Markers in DGAT1 and TG genes are not associated with intramuscular lipid content in the French beef breeds Charolais, Limousin and Blonde d'Aquitaine

G. Renand[1*], N. Payet[2], H. Levéziel[2], J.F. Hocquette[3], J. Lepetit[4], S. Rousset[5], C. Denoyelle[6], V. Dodelin[7] and A. Malafosse[8]

[1] INRA UR337 Station de Génétique Quantitative et Appliquée, 78352 Jouy en Josas Cedex, France. [2] INRA/Université de Limoges, Unité de Génétique Moléculaire Animale, Faculté des Sciences et Techniques, 87060 Limoges, France; [3] INRA UR1213 Unité de Recherches sur les Herbivores, 63122 Saint Genès Champanelle, France; [4] INRA Unité Qualité des Produits Animaux, 63122 Saint Genès Champanelle, France; [5] INRA Laboratoire de Nutrition Humaine, 58 rue de Montalembert, 63000 Clermont-Ferrand; [6] Institut de l'Elevage, Laboratoire d'Analyses et Technologies des Viandes, Villers Bocage, 14310, France; [7] Institut de l'Elevage, Service Sélection, 75975 Paris Cedex 12, France; [8] UNCEIA, 75975 Paris Cedex 12, France

Email: gilles.renand@jouy.inra.fr

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Introduction

Intramuscular lipid content is regarded as an important characteristic of beef meat in relation to sensory attributes or nutrition properties. Number of researches have been dedicated to detect QTL on the predisposition for meat marbling and to find markers that can be used for selecting superior animals. Several studies reported that two genes located in the centromeric region of the chromosome 14 were candidate genes for marbling: DGAT1 and TG (Barendse, 1999; Barendse *et al*., 2004; Fries and Winter, 2004; Moore *et al*., 2003; Thaller *et al*., 2003). Grisart *et al*. (2001) showed that the dinucleotide polymorphism at the 10 433 and 10 434 positions (AA vs GC) in exon 8 of DGAT1 was related to a modification of the protein (lysine (K) or Alanine (A) encoded at amino acid 232 respectively). The genotyping of this missense mutation was claimed to be useful for testing the predisposition for meat marbling (Fries and Winter, 2004). On the other hand, although no missense mutation could be found in the TG gene, Barendse (1999) claimed that a SNP in the 5' untranslated region (5'UTR) was associated with marbling.

As the above results were obtained in specific beef production systems (with particular breeds, gender and age) the utility of these markers for selecting the intramuscular lipid predisposition in the French conditions requires a powerful validation study. The present poster describes a large scale experiment for validating the putative association of markers in DGAT1 and TG with intramuscular lipid content in the specialised French beef breeds: Charolais, Limousin and Blonde d'Aquitaine.

Materials and Methods

The intramuscular lipid content was measured in a sample of 2 518 bull calves of the Charolais (CH, n=875), Limousin (LI, n=897) and Blonde d'Aquitaine (BA, n=746) beef breeds. All measures were performed via Soxhlet extraction method in a single laboratory in duplicates on a grounded sample of the *Longissimus thoracis* muscle excised from the 7th rib. The duplicates were averaged for each animal. These bull calves were pure bred progeny of 92 sires (41 CH, 27 LI and 24 BA) and were randomly procreated from unrelated dams in two successive years. The CH bull calves were fattened in 2 feed-lots and were slaughtered when they reached 729 kg live weight on average (504 days old). The LI and BA calves were fattened in a single feed-lot and were slaughtered when they reached 479 days (639 kg) and 417 days (623 kg) on average respectively.

DNA was extracted from blood sample of all the calves and sires and of 1991 dams. Markers in the two candidate genes were genotyped with the Taqman method (TaqMan 5' nuclease assay, 7900 HT Applied Biosystems). As the method failed for genotyping the 5'UTR polymorphism in TG, an other SNP (Single Nucleotide Polymorphism) located in intron 9 (Daskalchuk and Schmutz, 1997) was genotyped in order to seek for association with phenotypes. Comparison of the calve's genotypes with the sire's and dam's genotypes allowed the determination of the sire transmitted alleles (STA).

Associations between the calves' genotypes and lipid content were estimated in a linear model that included the fattening contemporary group (year x feed-lot) and the sire effects. The allele substitution effect was estimated via the difference, within heterozygous sires, between the two sire transmitted allele (STA) effects, either AA and GC for the DGAT1 dinucleotide marker or C and T for the TG SNP. This difference was pooled over the three breeds after the lipid content variable was normalised and standardised across the 3 breeds.

Results & Discussion

The lipid content was 1.52 % (Sp = 0.85), 1.22 % (Sp = 0.52) and 0.55 % (Sp = 0.37) in the CH, LI and BA breeds. The allele frequencies were estimated in each breed from the dams' genotype distributions. The AA (DGAT1) and the C (TG) allele frequencies were 0.08 and 0.17, 0.11 and 0.12, 0.29 and 0.17 in the CH, LI and BA breeds respectively.

DGAT1 polymorphism had no significant effect on lipid content (Table 1). For the TG SNP, a significant difference was found for homozygous Charolais [CC] calves that were slightly fatter than others: +0.50 %, i.e. +0.59 sp. This result was not confirmed in the two other breeds however. Lipid content was -0.13 sp in LI and -0.28 sp in BA [CC] calves and these differences were not significant.

Table 1 : DGAT1 and TG genotype frequencies and genotype effects on lipid contents.

Breed		DGAT 1 genotypes			Significance			TG genotypes			Significance		
		AA AA	GC AA	GC GC	df	F-value	Pr>F	C C	C T	T T	df	F-value	Pr>F
CH	LSM	1.41	1.39	1.52	2	1.28	0.28	1.98	1.45	1.50	2	4.73	0.009
	Freq.	7	118	734				26	238	564			
LI	LSM	1.25	1.18	1.22	2	0.57	0.56	1.14	1.19	1.22	2	0.33	0.72
	Freq.	24	204	650				6	177	698			
BA	LSM	0.49	0.56	0.55	2	1.14	0.32	0.44	0.54	0.56	2	0.59	0.55
	Freq.	75	324	336				13	181	537			

Among the 92 sires, 24 were heterozygous for the DGAT1 maker. The within sire differences between progeny that received AA versus GC allele ranged from -0.8 to 1.0 sp, averaged 0.0 sp and were not significant [Pr>F = 0.67]. Twenty five sires were heterozygous for the TG SNP. The within sire differences between progeny that received C versus T allele ranged from -1.0 to 0.7 sp, averaged 0.1 sp and were not significant [Pr>F = 0.40].

Conclusions

The present results show a lack of association between the genotypes for the DGAT1 and TG markers genotyped in this study and the intramuscular lipid content in the 3 French beef breeds. These markers cannot be used to select animals therefore. Moreover, DGAT1 and TG could hardly be considered as candidate genes, since no within sire linkage could be found in these populations between the sire transmitted allele (STA) and lipid content. If a causal mutation did exist in these genes, it would have been detected in the heterozygous sire families. These results do not exclude definitively this centromeric region of the chromosome 14 for including a QTL however. Two microsatellites in the same region will be added to these 2 markers in order to perform an interval mapping and definitively exclude or not this region as including a QTL for intramuscular lipid accretion.

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