

# QTL detection for muscle cholesterol content and fatty acid composition in a *Duroc* population



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#### INTRODUCTION

The amount and composition of intramuscular fat have a strong influence on the sensory, nutritional and technological properties of meat.

We have carried out a QTL study in pigs dealing with intramuscular fat content, fatty acid composition and cholesterol content of muscles Longissimus Dorsi and Gluteus Medius in a Duroc population.

## **MATERIAL AND METHODS**



#### **Animal material**

Animal material came from a high intramuscular fat commercial Duroc population used in the production of fine quality cured ham.

Experimental population: 370 castrated males distributed in five half-sib families. Barrows were kept under normal intensive conditions at control station CCP-IRTA.

<u>Variables measured</u> from samples of *Longissimus dorsi* (LD) and Gluteus medius (GM) collected in the slaughterhouse

- Percentage of intramuscular fat in GM and LD
- Cholesterol content in GM and LD
- Fatty acids composition in GM and LD (determination of fatty acids content in the C12 - C22 interval)

#### **Genomic information**

All individuals, plus the five parental sires, were genotyped for 110 informative microsatellites covering the whole genome.

## Available data

AND DESCRIPTION OF THE PARTY OF	Mean (Standard Deviation)				
	Longissimus Dorsi	Gluteus Medius			
Intramuscular Fat (%)	3.91 (1.53)	5.21 (2.05)			
Cholesterol content (mg/g)	58.59 (9.45)	64.64(11.06)			
Oleic acid content (%)	34.92 (5.18)	35.10 (4.48)			
Palmitic acid content	23.47 (1.63)	23.22 (1.42)			
Linoleic acid content (%)	14.16 (5.11)	14.95 (4.10)			
Stearic acid content (%)	11.71 (1.21)	11.21 (1.12)			

## Statistical analyses

Model:  $y_{ii} = \mu + f_i + \beta bft_{ii} + \alpha p_{ii} + e_{ii}$ p<sub>ii</sub> Probability of individual inheriting one Batch of fattening of alleles from the common parent Backfat thickness  $\alpha$  regression coefficient of phenotypes onto the probability p

Software: QTL express, half-sib analysis (Knott et al., 1996). Significance thresholds were determined by data permutation (chromosome-wise) and Bonferroni correction (genome-wise).

### **RESULTS**

Significant QTL for intramuscular fat, muscle cholesterol content and fatty acid composition of muscles Gluteus Medius and Longissimus Dorsi

	Gluteu	ıs Medius		Longi	ssimus Dorsi			
ssc	Position (cM)	(Familiy) F-value	ssc	Position (cM)	(Family) F-values			
Intramuscular Fat Content (%)								
1	16, 63	(3)6.98 <sup>+</sup> , (4)6.06 <sup>+</sup>	1	66	(4)6.50 <sup>+</sup>			
3	15	(3)12.64*	3	53, 85	(2)10.24 <sup>++</sup> , (5)10.73 <sup>+</sup>			
6	92	(1)11.70 <sup>++</sup>	6	6	(3)7.05+			
7	133	(1)16.48*	10		(5)7.27 <sup>+</sup>			
11	19	(1)9.24+	13 17	58, 110 9	(2)9.43 <sup>++</sup> , (3)7.15 <sup>+</sup> (2)8.85 <sup>+</sup>			
Cholesterol content (mg/g)								
11	66							
16	66 60	(4)9.63 <sup>+</sup> (4)7.02 <sup>+</sup>	<b>6</b> 8	<b>35</b> 42	<b>(2)14.92*</b> (4)7.82 <sup>+</sup>			
10	00	(4)7.02	11	62, 71	(1)8.56 <sup>+</sup> , (5)10.71 <sup>++</sup>			
			14	42	(4)7.35 <sup>+</sup>			
			17	0	(5)7.91 <sup>+</sup>			
			18	6	(5)11.15 <sup>++</sup>			

\*=p<0.05 and \*\*=p<0.01 at chromosome-wide level; \*=p<0.05 at genome-wide level

Gluteus Medius		Longissimus Dorsi					
SSC	Position (cM)	(Familiy) F-value	ssc	Position (cM)	(Family) F-values		
Oleic acid content (%)							
1 3 15	25 26 67, 72	(4)6.68 <sup>+</sup> (3)10.13 <sup>++</sup> (3)7.44 <sup>+</sup> , (5)10.07 <sup>+</sup>	1 2	29 121	(3)7.79 <sup>+</sup> (5)8.47 <sup>+</sup>		
Palmitic acid content (%)							
11 18	65, 71 40	(2)6.14 <sup>+</sup> , (5)8.66 <sup>+</sup> (3)14.96*	1 4 11	28 48, 49 71	(3)10.62 <sup>++</sup> (1)8.72 <sup>+</sup> , (2)6.72 <sup>+</sup> (5)7.70 <sup>+</sup>		
Linoleic acid content (%)							
3 15 16	51, 26 69, 103 45	(1)7.79 <sup>+</sup> , (3)11.37 <sup>*</sup> (3)9.98 <sup>+</sup> , (5)11.40 <sup>++</sup> (4)6.52 <sup>+</sup>	1 2	29 121	(3)6.58 <sup>+</sup> (5)8.74 <sup>+</sup>		

SSC = Sus Scrofa Chromosome =p<0.05 and \*\*=p<0.01 at chromosome-wide level; \*=p<0.05 at genome-wide level

Genomic regions with significant effects on both Longissimus **Dorsi and Gluteus Medius** muscles:

- at SSC 1, 3 and 6 for intramuscular fat content
- at SSC 11 for cholesterol and palmitic contents

Relevant QTL for intramuscular fat content affecting only one muscle: at SSC 7 for Gluteus Medius

at SSC 13 for Longissimus Dorsi

Genomic regions affecting both oleic and linoleic acids content:

- > at SSC 3 and 15 for Gluteus Medius
- at SSC 1 and 2 for Longissimus Dorsi

QTL affecting palmitic content: > at SSC 18 for GM at SSC 4 for LD

QTL involved in cholesterol content of LD at SSC 6 and 18.