Arch. Tierz., Dummerstorf **47** (2004) 3, 231-238

Department of Genetics, Mendel University of Agriculture and Forestry Brno

PAVEL HORÁK, TOMÁŠ URBAN and JOSEF DVOŘÁK

Genetic variability of the *CRC* and *MYF4* genes in genetic resource, Přeštice Black-Pied pig

Abstract

The study of molecular genetic variability in genetic resources of farm animals is necessary for optimal conduct of their breeding and for understanding of relations between molecular markers and traits. The determination of variability in the *CRC* and the *MYF4* genes and the evaluation of associations between these genetic markers and the total number born, the number born alive and the number weaned of piglets, weaning weight of piglets and farrowing interval were carried out in population of 102 Přeštice Black-Pied sows. The frequency of the allele CRC^n (0.083) was found out to be markedly lower than the frequency of the allele CRC^N and there was observed no sow of homozygous recessive genotype in the investigated sample population. In *MYF4* locus, the higher frequency of the MYF^B allele was detected (0.711). A significant influence of the *CRC* gene polymorphism on number of piglets alive born in the 1st and the 1st - 6th litters was discovered. In the total number of born piglets the significant disparity were ascertained between the $MYF4^A/MYF4^A$ and $MYF4^A/MYF4^B$, $MYF4^A/MYF4^A$ and $MYF4^B/MYF4^B$ sows in the 2nd - 6th litters and the 1st - 6th litters. The obtained data are exploitable in genetic structure mapping, management of breeding and improvement of this breed and comparison with other pig genetic resources.

Key Words: genetic resource, pig, Přeštice Black-Pied, litter size, *CRC* gene, *MYF4* gene

Zusammenfassung

Titel der Arbeit: **Variabilität der Gene *CRC* und *MYF4* im Genreservoir des Přešticer Schwarzbunten Schweines**

Die Analyse der molekular-genetischen Variabilität der genetischen Herkünfte der Haustiere ist für ein optimales Zuchtmanagement sowie das Verständnis der Beziehungen zwischen den Molekularmarkern und Nutzmerkmalen notwendig. Untersucht wurden die Beziehungen zwischen der Variabilität der genetischen Marker *CRC* und *MYF4* und der Anzahl gesamt geborener, lebend geborener und Absatzferkel, den Absatzgewichten am 21. Tag sowie der Zwischentragezeit in einer 102 Muttersauen umfassenden Herde des Přešticer Schwarzbunten Schweines. Es ergaben sich deutlich niedrigere Frequenzen der Allele CRC^n (0,083) als der Allele CRC^N und es wurden bei keiner Sau der untersuchten Population homozygot rezessive Genotypen gefunden. Am Lokus *MYF4* wurde eine höhere Allelfrequenz bei $MYF4^B$ (0,711) beobachtet. Sowohl bei den 1. als auch den 1. bis 6. Würfen wurde ein signifikanter Einfluss des *CRC* Genpolymorphismus auf die Anzahl lebend geborener Ferkel nachgewiesen. Nachweisbare Unterschiede fanden sich bei der Anzahl gesamt geborener Ferkel der Sauen mit den Genotypen $MYF4^A/MYF4^A$ und $MYF4^A/MYF4^B$, $MYF4^A/MYF4^A$ und $MYF4^B/MYF4^B$ bei den 2. bis 6. und den 1. bis 6. Würfen. Die gefundenen Ergebnisse sind sowohl zur Beurteilung der genetischen Struktur der Rasse, dem Zuchtmanagement und der Selektion als auch für den Vergleich mit anderen genetischen Schweineherkünften nutzbar.

Schlüsselwörter: Genreservoir, Schwein, Přešticer Schwarzbuntes Schwein, Wurfleistung, *CRC* Gen, *MYF4* Gen

Introduction

One of goals of animal genetics is to locate and identify the loci that are responsible for economical important traits. Genetic resources of farm animals are very interesting branch of research, because these populations are not influenced by selection as much as the commercial hybrid lines. For preservation and conservation is needful to study genetic polymorphisms and their associations with production traits, as in improved breeds of pigs.

