Effects of the Porcine LEPR Polymorphism (*Hpa*ii) on Carcass Traits in Large White × Landrace Crossbred Pigs

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Abstract
The aim of the study was to establish the relationship between leptin receptor (LEPR) gene polymorphism and carcass quality traits in pigs (LWxL). The genotypes of LEPR gene were determined in 106 hybrid pigs. The polymorphism of LEPR gene was analyzed by PCR-RFLP method using the *Hpa*II restriction enzyme. Three genotypes were identified, 45 being animals AA, 42 AB and 19 BB. The back-fat thickness (BFT) was higher and percentage of lean meat (LM) was lower in AA genotype compared to BB genotype (19.05 > 17.21, 54.53 < 55.68). The significant effect of back-fat thickness was observed between AA (19.05) to AB (17.46) and BB (17.21) genotypes. Statistically most significant were correlations between BFT (-0.7417) to LM percentage and percentage of thigh in BB genotype. Our results suggest that LEPR gene provide a useful tool to improve carcass/meat quality in pigs.

Keywords: LEPR (*Hpa*II), pig, polymorphism, production trait.

1. Introduction

Leptin and leptin receptor genetic variants are associated with obese phenotypes in humans and mice and are expected to influence fat deposition in pigs [1]. Leptin receptor has been localized to several hypothalamic nuclei, including the ventromedial hypothalamus, the medial preoptic area, the paraventricular nucleus, and the arcuate nucleus [2]. [3] localized the leptin receptor gene (*LEPR*) on chromosome 6 and is related to the control of feed intake and the regulation of energy balance in mammals since it modulates the leptin effect. [4] identified a *HinfI* polymorphism in *LEPR* gene. [5] identified two other types of polymorphism with the restriction enzymes *Hpa*II and *Rsa*I. The polymorphism analyzed is a *Hpa*II restriction site polymorphism [5] located in the fourth intron of the gene (accession numbers AJ223162 and AJ223163). The polymorphism has two alleles: *A* (with a fragment of 2 Kb) and *B* (with fragments of 1450 and 550 pb). [6] results suggested that differences in the locations of LEPR polymorphisms may be associated with production traits such as feed efficiency and back-fat thickness in different porcine breeds.

The objectives of the present study were to analyse of LEPR (HpaII) polymorphism and to estimate its genotypic and allelic frequencies in Landrace and Large White crossbred pigs. This study also aimed to investigate the associations of LEPR polymorphism with production traits of half carcass weight, lean meat percentage, thigh percentage, back-fat thickness and MLT area - *musculus longisimus thoracis*.

2. Materials and methods

A total of 106 pigs were used for experiment. This included domestic crossbreeds (Large White x Landrace). Blood samples were collected from

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every animal. The DNA samples were isolated from blood of hybrids Large White x Landrace (LW x LA). Genomic DNA was extracted from blood samples. All the samples were kept in an icebox. For amplification of specific fragments for *LEPR* gene detection the following oligonucleotide primers FOR and REV was taken from [5]:

FOR: 5´ - GGA AGG CAT TTG TTT CAG CAG TAA - 3´

REV: 5´ - CAA GTC CTC TTT CAT CCA GCA CTG - 3´

Table 1. PCR reaction temperature and time profile

	LEPR (*Hpa*II)	
Start	95 °C	2 min.
Denaturation	94 °C	1 min.
Annlealing	57 °C	1 min.
Polymerisation	72 °C	2 min.
Elongation	72 °C	10 min.
Cooling	15 °C	forever
Cycles	30	

Genotyping of pigs was done by PCR – RFLP methods with restriction enzyme *Hpa*II.

The observed carcass traits (half carcass weight, lean meat percentage, thigh percentage, back-fat thickness, MLT area) were measured by standard technical norm STN 466164.

