



INTRODUCTION

The fatty acid composition and melting point of fat are among the most important economic traits in pig breeding. The stearoyl-CoA desaturase (*SCD*) gene is located on SSC14, and is considered a candidate gene for fatty acid composition. We conducted whole-genome quantitative trait locus (QTL) analysis for fatty acid composition and melting point of inner and outer subcutaneous fat and inter- and intramuscular fat in a Duroc purebred population. We also performed positional candidate gene analysis to fine map the detected QTL on SSC14, to identify polymorphisms of *SCD* gene and to examine the effects of *SCD* gene on these traits.

MATERIALS AND METHODS

Duroc population and phenotype



The Duroc population used in this study had been selected on the basis of DG, LEA, BF, IMF (Suzuki et al., 2005).

The pigs were evaluated for fatty acid composition and melting point of 4 different tissues, and the number of pigs with phenotypes ranged from 479 to 521.

Trait	N	Average	SD	Trait	N	Average	SD
Inner subcutaneous fat				Outer subcutaneous fat			
C14:0	% 515	1.55	0.41	C14:0	% 513	1.58	0.40
C16:0	% 515	27.04	1.89	C16:0	% 513	25.28	2.05
C16:1	% 515	2.04	0.69	C16:1	% 513	2.76	0.84
C18:0	% 515	16.96	1.91	C18:0	% 513	13.89	1.70
C18:1	% 515	42.86	2.47	C18:1	% 513	45.79	2.47
C18:2	% 515	9.57	1.75	C18:2	% 513	10.59	1.72
Melting point C* 507		39.40	2.99	Melting point C* 507		34.67	3.19
Intermuscular fat				Intramuscular fat			
C14:0	% 479	1.70	0.45	C14:0	% 521	1.53	0.28
C16:0	% 479	27.12	2.13	C16:0	% 521	26.56	1.50
C16:1	% 479	2.79	0.81	C16:1	% 521	4.48	0.87
C18:0	% 479	15.43	1.91	C18:0	% 521	13.46	1.41
C18:1	% 479	43.35	2.58	C18:1	% 521	48.38	2.16
C18:2	% 479	9.57	1.76	C18:2	% 521	5.48	1.25

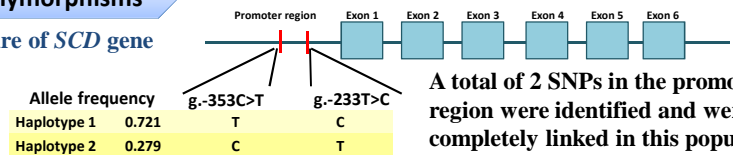
Genome-wide mapping

A total of 129 markers distributed along the porcine genome were genotyped for all autosomes, and total map length was 2,544.7 cM with the average spacing of markers of 19.7 cM based on Haldane map functions.

We conducted a pedigree-based multipoint variance components approach to test for linkage between QTLs and the phenotypic values using a maximum likelihood method implemented in the SOLAR software (Almasy and Blangero, 1998) and LOKI software (Health, 1997), and the LOD score was estimated.

SCD gene polymorphisms

The structure of *SCD* gene



A total of 2 SNPs in the promoter region were identified and were completely linked in this population.

Fine mapping and Candidate gene analysis

A total of 19 microsatellite markers on SSC14 and *SCD* haplotype were genotyped in all pigs, and then used for fine map.

To examine the effect of *SCD* gene, a mixed-inheritance animal model was used to evaluate the effects of *SCD* haplotype by using QxPak software (Perez-Enciso and Misztal, 2004).

RESULTS

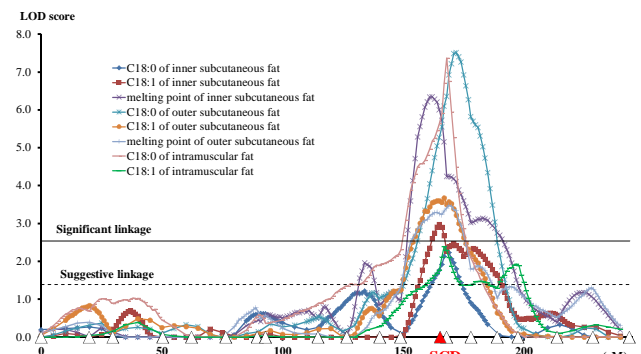
Summary of suggestive and significant QTLs