In the Czech Republic, the Přeštice Black-Pied pigs (PBP) have been declared as the genetic resource in 1991. At present, there are approximately 500 sows PBP bred in the Czech Republic, 350 of which are included in the population of genetic resources.
These pigs are bred mainly in West Bohemia. The following 16 breeds have participated in their genetic improvement: local Bavarian pigs, Large White, Middle White, Swabian – Hall, Berkshire, Large Black, Suffolk, Sussex, Essex, Mirgorod, Livny, Wessex Saddleback, Pietrain, Welsh, Landrase and Hampshire (FIEDLER and SMITAL, 2001). The Přeštice Black-Pied pigs are characterised by high fertility and excellent maternal properties but their disadvantage is higher back-fat thickness, lower % of lean muscle and worse conversion of fodder.
The effect of the *CRC* gene (ryanodine receptor 1) on the manifestation of malignant hyperthermia syndrome (MHS), carcass traits and meat quality in pigs has been studied in detail (FUJII et al., 1991; FISHER and MELLETT, 1997; de SMET et al., 1998). In the CRC^N/CRC^N genotype higher pH_1 and pH_{24}, backfat thickness and average daily gain and lower carcass lean were discovered (LARZUL et al., 1997; KUHN et al., 1998; KŘENKOVÁ et al., 1999; TOR et al., 2001). The sows of CRC^n/CRC^n genotype achieve lower total number of born piglets, number of piglets born alive, number of weaned piglets and number of litters per life (WITTMANN et al., 1992; DVOŘÁK, 1994). Likewise , the negative influence of CRC^n allele on sperm quality traits (volume, sperm concentration, mobility) in boars has proven (GREGOR and HARDGE, 1995; URBAN and KUCIEL, 2001).
The myogenin gene (*MYF4*), as well as *MYF3*, *MYF5* and *MYF6* genes, is a member of MYOD gene family (WEINTRAUB et al., 1991). The MYOD gene family controls a muscle fibre formation during embryonic development in mammals; the myogenin together with the *MYF3* gene induce the terminal transformation of myoblasts into myofibers (te PAS and VISSCHER, 1994). In the *MYF4* gene three *Msp*I polymorphic sites, in the promoter region, the second intron and the 3´side of the gene, have been observed (ERNST et al., 1993; SOUMILLION et al., 1997).
The polymorphism at the 3´side of the *MYF4* gene impacts on carcass traits and lean meat content in pigs. For example, CIESŁAK et al. (2000) noted, that $MYF4^A/MYF4^A$ homozygous animals obtain significantly higher half carcass meat weight, meat (%), ham meat weight, ham meat ratio, loin meat weight, loin meat ratio and loin eye area. Not much is known about the relationship between the polymorphism at the 3´side and fertility in pigs. It is associated with birth weight and mortality of piglets (te PAS et al., 1999). KANIAK – POLOK et al. (2001) described differences in several reproductive traits (e.g. number of piglets born alive, number of piglets at the 21 day, farrowing interval) between the sows of $MYF4^A/MYF4^A$ and $MYF4^B/MYF4^B$ genotypes.
The primary target of this study is to assess the genetic variation within Přeštice Black-Pied pigs by means of molecular genetic markers *CRC* and *MYF4*. A secondary aim is to evaluate the associations between polymorphism of these genes and reproduction traits in sows.

Materials and Methods

In the investigated population, there were included 102 Přeštice Black-Pied sows from several pedigree breedings. The genomic DNA was isolated from blood samples by using QIAamp®DNA Blood Mini Kit (QIAGEN GMBH).

The particular parts of the *CRC* and *MYF4* gene sequences were amplified by polymerase chain reactions as described by BRENIG and BREM (1992) and SOUMILLION et al. (1997), respectively. The predicted sizes of PCR products were 134 bp (the *CRC* gene) and 353 bp (the *MYF4* gene).

