The effects of single and epistatic QTL for fatty-acid composition in a Meishan × Duroc crossbred population

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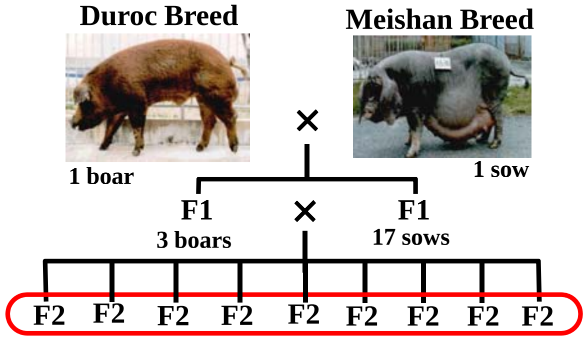
INTRODUCTION

We performed a whole genome quantitaitve trait locus (QTL) analysis to confirm the existence of QTLs affecting fatty acid compositon of backfat, and to investigate the effects of additive, dominance, imprinting, and epistatic interactions between QTLs for these traits in a Meishan × Duroc crossbred population.

MATERIALS AND METHODS

F2 resource population



A total of 166 F2 barrows

F2 barrows were slaughtered at a body weight of 90 kg and their fatty acid composition of backfat were measured.

Genotyping and Linkage map

A total of 180 markers distributed along the porcine genome were genotyped for 18 autosomes and the sex chromosome, and total map length was 2,263.6 cM with the average spacing of markers of 12.6cM.

Statistical Analysis

The single and epistatic QTL analysis were performed with Qxpak softwere (Pérez-Enciso and Misztal, 2004).

Single QTL analysis

$$\mathbf{H_0}:\ y_{ijk} = group_i + parity_j + bx_{ijk} + u_k + e_{ijk}$$

$$\mathbf{H_1}:\ y_{ijk} = group_i + parity_j + bx_{ijk} + C_a a + C_d d + u_k + e_{ijk}$$ (Additive and dominance model)

$$y_{ijk} = group_i + parity_j + bx_{ijk} + C_{\mathrm{imprint}} a + u_k + e_{ijk}$$ (Imprinting model)

Epistatic QTL analysis

$$\mathbf{H_0}:\ y_{ijk} = group_i + parity_j + bx_{ijk} + C_{a1}a_1 + C_{d1}d_1 + C_{a2}a_2 + C_{d2}d_2 + u_k + e_{ijk}$$

$$\mathbf{H_1}:\ y_{ijk} = group_i + parity_j + bx_{ijk} + C_{a1}a_1 + C_{d1}d_1 + C_{a2}a_2 + C_{d2}d_2 + C_{a\times a}I_{a\times a} + C_{a\times d}I_{a\times d} + C_{d\times a}I_{d\times a} + C_{d\times d}I_{d\times d} + u_k + e_{ijk}$$

Fixed effect: group, parity , Covariate (bx): backfat thickness
Random effect (u): infinitesimal genetic effect
Epistatic model were followed by Cockerham (1954) model.

RESULTS

Trait measurement

Trait	Label	N	mean	SD
C14:0, %	Myristic acid	166	1.1	0.2
C16:0, %	Palmitic acid	166	27.7	2.7
C16:1, %	Palmitoleic acid	166	1.6	0.4
C18:0, %	Stearic acid	166	18.1	2.5
C18:1, %	Oleic acid	166	43.1	3.8
C18:2, %	Linoleic acid	166	5.8	0.8
C18:3, %	Linolenic acid	166	0.3	0.1

Estimated linkage map

SSC	Number of markers	map length (cM)	average marker interval
1	11	149.5	13.6
2	12	132.3	11.0
3	11	146.3	13.3
4	12	137.7	11.5
5	9	125.2	13.9
6	13	171.4	13.2
7	12	165.1	13.8
8	10	120.8	12.1
9	11	138.2	12.6
10	10	124	12.4
11	6	62.7	10.5
12	7	85.3	12.2
13	10	116.5	11.7
14	8	105.3	13.2
15	8	101.1	12.6
16	8	87.2	10.9
17	7	91.8	13.1
18	5	79.5	15.9
X	10	123.8	12.4
total	180	2263.7	12.6

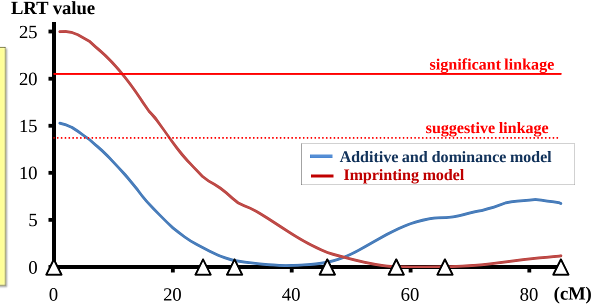
Effects of additve, dominance, and imprinting QTL

Trait	SSC	Location (cM)	Marker interval	LRT	P-value	Additive		Dominance		Imprinting	
						mean	SE	mean	SE	mean	SE
C14:0	12	1	S0143 - SW957	15.3 *	4.8×10^{-4}	-0.09	0.02	0.06	0.03		
	12	2	S0143 - SW957	25.0 **	5.7×10^{-7}					-0.10	0.02
C18:2	5	49	SW70 - S0005	24.4 **	5.1×10^{-6}	-0.39	0.10	0.35	0.16		

*: suggestive linkage, **: significant linkage

Chromosome 12

For C14:0, a suggestive QTL and a significant QTL with a paternal imprinting effect were detected at the same loci of SSC 12 (near S0143 marker). The QTLs found in this study are approximately at the FASN locus.



Effects of epistatic QTL

Trait	QTL positions SSC, Location (cM), Marker interval								LRT	P-value	Epistatic QTL effects							
	QTL1				QTL2						$I_{a\times a}$		$I_{a\times d}$		$I_{d\times a}$		$I_{d\times d}$	
											mean	SE	mean	SE	mean	SE	mean	SE
C14:0	SSC16	34	SWR2086	SW977	SSC16	11		SW2411	67.3	8.4×10^{-14}	-0.59	0.08	-0.65	0.10	0.51	0.09	0.48	0.11
C18:0	SSC4	43	S0001	SW752	SSC10	17	SW830	SW249	31.3	2.7×10^{-6}	1.17	0.40	-0.89	0.64	-1.98	0.53	2.95	0.84
C18:1	SSC4	43	S0001	SW752	SSC10	19	SW830	SW249	34.9	4.8×10^{-7}	-1.06	0.61	1.57	0.92	3.19	0.80	-4.00	1.23
C18:2	SSC2	51	SW1201	SWR468	SSC5	47	SW70	S0005	26.2	2.9×10^{-5}	0.02	0.15	0.34	0.24	-1.02	0.22	0.38	0.38
C18:3	SSC5	91	IGF1	SWR1112	SSC9	16	SW21	S0024	30.8	3.4×10^{-6}	-0.02	0.01	-0.08	0.02	0.02	0.02	0.15	0.03

CONCLUTIONS

1. Single QTL analysis

Two QTLs for C14:0 and C18:2 were detected on SSC 12 and 5, respectively, and imprint QTL were also detected on SSC12.

2. Epistatic QTL analysis

A total of five epistatic pairs were located on SSC 4, 5, 9, and 16.

➡ The present study constitutes one of the first reports on the mapping of imprinting QTLs and epistatic pairs between QTLs affecting fatty acid composition in a swine population.