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

3. Results and discussion

Three genotypes were identified in the set of pigs, AA (45), AB (42) a BB (19). Allele A showed higher frequency than allele B (0.6226 vs. 0.3774). Allele and genotype frequencies are presented in Table 2. These results are not similar to the reported by [5], where the B allele was the predominant in the Landrace, Meishan, Large White and Czech meat pig. [7] confirmed high occurrence of B allele (0,651) in Large White and Landrace breeds.

[8] studied Lepr (*Hpa*II) genotypes and their association with a differential level of plasma Lep concentration as well as with phenotypic variation at several production traits in a Landrace population and confirmed the high frequency of BB genotype (AA: 0.034, AB: 0.307 and BB: 0.659).

Table 2. Frequencies of genotypes and alleles of *LEPR* gene in the pig population

Group	n	LEPR genotypes			LEPR allele	
		AA	AB	BB	A	B
Total	106	0.425	0.396	0.179	0.6226	0.3774

Table 3. The effect of *LEPR* genotypes on carcass and meat quality traits in crossbred pigs

Traits	min./max.	Genotype		
		AA (45)	AB (42)	BB (19)
Half carcass weight (kg)		$41.09\pm1.03^{++}$	$40.38\pm1.28^{++}$	40.87±1.24
	min.	38.55	37.64	39.62
	max.	43.37	43.16	44.69
Lean meat (%)		54.53±1.91	54.95±2.20	55.68±2.24
	min.	49.74	50.73	50.27
	max.	57.51	59.68	59.10
Thigh percentage (%)		22.41±1.32	22.18±1.34	22.78±1.19
	min.	19.59	19.37	19.98
	max.	26.67	25.34	24.80
Back-fat thickness (mm)		$19.05\pm3.57^{+*}$	$17.46\pm3.60^{+}$	$17.21\pm2.88^{*}$
	min.	13.00	11.33	12.67
	max.	27.00	25.67	23.33
MLT area (cm^2)		43.84±3.78	43.68±4.84	43.28±3.93
	min.	37.40	37.10	37.90
	max.	55.00	61.70	50.60

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

The observed associations of individual genotypes of LEPR gene with parameters of carcass traits are presented in Table 3. In the group of pigs was found significant differences between genotypes AA (41.09±1.03) and AB (40.38±1.28) for half carcass weight. We found significant differences between genotype AA for BFT (19.05±3.57) in comparison with AB

(17.46±3.60) and BB (17.21±2.88) on the lowest level of significance. [9] showed that Lepr genotypes are associated with backfat thickness and intramuscular fat content. [8] experiment allowed to demonstrate the existence of one QTL at 60–100 cM, with effects on backfat thickness and weight of the ribs with sternum, and another one peaking at 130–132 cM with highly significant effects on diverse fatness and carcass traits.

Correlations among meat quality traits are presented in Table 4. Negative high correlations (−0.6101, −0.5124, -0.7417) were estimated for BFT with percentage of LM in all genotypes. Very high (0.8356, 0.8947) and moderate (0.6073) correlations were estimated for percentage of thigh with percentage of LM.

Table 4. Likelihood estimates of correlations between carcass/meat traits in the *LEPR* genotypes

Trait	genotype	HCW	LM	Thigh	BFT
LM	AA	-0.1322			
Thigh		0.1122	0.6073		
BFT		-0.0290	-0.6101	-0.2422	
MLT		-0.1286	0.3533	0.3533	-0.0721
LM	AB	0.1597			
Thigh		0.0180	0.8356		
BFT		-0.1404	-0.5124	-0.4879	
MLT		0.3092	0.5070	0.3315	-0.0671
LM	BB	-0.2552			
Thigh		-0.2784	0.8947		
BFT		0.3465	-0.7417	-0.8167	
MLT		0.1841	0.4056	0.3324	0.0202

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

4. Conclusions

In summary, we were able to detect porcine LEPR gene polymorphisms by PCR and PCR-RFLP. The results presented here identify some important carcass traits of LEPR (HpaII) between genotypes. We found possible association of LEPR polymorphisms with production traits. The results presented here were obtained on a relatively small number of animals, their attestation needs further study.

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