For the detection of mutant alleles the RFLP method was used. The restriction of the *CRC* gene PCR product was carried out by endonuclease *Hin6*I (FUJII et al., 1991). If the restriction site is present (wild allele CRC^N), the PCR product is cut into two fragments (84 and 50 bp). In the presence of the mutant allele (allele CRC^n), the PCR product stays intact. The PCR product of the *MYF4* gene is digested by endonuclease *Msp*I into 219 bp and 134 long fragments (allele $MYF4^A$). No restriction site is involved in the allele $MYF4^B$. Therefore, the PCR product is not cleaved (SOUMILLION et al., 1997).

The polymorphism degree of these candidate loci was determined by rate of heterozygosity (NEI, 1978) and polymorphism information content - PIC (BOTSTEIN et al., 1980). A general linear model (SAS, 2000) was used for the analysis of the associations between polymorphisms in the *CRC* and *MYF4* genes and total number of born piglets - TNB, number of piglets born alive - NBA, number of weaned piglets - NW, weaning weight of piglets (at the age of 21 days) - WW and farrowing interval - IF. Because of low significance of the 1st litters, we evaluated the effect of *CRC* and *MYF4* genotypes on reproductive traits in sows for the 1st, the 2nd – 6th and the 1st – 6th litters separately. In the fixed effect were included: genes *MYF4, CRC*, herd, year of sow birth and litter parity.

The models were as follows:

for the 1st litters

$$Y_{ijkl} = \mu + MYF4_i + CRC_j + H*Y_k + e_{ijkl}$$

and for the 2nd – 6th and the 1st – 6th litters

$$Y_{ijklm} = \mu + MYF4_i + CRC_j + H*Y_k + L_l + e_{ijklm}$$

where: $Y_{ijkl\,(m)}$ – trait value, μ – general mean, $MYF4_i$ – the effect of *MYF4* genotype (i = 1, 2, 3), CRC_j – the effect of *CRC* genotype (j =1, 2), $H*Y_k$ – the effect of the interaction between the herd and the year of sow birth (k = 1, 2, 3, 4, 5, 6, 7, 8, 9), L_l – the effect of the litter parity (l = 1, 2, 3, 4, 5, 6), $e_{ijkl(m)}$ – random residual

Table 1
Frequencies of genotypes and alleles in the *CRC* and *MYF4* genes in Přeštice Black-Pied sows (n = 102) (Genotypen- und Allelfrequenz der Gene *CRC* und *MYF4* bei Sauen der Rasse Přešticer Schwarzbuntes Schwein (n - 102))

Locus	Genotype	Frequency of genotypes	Allele	Frequency of alleles
CRC	CRC^N/CRC^N	0.833	CRC^N	0.917 ± 0.019
	CRC^N/CRC^n	0.167	CRC^n	0.083 ± 0.019
	CRC^n/CRC^n	0		
MYF4	$MYF4^A/MYF4^A$	0.078	$MYF4^A$	0.289 ± 0.032
	$MYF4^A/MYF4^B$	0.422	$MYF4^B$	0.711 ± 0.032
	$MYF4^B/MYF4^B$	0.500		

Results

Genetic variability in the *CRC* and *MYF4* gene

In our study a lower frequency of the allele CRC^n (0.083) than the frequency of the allele CRC^N in PBP sows was observed. There was no sow with genotype CRC^n/CRC^n in the investigated population. The frequency of dominant homozygous genotypes CRC^N/CRC^N was very high compared to genotypes CRC^N/CRC^n (Table 1).

The frequency of the allele $MYF4^B$ was found to be higher than the frequency of allele $MYF4^A$. There were more sows with $MYF4^B/MYF4^B$ genotypes than $MYF4^A/MYF4^B$ heterozygotes in the population of PBP. The frequency of genotypes $MYF4^A/MYF4^A$ was clearly the lowest (Table 1).

