

Introduction

Leptin is primarily known for its role in the regulation of food intake, body weight and whole-body energy balance, although it exerts some effects also on reproductive and immune system. In cattle, several polymorphism within the locus of *leptin* gene have been described and associated to phenotypic traits (Liefers *et al.*, 2002; Nkrumah *et al.*, 2005). The purpose of this study was to evaluate the effects of polymorphisms in the *leptin* gene (coding and regulating sequences) on beef performance traits measured at slaughter and dissection, and on some meat rheological and colorimetric characteristics.



Materials and Methods

Twenty Italian Friesian young bulls, reared at the experimental farm and fed with two different type of protein (field bean or pea), were slaughtered at the age of 15 months with an average body weight of 544 ± 9.9 kg. DNA of each animal was extracted from blood and amplified for genotyping 31 Single Nucleotide Polymorphisms (SNP) in the *leptin* gene. Seventeen of these SNP (14 in the promoter region, 2 in exon 2 and 1 in exon 3) were not in linkage disequilibrium; therefore, for them, the allele substitution effect, on each trait, was estimated by regressing the number of copies of each allele, using a linear model, which included the age and the weight at the start of the trial, and the fixed effect of type of protein in the diet.

Data analysis was performed by ALLELE and GLM procedures of the SAS/STAT (2007).

Table 1. Genotyped SNP in the *leptin* gene.

Name	Allele substitution	PIC	Heterozygosity	P-value HWE	MAF	Minor allele
g.1540	G>A*	0.37	0.55	0.65	0.48	A
g.1545	G>A*	0.37	0.55	0.58	0.43	A
rs109337813	A>G	0.37	0.65	0.18	0.48	G
g.1661	T>C*	0.29	0.35	0.99	0.23	C
g.1935..37	del GTT*	0.37	0.60	0.34	0.45	del
rs29004468	T>A	0.37	0.70	0.07	0.50	A
rs29004171	G>A	0.29	0.35	0.99	0.23	A
rs29004173	G>A	0.13	0.15	0.72	0.08	A
rs29004469	del G	0.37	0.55	0.58	0.43	del
rs29004470	C>T	0.35	0.40	0.59	0.35	T
rs29004472	A>G	0.37	0.50	0.96	0.45	G
rs29004474	C>T	0.16	0.10	0.05	0.10	T
rs29004475	T>C	0.37	0.55	0.65	0.48	C
rs29004476	T>C	0.36	0.45	0.86	0.38	C
rs29004484	C>T	0.37	0.55	0.58	0.43	T
rs29004488	C>T	0.37	0.65	0.18	0.48	T
rs29004508	C>T	0.27	0.40	0.26	0.20	T

* Taniguchi *et al.*, 2006.

Table 2. Name and allele substitution.

Trait	mean	SD	g.1540 G>A		g.1935..37 del GTT		rs29004468 T>A		rs29004171 G>A		rs29004173 G>A	
			Effect	p-value	Effect	p-value	Effect	p-value	Effect	p-value	Effect	p-value
Carcass weight	304.13	9.87	-5.251	0.029	-	ns	-	ns	-	ns	14.482	0.002
% Longissimus Dorsi	34.24	2.90	-	ns	-	ns	-	ns	-	ns	-	ns
Fat score	4.06	0.88	0.569	0.054	0.614	0.053	-	ns	0.766	0.026	-	ns
% Other tissues	1.24	0.43	-	ns	-	ns	-	ns	-	ns	-0.725	0.01
Cooking loss	25.77	3.09	-	ns	-	ns	1.814	0.046	2.052	0.015	-	ns

Trait	Effect	p-value	rs29004469 del G		rs29004470 C>T		rs29004474 C>T		rs29004476 C>T		rs29004508 C>T	
			Effect	p-value	Effect	p-value	Effect	p-value	Effect	p-value	Effect	p-value
Carcass weight	-	ns	-	ns	-	ns	7.596	0.029	-	ns	-8.273	0.026
% Longissimus Dorsi	-	ns	-	ns	-	ns	2.657	0.059	-	ns	-	ns
Fat score	-	ns	-	ns	-	ns	-	ns	-	ns	-	ns
% Other tissues	-	ns	-	ns	-	ns	-	ns	-	ns	-	ns
Cooking loss	1.548	0.038	1.338	0.054	-	ns	-	ns	-	ns	-	ns

Results

Only two of the seventeen SNP were not in agreement with Hardy-Weinberg equilibrium (HWE): **rs29004468 T>A** and **rs29004474 C>T** (Table 1).

Carcass weight was affected by the SNP in: **promoter region: g.1540 G>A, rs29004173 G>A, rs29004474 C>T; exon 3: rs29004508 C>T** (P<0.03 ÷ 0.002 - Table 2).

Fat score was affected by: **g.1540 G>A, g.1935..37 del GTT and rs29004171 G>A** (P<0.05÷0.03 - Table 2).

Cooking loss, that contributes to defining the juiciness of meat, is influenced by: **rs29004468 T>A, rs29004171 G>A, rs29004469 del G, g.2004478 C>T and rs29004476 T>C** of the promoter region (P < 0.05 ÷ 0.02 - Table 2).

Conclusion

Considering that leptin hormone regulates energy metabolism and therefore beef attitude in cattle, our results confirm the importance of the *leptin* gene, where some polymorphisms showed their influence on some important beef traits.

The detected polymorphisms, if confirmed by further investigations on different cattle populations, could be used as markers in selection programs to improve meat quality.

References

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