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Short Communication

Polymorphism in the gene *FABP*3 and its association with indicators of meat quality in pigs

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The objective of this study was to analyze the variability of the *FABP*3 gene (heart fatty acid-binding protein) in the population of pig Czech large white breed and to analyze the association with parameters of meat quality. *FABP*3 belongs to multigene family of *FABP*s (fatty acid binding proteins affecting the transport of long chain fatty acids). Analyzed polymorphism was at position X98558:g.1321 *G* > *C* in the 5′ UTR region. The relative frequencies of genotypes were: *HH* = 0.87and *Hh* = 0.13. Genotype hh was not detected in the population. The frequencies of alleles were as follows: *H* = 0.93 and *h* = 0.07. There were statistically significant associations between genotypes and values of stearic acid and linoleic acid. Highly statistically significant difference was observed with palmitic acid.

Keywords: SNP polymorphism, *FABP*3, pig, fatty acids

1 Introduction

Meat quality is defined by the characteristics of sensory experience and meat technological quality traits. A higher level of intramuscular fat (IMF) has a positive influence on the pork sensory characteristics and shows a positive correlation with meat tenderness, juiciness, and taste (Fernandez et al., 1999; Reardon et al., 2010). The fatty acid composition of pork has been analyzed due to its effects on meat quality and its association with human health (Wang et al., 2013).

Porcine fatness traits are changed through genetics (selective breeding) and candidate genes have been as well identified. Significantly associated candidate genes are *FABP*3 and LEPR gene (Tyra et al., 2010; Chmurzyńska, 2006), MASTR (Han et al., 2012), MC4R (Wang et al., 2013), MTTP and FASN (Maharani et al., 2012).

The objective of this investigation was to correlate the variability in *FABP*3 gene (heart fatty acid-binding protein) with the IMF content and fatty acid composition in muscle of Czech Large White pigs.

2 Material and methods

For this study, 104 pigs of the breed Czech Large White were selected from nucleus herd. Blood samples were collected immediately after slaughter into EDTA tubes. Meat quality was evaluated in all individuals by the following features: meat color (L, a, b), pH ultimate, drip loss, the electrical conductivity of the meat, dry matter, the percentage and content of intramuscular fat, and fatty acids composition.

Polymorphism was analyzed by PCR-RFLP method. Primers for amplification of the fragments were taken from a study of Pang et al. (2006) with modifications for the specific conditions of our laboratory: FW: 5′-GGACCCAAGATGCCTACGCCG-3′ and RV: 5′-CTGC AGCTTTGACCAAGAGG-3′. The size of the resulting PCR product was 693 bp. The PCR reaction mixture was prepared on ice in a total volume of 25 μl containing 2 μl of genomic DNA, 0.5 μl dNTP mix, 0.5 μl, FW primer, 0.5 μl RV primer, 0.2 μl polymerase pd. Unis, 2.5 μl buffer, and 18.8 μl H_2O. The amplification conditions were as follows: 94 °C for 3 min, 35 cycles of 94 °C for 30 s, 62 °C for 30 s, 72 °C for 50 s, and a final extension of 72 °C for 10 min.

SNP X98558 g.1321 *G* > *C* in 5′ UTR region of *FABP3* was analyzed by *Hinf*I restriction endonuclease. PCR product was digested overnight with 3 U *Hinf*I in a total volume of 15 μl at 37 °C, and subsequently size-separated on 3.0% agarose gel.

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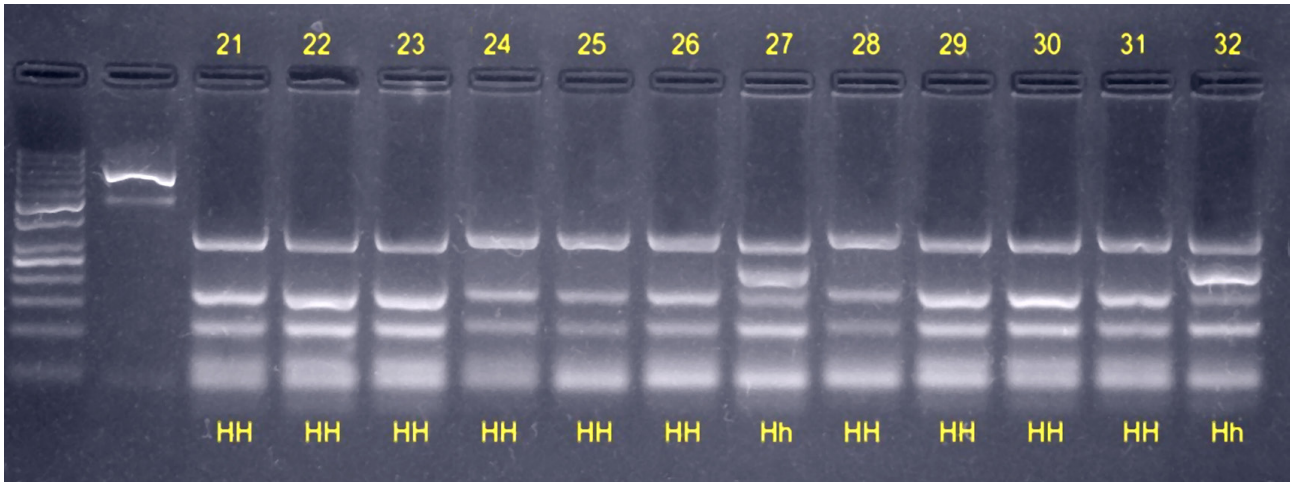