CRC locus showed lower heterozygosity and polymorphism information content than *MYF4* (Table 2), because of missing recessive homozygotes CRC^n/CRC^n.

Table 2
Summary of the polymorphism level for both loci in Přeštice Black-Pied pigs: heterozygosity (Het.) - NEI (1978); polymorphism information content (PIC) - BOTSTEIN et al. (1980) (Polymorphismus-Niveau beider Loci der untersuchten Sauen)

Locus	Het.	PIC
CRC	0.1538	0.1400
MYF4	0.4151	0.3270
Average Het.	0.2844	

Associations of the polymorphism in the *CRC* gene with reproduction traits

In the 1st litters the polymorphism in the *CRC* gene influenced significantly NBA ($P \leq 0.05$). The dominant homozygous sows showed also higher TNB, NW and WW than heterozygous sows (Table 3). No significant differences were found out between CRC^N/CRC^N and CRC^N/CRC^n genotypes in the 2nd – 6th litters, although homozygous sows were better in TNB, NBA, NW and WW as well as in the 1st litters. However, the sows of CRC^N/CRC^n genotypes had shorter farrowing interval.

Table 3
Associations between reproduction traits and genotypes of the *CRC* gene and the *MYF4* gene in Přeštice Black-Pied sows (least-square means LSM ± standard error S_E) (Beziehungen zwischen den Wurfleistungsmerkmalen und Genotypen der Gene *CRC* und *MYF4* der untersuchten Sauen (LSM und S_E))

Genotypes	NL	TNB	NBA	NW	WW	IF
			the 1st litters			
CRC^N/CRC^N	85	11.52 ± 0.32	10.57^{*} ± 0.32	9.81 ± 0.29	54.40 ± 1.88	-
CRC^N/CRC^n	17	10.68 ± 0.65	9.17^{*} ± 0.64	9.06 ± 0.59	49.32 ± 3.58	-
$MYF4^A/MYF4^A$	8	11.03 ± 0.91	9.34 ± 0.90	9.19 ± 0.83	50.52 ± 5.21	-
$MYF4^A/MYF4^B$	43	11.19 ± 0.43	10.11 ± 0.42	9.61 ± 0.39	52.70 ± 2.34	-
$MYF4^B/MYF4^B$	51	11.08 ± 0.36	10.16 ± 0.36	9.51 ± 0.33	52.36 ± 2.03	-
			the 2nd - 6th litters			
CRC^N/CRC^N	368	13.11 ± 0.21	11.86 ± 0.19	10.33 ± 0.17	58.17 ± 1.24	169.76 ± 3.08
CRC^N/CRC^n	83	12.57 ± 0.40	11.28 ± 0.36	10.23 ± 0.32	56.95 ± 2.19	165.62 ± 5.81
$MYF4^A/MYF4^A$	39	$14.06^{**,***}$ ± 0.55	11.92 ± 0.50	10.12 ± 0.45	56.34 ± 3.05	165.58 ± 8.10
$MYF4^A/MYF4^B$	186	12.04^{***} ± 0.27	11.28 ± 0.25	10.27 ± 0.22	57.65 ± 1.51	169. 44 ± 3.99
$MYF4^B/MYF4^B$	226	12.44^{**} ± 0.24	11.52 ± 0.21	10.45 ± 0.19	58.68 ± 1.31	168.05 ± 3.46
			the 1st - 6th litters			
CRC^N/CRC^N	453	12.85 ± 0.18	11.65^{*} ± 0.16	10.27 ± 0.15	57.74 ± 1.03	-
CRC^N/CRC^n	100	12.25 ± 0.35	10.93^{*} ± 0.32	10.04 ± 0.28	55.98 ± 1.87	-
$MYF4^A/MYF4^A$	47	$13.52^{**,**}$ ± 0.48	11.47 ± 0.44	9.96 ± 0.40	55.66 ± 2.65	-
$MYF4^A/MYF4^B$	229	11.92^{**} ± 0.24	11.10 ± 0.22	10.19 ± 0.19	57.07 ± 1.27	-
$MYF4^B/MYF4^B$	277	12.22^{**} ± 0.20	11.30 ± 0.18	10.32 ± 0.17	57.85 ± 1.09	-

