 6. The evaluation of the results of CLW breed indicated statistically significant differences between genotypes *AA* and *BB* in the traits MLLT area, percentage of main lean cuts and weight of main lean cuts in favour of *BB* genotype on a significance level $P \leq 0.05$. It corresponds to the lowest backfat thickness in pigs with *BB* genotype. These findings are different from the results of Pietruzsky *et al.* (2002). They reported higher meatiness of pigs with *AA* genotype. In the traits MLLT area and weight of main lean cuts statistically significant differences were determined between *AB* and *BB* genotypes. Higher phenotypic values were reached by pigs with *BB* genotype. Statistical significance was not found for the differences in phenotypic levels of lean meat content between the particular genotypes.

Kahánková (1998) analysed backfat thickness and lean meat percentage in sows of Czech Large White and Landrace breeds according to genotypes of *MYF4* gene and she found out that pigs with *AA* genotype had higher lean meat percentage and lower backfat thickness in comparison with animals with *Aa* genotype.

The evaluation of phenotypic levels of the studied carcass value traits in detected genotypes of *MYF4* gene in Landrace pigs indicated differences in favour of heterozygotes *AB* in comparison with homozygotes *AA*. The differences were not statistically significant. Kaniak and Jasek (1999) reported significantly higher meatiness of heterozygotes *AB* in comparison with homozygotes *AA*. Kahánková and Dvořák (1998) mentioned lower meatiness in animals with recessive allele *B* in comparison with homozygotes *AA*.

Comparing the results of carcass value the identical tendency for determined genotypes in both breeds was not found out.

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ABSTRAKT

Analýza jatečné hodnoty u prasat různých genotypů

Byla provedena analýza vybraných ukazatelů jatečné hodnoty u prasat plemene bílé ušlechtilé a landrase diferencovaně podle genotypů *C-MYC* a *MYF4* genu, pro jejichž určení byla použita metoda PCR-RFLP. U prasat plemene LW byly určeny tři genotypy genu *C-MYC* s frekvencí alely *A* 0,714 a *B* alely 0,286; u plemene landrase genotyp *BB* detekován nebyl. Frekvence alel *A* a *B* genu *MYF4* byla u plemene bílé ušlechtilé 0,660 a 0,340: u plemene landrase 0,917 a 0,083. Statisticky průkazný rozdíl mezi fenotypovými úrovněmi plochy svalu MLLT ($P \leq 0,05$) byl zjištěn mezi genotypy *AA*, *AB* a *BB C-MYC* genu u plemene LW. U prasat tohoto plemene byly také vypočteny statisticky průkazné rozdíly ($P \leq 0,05$) mezi genotypy *AA* : *BB* u ukazatelů plocha MLLT, procento HMČ a hmotnost HMČ (hlavních masitých částí) ve prospěch genotypu *BB* genu *MYF4*. Signifikantní rozdíly v naměřených úrovních ukazatelů jatečné hodnoty mezi různými genotypy genu *MYF4* prasat plemene landrase nebyly zjištěny.

Klíčová slova: prasata; plemena; jatečná hodnota; genotyp; *C-MYC; MYF4*

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