

QTL DETECTION ON SSC12 FOR FATTY ACID COMPOSITION OF INTRAMUSCULAR FAT AND EVALUTATION OF PORCINE *ACLY* AS CANDIDATE GENE

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INTRODUCTION

- ❖ 3 SSC12 QTLs affecting backfat (BF) fatty acid (FA) composition were detected in a previous study in an experimental F2 cross Iberian x Landrace.
- ❖ Differences in FA profile have been reported between BF and Intramuscular fat (IMF).

→ **OBJECTIVES** {

1. To carry out a QTL scan on SSC12 for fatty acid composition on IMF in the intercross Iberian x Landrace material.
2. To test porcine *ACLY* as a possible candidate gene underlying the detected QTL.

MATERIAL AND METHODS



Iberian x Landrace
 •56 F3
 •79 BC (F2xLandrace)

❖ 2 Iberian
 2 Landrace → cDNA sequencing → SNPs detection

❖ 23 FA measured on IMF

❖ Genotyping of {
 ✓ 7 SNPs on Candidate Genes: *ACACA*, *ACLY*, *ACOX*, *FASN*, *GH*, *GIP*, *SREBF*
 ✓ 6 Microsatellites: *S0106*, *S0143*, *SW874*, *SWR1021*, *SWR1307*, *SWR1802*

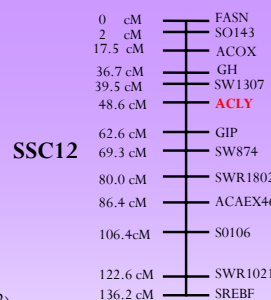
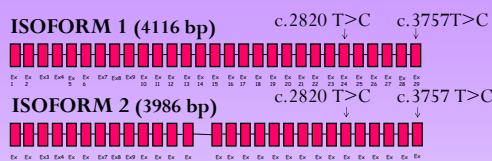
❖ Linkage mapping of SSC12

❖ Statistical models {
 1. QTL Model
 2. SNP Association Model
 3. SNP + QTL Model



RESULTS

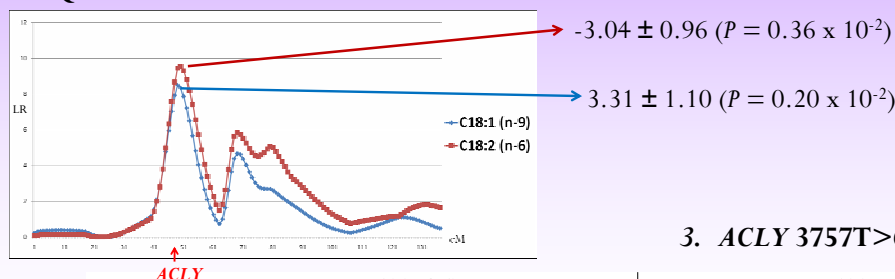
ACLY



2. SNP *ACLY* 3757T>C

Trait	LR	P value	a (SE)
C18:1 (n-9)	6.32	0.12 x 10 ⁻¹	-1.14 (0.44)
C18:2	5.63	0.18 x 10 ⁻¹	0.93 (0.39)

1. QTL



3. *ACLY* 3757T>C + QTL

QTL + SNP					QTL			SNP		
Trait	Position	LR	P value	QTLa (SE)	Position	LR	P value	QTLa (SE)	LR	P value
C18:1 (n-9)	48	13.92	0.95 x 10 ⁻³	3.10 (1.10)	48	7.60	0.58 x 10 ⁻²	3.10 (1.10)	7.94	0.48 x 10 ⁻²
C18:2	50	13.99	0.91 x 10 ⁻³	-2.79 (0.95)	50	8.36	0.38 x 10 ⁻²	-2.80(0.94)	6.97	0.83 x 10 ⁻²
										SNPa (SE)
										-1.27 (0.44)
										1.04 (0.34)

REMARKS

- ❖ The detected QTL does not match the QTLs for fatty acid composition of BF previously located on SSC12.
- ❖ These results support the hypothesis of different genetic control underlying FA metabolism on IMF and BF.
- ❖ The model fitting both QTL and SNP provides the best explanation of the observed effects on C18:1 and C18:2