Note: NL-number of investigated litters, TNB- total number of born piglets, NBA- number of piglets born alive, NW-number of weaned piglets, WW - weaning weight of piglets (at the age of 21 days), IF - farrowing interval;
Values with superscripts in columns show significant differences: * $P \leq 0.05$, ** $P \leq 0.01$, *** $P \leq 0.001$

The significant associations ($P \leq 0.05$) between polymorphism in the *CRC* gene and NBA were also observed in a joint analysis of the $1^{st} – 6^{th}$ litters.

Associations of the polymorphism in the *MYF4* gene with reproduction traits

The highest TNB, NW and WW in the 1^{st} litters were recorded in heterozygous sows. The $MYF4^B/MYF4^B$ sows produced most born alive piglets but no differences were significant (Table 3). In the $2^{nd} – 6^{th}$ litters, we determined significant differences between sows of $MYF4^A/MYF4^A$ and $MYF4^B/MYF4^B$ genotypes ($P \leq 0.01$) and between sows of $MYF4^A/MYF4^A$ and $MYF4^A/MYF4^B$ genotypes ($P \leq 0.001$) in TNB. Homozygous $MYF4^A/MYF4^A$ sows excelled in number of born alive piglets. NW and WW from $MYF4^B/MYF4^B$ sows were higher than those from other genotypes. The longest farrowing interval was found out in heterozygous sows.

The similar results we detected in the $1^{st} – 6^{th}$ litters, where significant differences ($P \leq 0.01$) in TNB between sows of $MYF4^A/MYF4^A$ and $MYF4^B/MYF4^B$ genotypes as well as between sows of $MYF4^A/MYF4^A$ and $MYF4^A/MYF4^B$ genotypes were evaluated.

Discussion

The absence of CRC^n/CRC^n genotypes and low frequency of the recessive allele in *CRC* loci were surprising. On the basis of references, we supposed the incidence of the CRC^n allele in PBP sows is more frequent. For instance, ČEPICA et al. (1982) described that an occurrence of this allele is 0.348 (more recent data about PBP are not available). The substantial reduction of the recessive allele numerousness must have been caused by efforts of exclusion of CRC^N/CRC^n and CRC^n/CRC^n genotypes from reproduction in pedigree breedings that were performed despite declaration of Přeštice Black-Pied pigs as the gene reserve. Thereby, the immigration of CRC^n alleles from Landrase breed that was used for the genetic improvement of PBP in 1986 (KLUSÁČEK et al., 1991), could not increase the frequency of the recessive allele in PBP sows either.

If we compared our data with references about the *CRC* gene variability in Landrase (L) and Large White (LW) breed in the Czech Republic, we found slight differences only. BEČKOVÁ et al. (2002) and MATOUŠEK et al. (2003) noted the frequency of the recessive allele 0.01 in Landrase sows and 0.025 – 0.045 in Large White sows. However, the incidence of the CRC^n allele in L and LW breed was far higher a few years ago – 0.22 and 0.06, respectively (KAHÁNKOVÁ et al., 1996). Well, just as the frequency of the recessive allele has dropped in L and LW breed, so it has in Přeštice Black-Pied sows.

There are no original data about the *Msp*I variability of the *MYF4* gene in Přeštice Black-Pied pigs accessible, so we could not assess if changes of genotypes and alleles frequencies have happened within evolution of this breed. It is remarkable that similar results ($MYF4^B = 0.68$) were obtained in autochthonous breed – Zlotnicka Spotted in Poland (CIESŁAK et al., 2000). In contrast to the PBP breed, there is more frequent occurrence of the $MYF4^A$ allele than the $MYF4^B$ allele in L (0.545 – 0.680) and LW (0.750) breed (KOLAŘÍKOVÁ et al., 2002; PUTNOVÁ et al., 2001). These dissimilarities may be explained by more stringent selection to carcass characteristics and meat quality in L and LW breed, because the $MYF4^A$ allele conditions a superior level of these traits (te PAS et al., 1999).