Figure 1 Results of PCR product and PCR-RFLP (*Hinf*I – digestion of the 693 PCR product, Lanes 21–26, 28–31: *HH*; 27 and 32 *Hh*)

Association analysis was performed in SAS (Ver. 9.1.4, SAS Institute, Cay, NC, USA) by general linear model with one fixed effect of genotype of *FABP*3 gene.

3 Results and discussion

The polymorphism X98558g.1321*G* > *C* detected in 5´ UTR region of *FABP*3 gene was genotyped in Czech Large White pigs (Figure1). The 693 bp PCR product of the *G/C* polymorphism of 5'UTR of the *FABP*3 gene was digested with *Hinf*I, cleaving the H allele into four fragments (339, 172, 98 + 59 bp) and cleaving the h allele into four fragments (339, 231, 98 +25 bp).

Frequencies of alleles *H* and *h* were 0.93 and 0.07, respectively. The genotype frequencies *HH* = 0.87 and *Hh* = 0.13 were at Hardy-Weinberg equilibrium.

Association analysis performed with studied SNP revealed statistically significant differences between genotypes of *FABP*3 gene and quality of pork (Table 1).

Table 1 Association of *FABP*3 gene with meat quality traits in pig (LSM ±SE)

Traits	*FABP*3 genotypes	
	HH	*Hh*
L	61.62 ±0.53	59.55 ±1.35
a	1.92 ±0.17	1.77 ±0.44
b	12.51 ±0.18	11.69 ±0.47
pH_{ult}	5.54 ±0.02	5.60 ±0.05
EV_{24} (mS)	8.97 ±0.22	9.07 ±0.55
Drip loss (%)	3.04 ±0.04	2.86 ±0.11
Dray matter (%)	29.58 ±0.35	29.72 ±0.90
Myristoleic acid (%)	1.48 ±0.03	1.46 ±0.07
Palmitic acid (%)	28.88 ±2.70 **	49.24 ±6.85 **
Palmitoleic acid (%)	4.44 ±0.42	4.23 ±1.08
Stearic acid (%)	15.58 ±0.24 *	17.29 ±0.62 *
Oleic acid (%)	46.32 ±2.07	40.96 ±5.26
Arachidonic acid (%)	0.44 ±0.07	0.55 ±0.12
Linoleic acid (%)	3.41 ±0.08 *	3.90 ±0.21 *
EPA (%)	0.25 ±0.01	0.23 ±0.03
IMT (g)	1.31 ±0.05	1.13 ±0.14
IMT (%)	3.87 ±0.16	3.44 ±0.41

Meat color: L – lightness, a – redness and greenness, b – yellowness and blueness; pHult – value of pH and EC24 – electric conductivity after 24 hours post mortem, EPA – eicosapentaenoic acid, IMF – Intramuscular fat. *$P < 0.05$, **$P < 0.01$

It can be concluded that *HH* genotype had a lighter meat color, lower pH (more acidic) and thus drip loss was higher than in genotype *Hh*. But these values are not statistically significant. *HH* genotype tended to a higher proportion of red and yellow meat color. Furthermore, this genotype shows tendency to higher content of fatty acids: myristoleic acid, palmitoleic acid, oleic acid and EPA, and intramuscular fat content. *Hh* genotype was found with higher content of palmitic ($P < 0.01$), stearic ($P < 0.05$), arachidonic, linoleic ($P < 0.01$) acids, and genotype *Hh* has also been found to have higher percentage of dry matter content. However, only differences in content of stearic acid, linoleic acid and palmitic acid were statistically significant.

4 Conclusions

The porcine *FABP*3 gene showed significant association with content of palmitic acid, stearic acid and linoleic acid: animals of genotype *Hh* had higher content of palmitic and linoleic acids than those of genotype *HH* ($P < 0.01$), and individuals with *Hh* genotype had higher content of stearic acid than those with *HH* genotypes ($P < 0.05$).

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