Association of H-FABP (*Hinf*I) Gene with Carcass and Meat Quality Characteristics in Pigs

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Abstract
Our aims were to analyze how this polymorphism influence to carcass traits in crossbred pigs. For our experiment we used biological material from pigs of hybrid combination Large White and Landrace. A total of 106 animals were genotyped using the *Hinf*I restriction enzyme. Three genotypes were identified, 51 being animals HH, 41 Hh and 14 hh. The carcasses of hh pigs had higher carcass percentage of lean meat LM (55.26), MLT area (45.30), (statistically significant higher in comparison hh to HH genotype), half carcass weight (40.84) and back-fat thickness BFT (18.57), as compared with the Hh and HH pigs. We confirmed a statistically significant correlation between carcass traits of genotypes. Statistically most significant were correlations between LM to BFT (-0.8336) and half carcass weight to MLT area (0.5902) in genotype hh. In the other genotypes was a similar trend but with a lower significance. Our results showed the potential of the H-FABP gene in selection programs for carcass traits in pigs.

Keywords: carcass trait, H-FABP (*Hinf*I), pig, polymorphism.

1. Introduction

During the past few decades, advances in molecular genetics have led to the identification of multiple genes or genetic markers associated with genes that affect traits of interest in livestock, including genes for single-gene traits and QTL or economic regions that affect quantitative traits. The main application and potential for use of markers to enhance genetic improvement in livestock is through within-breed selection. This requires markers that trace within-breed variability [1]. Due to the demand for inexpensive and lean pork during the last decades, a considerable reduction of the fat content of carcasses has been registered in pig populations [2].

Fatty acid binding proteins (FABPs) are proteins of ~15 kDa that constitute a family of intracellular lipid-binding proteins [3].

The H-FABP gene, which is generally considered to be a candidate gene for fatness traits in the pig, is involved in the regulation of fatty acid utilization in skeletal muscle [4]. Some studies reported that a significant association between the H-FABP gene and intramuscular fat (IMF) content. [5,6,7] located pig *H-FABP* gene on the sixth chromosome and discovered *Msp*I, *Hae*II and *Hinf*I polymorphism of the H-FABP gene that is related to intramuscular fat content.

[6] Reported association of H-FABP gene on backfat thickness in Duroc breed. They also shown difficult evaluation of H-FABP protein association on backfat thickness because of this protein does not express in cells of adipose tissue. They consider that the thickness of fat affect genes that are in linkage with H-FABP gene, such as genes coding for phosphogluconate dehydrogenase (PGD), glucosephosphate isomerase (GPI) and RYR1.

In view of the HFABP gene playing an important role in carcass/meat traits, this work was conducted to investigate the polymorphism of this gene and its effect on carcass characteristics (half

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carcass weight, percentage of lean meat, percentage of thigh, back-fat thickness, MLT area) in the Large White x Landrace crossbred pig populations, to obtain information which would assist in their selection.

2. Materials and methods

The material involved 106 pigs (51 boars, 55 sows) randomly selected. The population of pigs consisted of hybrids Large White x Landrace (LW x LA).

Genomic DNA was extracted from blood samples and PCR–RFLP *Hinf*I test was used to identify genotypes in the H-FABP gene according to the protocol described by [5].

The observed carcass traits (half carcass weight, lean meat percentage, thigh percentage, back-fat thickness and MLT area - *musculus longisimus thoracis*) were measured by standard methodology [8].

T-test was used to calculate basic statistical characteristics and to determine significant differences between H-FABP genotypes to carcass characteristics.

3. Results and discussion

We identified three genotypes in the set of pigs, HH(51), Hh(41) a hh(14). Allele H showed higher frequency than allele h (0.6745 vs. 0.3255). Allele and genotype frequencies are presented in Table 1. [9] confirmed high occurrence of H allele in Large White and Landrace breeds and not found hh genotype in Large White pigs. Frequencies of genotypes and alleles at H-FABP (*Hinf*I) were previously studied [10] in pigs (Large White, Landrace, Duroc) with the following results: HH (0.481), Hh (0.438), hh (0.081), allele H (0.700 ± 0.026) and h (0.300 ± 0.026). [11] and [12] found a similar frequency of allele H (0.678 or 0.686) in Large White x Landrace crossbred. [13] found a very high frequency of H allele in a commercial Norwegian three-way pig cross. [14]) also found high frequency of H allele (0.64) in Berkshire pigs. Our results are consistent with the finding of the authors, whereas in our group of pigs was a similar occurrence of the allele H (0.6745).