It is obvious from Table 2, that *CRC* and *MYF4* loci demonstrate a different degree of polymorphism measured by heterozygosity and by polymorphism information content in the PBP population. This finding can be elucidated by marker assisted selection implemented in the *CRC* gene as opposed to the *MYF4* gene.

The evaluation of associations between the variability in the *CRC* gene and reproductive traits in PBP sows proved the outcomes in other maternal breeds (DVOŘÁK, 1994; KMIEĆ et al., 2002), because the sows of CRC^N/CRC^N genotypes showed the higher TNB, NBA and NW than the heterozygous ones.

Piglets of $MYF4^A/MYF4^A$ genotypes have greater birth weight, which decreases their mortality (te PAS et al., 1999). Therefore, we expected the sows of $MYF4^A/MYF4^A$ genotypes would achieve more weaned piglets compared to $MYF4^B/MYF4^B$ or $MYF4^A/MYF4^B$ genotypes. These assumptions were not shown to be correct in this study. The homozygous $MYF4^A/MYF4^A$ sows surpassed the sows of $MYF4^A/MYF4^B$ and $MYF4^B/MYF4^B$ genotypes in TNB and NBA in the 2^{nd} – 6^{th} and the 1^{st} – 6^{th} litters. Nevertheless, in NW as well as in WW were the sows of $MYF4^B/MYF4^B$ genotypes the best. Some researches point out potential associations of the polymorphism at the 3´side of the *MYF4* gene on fertility (KANIAK – POLOK et al., 2001), but this hypothesis neither has been confirmed nor has been disproved so far.

That said data could assist in genetic structure assessing, the proposal of measures concerning the breeding and improvement of this breed as well as for comparison with other genetic resources of pigs. The loci described here are utilized for this purpose well. The increment of loci number and inclusion of all chromosomes in the evaluation are essential (WITTMANN and DOHY, 1999) for proper genetic appraisal of Přeštice Black-Pied pigs.

Acknowledgements

The authors would like to thank S. CAPSTICK for linguistic revision of a manuscript and Bc. I. VRTKOVÁ for technical assistance. This study was supported by grant MSM 432100001 and Czech Science Foundation (Project No. 523/03/H076).

References

BEČKOVÁ, R.; DVOŘÁK, J.; DANĚK, P.; ROZKOT, M.:
Genetic fertility markers in Landrace pigs in the Czech Republic. Ann. Anim. Sci. **2** (2002), 103 - 108

BOTSTEIN, D.; WHITE, R.L.; SKOLNICK, M.; DAVIS, R.W.:
Construction of genetic linkage map in man using restriction fragment length polymorphisms. Am. J. Hum. Genet., **32** (1980), 314 – 331

BRENIG, B.; BREM., G.:
Molecular cloning and analysis of the porcine "halothane" gene. Arch. Tierz., Dummerstorf **35** (1992), 129-135

CIESŁAK, D.; KAPELAŃSKI, W.; BLICHARSKI, T.; PIERZCHALA, M.:
Restriction fragment length polymorphisms in *myogenin* and *myf3* genes and their influence on lean meat content in pigs. J. Anim. Breed. Genet., **117** (2000), 43-55

ČEPICA, S.; HOJNÝ, J.; HRADECKÝ, J.; KLAUDY J.:
Study on the sensitivity to halothane and associations between HAL and PHI, H-loci, A-loci, and S-loci in the pigs of Prestitzer black-pied breed (in Czech). Živočišná výroba **27** (1982), 587 – 593

DVOŘÁK, J.:
Genetical analysis of susceptibility to stress and its effect on reproduction and selection breeding in pigs (in Czech). Acta univ. agric. Brno, fac. agron. (1994), 179-189