Trait	SSC	Position (cM)	Marker interval ¹	LOD score	Trait	SSC	Position (cM)	Marker interval ¹	LOD score
Inner subcutaneous fat					Intermuscular fat				
C14:0	9	0	SW21	1.45*	C16:0	6	42	SW2525	1.55*
	12	34	SW957	2.28*		8	32	SW2410 to S0098	3.92**
C16:0	2	165	SWR2157 to SW1844	1.52*		10	38	SW767	2.33*
	11	90	SW1494	1.52*		15	117	SW1983 to SW1119	3.14**
C18:0	2	99	SW1686 to SW776	1.46*	C18:0	14	70	SW857 to SW104	2.35**
	9	65	SWR1848 to SW940	2.23*	C18:1	4	99	SW270 to S0067	1.66*
	10	73	SWC19	2.23*		6	152	SW1881_CA to SW322	1.96*
C18:1	10	73	SWC19	1.56*	C18:2	2	93	SW1686 to SW776	1.99**
	14	105	S0007 to SW761	2.08*		9	150	SW2093	3.02**
C18:2	4	38	KVL2754 to SW2409	1.79*		10	73	SWC19	1.67*
	6	189	SW2052	2.73**		14	70	SW857 to SW104	2.30*
	10	147	SW1991 to SW951	1.67*	Intramuscular fat				
	18	0	SW1023	1.90*	C16:0	4	123	S0067	1.71*
Melting point	14	102	S0007 to SW761	3.25**	C16:1	9	60	SWR1848	1.76*
Outer subcutaneous fat					C18:0	2	77	SWR1445 to SW1686	2.09*
C16:0	18	0	SW1023	1.53*		10	68	SW497 to SWC19	1.98*
C18:0	8	98	SW933	1.87*		14	99	S0007	5.78**
	14	102	S0007 to SW761	4.49**	C18:1	14	106	S0007 to SW761	3.43**
C18:1	14	100	S0007 to SW761	2.67**	C18:2	9	62	SWR1848 to SW940	1.77*
C18:2	4	8	KVL3115 to KVL2754	1.67*					
	11	84	SW1377 to SW1494	1.65*					
	18	0	SW1023	2.45*					
Melting point	14	102	S0007 to SW761	3.03**					

¹The primers of new microsatellite markers were described by Soma et al. (2011).
²Suggestive linkage (LOD = 1.39), **Significant linkage (LOD = 2.54).

¹LRT = likelihood ratio test statistics.
²Additive and dominance effects were genotypic value of (H1H1 - H2H2)/2 and H1H2 - (H1H1 + H2H2)/2, respectively.
³Variance (%) = the proportion of additive genetic variance accounted for by the SNP effect of *SCD* promoter region.

Fine mapping on SSC14 and candidate gene analysis



Trait	LRT ¹	P-value	Additive effect ² Mean	SE	Dominance effect ² Mean	SE	Variance ³ (%)
Inner subcutaneous fat							
C18:0	21.5	2.2 × 10 ⁻⁵	0.54	0.14	-0.11	0.18	9.9
C18:1	24.1	5.9 × 10 ⁻⁶	-0.77	0.18	0.01	0.22	17.0
Melting point	52.7	3.5 × 10 ⁻¹²	1.34	0.20	-0.05	0.25	22.3
Outer subcutaneous fat							
C18:0	52.4	4.1 × 10 ⁻¹²	0.80	0.12	0.11	0.14	22.1
C18:1	36.4	1.2 × 10 ⁻⁸	-0.90	0.16	-0.15	0.20	24.1
Melting point	48.0	3.8 × 10 ⁻¹¹	1.22	0.20	-0.10	0.25	27.1
Intramuscular fat							
C18:0	69.8	6.7 × 10 ⁻¹⁶	0.69	0.10	-0.16	0.12	31.4
C18:1	38.7	3.9 × 10 ⁻⁹	-0.78	0.16	0.21	0.19	30.5

CONCLUSIONS

Genome-wide QTL mapping

- A total of 10 QTLs with significant linkages and 30 QTLs with suggestive linkages for these traits were detected.

Fine mapping and Candidate gene analysis

- Two SNPs (g.-353C>T and g.-233T>C) in the promoter region of the *SCD* gene were identified and completely linked.
- Especially, a significant association was found between *SCD* gene and C18:0, C18:1 and melting point of fat.

➔ The *SCD* gene have a strong effect for fatty acid composition and melting point of fat.