The observed significant associations of individual genotypes of H-FABP gene with parameters of carcass and meat production are presented in Table 2. Highly significant differences were found between genotypes hh (45.30±3.02) and HH (43.02±4.46) for MLT area. Significant differences were not found in the other parameters. The hh genotype was associated with the highest carcass weight, LM and MLT area among the H-FABP RFLP genotypes groups. Therefore, there appeared to be the best genotype hh, although to attain the highest back-fat thickness (18.57±4.37). [9] detected non significant differences between individual genotypes of Large White, Pietrain and Landrace breeds in percentage of LM and their results are slightly different from our findings. [14] not found significant differences between genotypes in carcass weight and BFT and their findings in the evaluation of BFT had a similar tendency as our results: HH (24.23 ± 0.67), HH (23.79 ± 0.73), hh (3.25 ± 1.06), as well as for carcass weight.

Correlations among carcass/meat quality traits are presented in Table 3. Negative very high (-0.8336) and high (-0.5173, -0.5938) correlations were estimated for BFT with percentage of LM. Very high (0.8315, 0.8279) and moderate (0.4102) correlations were estimated for percentage of thigh with percentage of LM. High correlations of 0.5583 and 0.5902 were estimated between half carcass weight with percentage of thigh and MLT area in hh genotype. This study reported negative high correlation between BFT with percentage of LM (-0.5938) and percentage of thigh (-0.5547). [15] identified correlation of H-FABP genotype of parents with muscle thickness of offsprings and the influence of maternal genotype for lean meat percentage.

Table 1. Frequency of genotypes and alleles of *H-FABP* gene in the pig population

Group	n	H-FABP genotypes			H-FABP allele	
		HH	Hh	hh	H	h
Boars	51	0.530	0.333	0.137	0.6961	0.3039
Sows	55	0.436	0.436	0.128	0.6545	0.3455
Total	105	0.481	0.387	0.132	0.6745	0.3255

Table 2. The effect of *H-FABP* genotypes on carcass and meat quality traits in crossbred pigs

Traits	min./max.	Genotype		
		HH (51)	Hh (41)	hh (14)
Half carcass weight (kg)		40.73±0.90	40.80±1.43	40.84±1.54
	min.	38.75	37.64	38.67
	max.	42.88	44.69	43.37
Lean meat (%)		54.76±2.00	54.95±2.17	55.26±2.42
	min.	50.27	50.16	49.74
	max.	58.46	59.68	59.10
Thigh percentage (%)		22.23±1.14	22.51±1.34	22.62±1.79
	min.	19.98	19.37	19.65
	max.	24.84	25.34	26.67
Back-fat thickness (mm)		18.04±3.94	17.99±2.67	18.57±4.37
	min.	11.33	11.66	13.67
	max.	27.00	23.67	26.67
MLT area (cm^2)		43.02±4.46^{+}	43.93±4.17	45.30±3.02^{+}
	min.	37.20	37.10	41.80
	max.	61.70	55.00	50.60

$^{+}$ = P ≤0.05, $^{++}$ = P ≤0.01, $^{+++}$ = P ≤0.001

Table 3. Likelihood estimates of correlations between carcass/meat traits in the H-FABP genotypes

Trait*	genotype	HCW	LM	Thigh	BFT
LM	HH	-0.1308			
Thigh		-0.1748	0.8279		
BFT		0.1643	-0.5938	-0.5547	
MLT		0.0175	0.4163	0.3491	-0.0195
LM	Hh	-0.0406			
Thigh		-0.0875	0.8315		
BFT		0.0205	-0.5173	-0.4346	
MLT		0.1349	0.4453	0.3242	-0.0563
LM	hh	0.1188			
Thigh		0.5583	0.4102		
BFT		-0.2217	-0.8336	-0.1213	
MLT		0.5902	0.3038	0.4145	-0.2485

*HCW-half carcass weight, LM-percentage of lean meat, Thigh-percentage of thigh, BFT-back-fat thickness, MLT-musculus longisimus thoracis area

4. Conclusions

The results presented here, shows the existence associations between carcass traits and H-FABP genotypes in crossbred pigs. The study showed that in analyzed lines of pigs H-FABP (polymorphism *Hinf*I) could be associated to carcass traits of economic relevance. It is therefore still not possible to draw any clear conclusion based on our results.

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