ERNST, C.W.; VASKE, D.A.; LARSON, R.G.; ROTHSCHILD, M.F. :
MspI restriction fragment length polymorphism at the swine MYOG locus. J. Anim. Sci. **71** (1993), 3479

FIEDLER, J.; SMITAL, S.:
The look into history of pig breeding (in Czech). Náš chov **9** (2001), 35-38
FISHER, P.; MELLETT, F.D.:
Halothane genotype and pork production.1 growth, carcass and meat quality characteristics. S. Afr. Tydskr. Veek., 27/1 (1997), 22-26
FUJII, J.; OTSU, K.; ZORZATO, F.; DE LEON, S.; KHANNA, V.K.; WEILER, E.J.; O´BRIEN, P.J.; MACLENNAN, D.H.:
Identification of a Mutation in Porcine Ryanodine Receptor associated with Malignant Hyperthermia. Science **26** (1991), 448-451
GREGOR, G.; HARDGE, T.:
Zum Einfluss von Ryanodin-Rezeptor-Genvarianten auf Spermaqualitätsmerkmale bei KB-Ebern. Arch. Tierz., Dummerstorf **38** (1995), 527-538
KAHÁNKOVÁ, L.; DVOŘÁK, J.; NEBOLA, M.; VRTKOVÁ, I.; HRADIL, R.:
Diversity of the populations of Large White and Landrase breed in the Czech Republic in the 1995 from the standpoint of genotypes RYR (in Czech). Živočišná výroba **41** (1996), 285-289
KANIAK-POLOK, M.; POLOK, P.; JASEK., S.:
The influence of polymorphism on the porcine myogenin locus on certain reproductive traits of sows PBZ (in Polish). In Sb.: Zeszyty naukowe Akademii Rolniczej we Wroclawiu – Konferencje XXXI (2001), 101-110
KLUSÁČEK, J.; DIBLÍK, T.; SVOBODA, V.; DOMABYL, V.:
Production potential of the Prestice Black-Pied and improved Prestice Black- Pied pigs (in Czech). Živočišná výroba **36** (1991), 649-650
KOLAŘÍKOVÁ, O.; VRTKOVÁ, I.; URBAN, T.; ADÁMEK, J.; DVOŘÁK J.:
Influence of polymorphism of MYOGENIN gene on growth and meat efficiency in pigs. Acta univ. agric. et silvic. Mendel. Brun. (Brno), **5** (2002), 15 – 19
KŘENKOVÁ, L.; KUCIEL, J.; URBAN, T.:
Association of the *RYR1, GH, LEP* and *TF* genes with carcass and meat quality traits in pigs. Czech J. Anim. Sci., **44** (1999), 481-486
KMIEĆ, M.; DVOŘÁK, J.; VRTKOVÁ, I.:
Relation between the polymorphism in the ryanodine receptor gene (*RYR1*) and certain reproductive traits of sows in a herd of Polish Landrace pigs. Anim. Sci. Pap. and Rep., 18 (2002), 277-283
KUHN, G.; HARTUNG, M.; NÜRNBERG, K.; FIEDLER, I.; FALKENBERG, H.; NÜRNBERG, G.; ENDER, K.:
Körperzusammensetzung und Muskelstruktur von genetisch differenten Schweinen in Abhängigkeit vom MHS-Status. Arch. Tierz., Dummerstorf **41** (1998), 589-596
LARZUL, C.; LE ROY, P.; GUEBLEZ, R.; TALMANT, A.; GOGUE, J.; SELLIER, P.; MONIN, G.:
Effect of halothane genotype (*NN, Nn, nn*) on growth carcass and meat quality traits of pigs slaughtered at 95 kg or 125 kg live weight. J. Anim. Breed. Genet., **114** (1997), 309-320
MATOUŠEK, V.; KERNEROVÁ, N.; KOLAŘÍKOVÁ, O.; KŘÍŽOVÁ, H.; URBAN, T.; VRTKOVÁ, I. :
Effect of *RYR1* and *ESR* genotypes on the fertility of sows of Large White breed in elite herds. Czech J. Anim. Sci. **48** (2003), 129 - 133
NEI, M.:
Estimation of average heterozygosity and genetic distance from a small number of individuals. Genetics, **89** (1978), 583 – 590
PUTNOVÁ, L.; KOLAŘÍKOVÁ, O.; NATOLOCZNA-KOTARA, A.; KANIAK-POLOK, M.; VRTKOVÁ, I.; DVOŘÁK, J.:
Polymorphism of OPN, ESR2, PRLR, MYF4 genes of the pig in the Czech Republic and Poland. Zeszyty naukowe Akademii rolniczej we Wroclawiu, (2001), 225-233
SAS.SAS/STAT:
User´s Guide (Release 8.01). SAS Inst. Inc. Cary, NC. (2000)
SOUMILLION, A.; ERKENS, J.H.F.; LENSTRA, J.A.; RETTENBERGER, G.; TE PAS, M.F.W.:
Genetic variation in the porcine myogenin gene locus. Mammalian Genome **8** (1997), 564-568
de SMET, S.; BLOEMEN, H.; van der VOORDE, G.; SPINCEMAILLE, G.; BERCKMANS, D.:
Meat and carcass quality in two pig lines of different stress susceptibility genotype and their crosses. Anim. Sci., **66** (1998), 441-447
te PAS, M. F. W.; SOUMILLION, A.; HARDERS, F. J.; VERBURG, F. J.; VAN DER BOSCH, T. J.; GALESLOOT, P.; MEUWISSEN, T. H. E.:
Influences of Myogenin Genotypes on Birth Weight, Growth Rate, Carcass Weight, Backfat Thickness, and lean Weight of Pigs. J. Anim. Sci. **77** (1999), 2352-2356
te PAS, M.F.W.; VISSCHER, A.H.:
Genetic regulation of meat production by embryonic muscle formation – a review. J. Anim. Breed. Genet., **111** (1994), 404-412

TOR, M.; ESTANY, J.; VILLALBA, D.; CIBILÓ, D.; TIBAU, J.; SOLER, J.; SANCHEZ, A.; NOGUERA, L.:
A within-breed comparison of RYR1 pig genotypes for performance, feeding behaviour, and carcass, meat and fat quality traits. J. Anim. Breed. Genet., **118** (2001), 417-427

URBAN, T.; KUCIEL, J.:
The effect of point mutation in the RYR1 gene on the sperm quality traits in boars of Large White and Landrace breeds. Czech J. Anim. Sci. **46** (2001), 460 - 464

WEINTRAUB, H.; DAVIS, R.; TAPSCOTT, S.; THAYER, M.; KRAUSE, M.; BENEZRA, R.; BLACKWELL, T.K.; TURNER, D.; RUPP, R.; HOLLENBERG, S.; ZHUANG, Y.; LASSAR, A.:
The *myoD* Gene Family: Nodal point During Specification of the muscle Cell Lineage. Science (1991), 761-765

WITTMANN, W.; DOHY, J.:
On some possibilities and prospects of gene conservation and utilisation of pig breeds. Arch. Tierz., Dummerstorf **42** (1999), 57-66

WITTMANN, W.; HOJNY, J.; CWICK, S.; SCHMID D.O.; KRAUS, H.; HAUSER, M.; BLENDL, M.H.:
Selektion homozygot streßresistenter Linien bei DL-Schweinen mittels Markergenen. Arch. Tierz., Dummerstorf **35** (1992), 119-127

Received: 2003-09-23

Accepted: 2004-05-12

Author´s address
Ing. PAVEL HORÁK, Ing. TOMÁŠ URBAN, PhD., Prof. Ing. JOSEF DVOŘÁK, CSc.
Department of Genetics
Mendel University of Agriculture and Forestry Brno
Zemedelska 1
635 00 BRNO
Czech Republic

E-Mail: horakpav@email.cz