

QTL mapping for growth and carcass traits in an Iberian by Landrace pig intercross: additive, dominant and epistatic effects

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Summary

Results from a QTL experiment on growth and carcass traits in an experimental F₂ cross between Iberian and Landrace pigs are reported. Phenotypic data for growth, length of carcass and muscle mass, fat deposition and carcass composition traits from 321 individuals corresponding to 58 families were recorded. Animals were genotyped for 92 markers covering the 18 porcine autosomes (SSC). The results from the genomic scan show genomewide significant QTL in SSC2 (longissimus muscle area and backfat thickness), SSC4 (length of carcass, backfat thickness, loin, shoulder and belly bacon weights) and SSC6 (longissimus muscle area, backfat thickness, loin, shoulder and belly bacon weights). Suggestive QTL were also found on SSC1, SSC5, SSC7, SSC8, SSC9, SSC13, SSC14, SSC16 and SSC17. A bidimensional genomic scan every 10 cM was performed to detect interaction between QTL. The joint action of two suggestive QTL in SSC2 and SSC17 led to a genome-wide significant effect in live weight. The results of the bidimensional genomic scan showed that the genetic architecture was mainly additive or the experimental set-up did not have enough power to detect epistatic interactions.

1. Introduction

Development of gene-mapping technologies has provided useful tools to conduct genomewide search for genes affecting quantitative traits. Since the publication of the genetic maps of microsatellite markers in swine (Archibald *et al.*, 1995; Marklund *et al.*, 1996; Rohrer *et al.*, 1994, 1996), several studies have detected quantitative trait loci (QTL) along the 18 porcine autosomes (SSC), mainly from F₂ crosses between populations of different genetic origin (Rothschild & Plastow, 1999).

Most of the published studies have used a single-QTL model, analysing every location of the genome and assuming independence of genetic effects. However, there is some evidence of epistatic interaction between QTL for lung cancer (Fijneman *et al.*, 1996), growth (Routman & Cheverud, 1997; Brockmann *et*

al., 2000), alcohol preference (Fernandez *et al.*, 2000) and circadian behaviour (Shimomura *et al.*, 2001) in mice.

In the present study, we used data from an intercross between Iberian and Landrace pigs, developed to detect QTL in growth, carcass, meat quality and histochemical traits. From a subset of the same experiment, results for SSC4 in fatty acid metabolism (Pérez-Enciso *et al.*, 2000), and for SSC6 in fat deposition traits, have been reported (Ovilo *et al.*, 2000*a*). The objective of this paper is to carry out a whole-genome QTL scan for growth and carcass traits using 92 markers along the 18 porcine autosomes, and to investigate epistatic interaction between QTL for these traits.

2. Materials and methods

(i) Experimental design and traits analysed

Three Iberian boars from the genetically isolated Guadyerbas line (Toro *et al.*, 2000) were mated with

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Table 1. Main statistics of growth and carcass traits analysed in the population

Description	Trait	Mean	SD
<i>Weight and carcass length traits</i>			
Live weight (kg)	LW	101.26	12.64
Carcass weight (kg)	CW	74.90	9.82
Length of carcass (cm)	LC	79.26	3.96
<i>Muscle traits</i>			
Loin depth at the last ribs (mm)	DLO	47.48	6.38
FOM loin depth (mm)	FLO	44.86	7.04
Loin muscle area (cm ²)	LDA	34.66	5.03
<i>Fat deposition traits</i>			
Backfat depth at last rib (mm)	DFAT	28.31	7.90
FOM backfat depth (mm)	FFAT	25.75	5.85
Backfat thickness at first rib (cm)	BF1	4.68	0.67
Backfat thickness at last rib (cm)	BF2	2.83	0.54
<i>Carcass composition traits</i>			
Weight of right ham (kg)	RHAM	10.96	1.40
Weight of left ham (kg)	LHAM	10.89	1.38
Weight of right shoulder (kg)	RSH	5.58	0.69
Weight of left shoulder (kg)	LSH	5.66	0.73
Weight of right loin with backfat (kg)	RLO	9.51	1.36
Weight of left loin without backfat (kg)	LLO	6.25	1.02
Weight of right ribs with sternum (kg)	RRIB	7.94	1.39
Weight of left ribs (kg)	LRIB	6.68	1.15
Weight of belly bacon (kg)	BELL	2.51	0.76

31 non-inbred Landrace sows. Six boars and 73 sows of their offspring, the F₁ generation, were parents of 577 F₂ animals. Iberian pig breed is characterized by extreme fat body composition, whereas the Landrace line is a maternal line used in the experimental farm Nova Genètica S.A. The parental lines differ substantially for growth, carcass and meat quality traits (Serra *et al.*, 1998).

All parental individuals from both populations were normal homozygous *RYR1* genotypes (NN). The F₂ pigs were raised under normal intensive conditions in the experimental farm Nova Genètica. Feeding was *ad libitum*, and males were not castrated. The pigs were slaughtered and each carcass was divided into standardized commercial joints. Records for 321 individuals of 58 full-sib families were obtained for the growth and carcass traits presented in Table 1. The average age at slaughter was 175.5 ± 5.5 days.

(ii) Genotyping

DNA from the parental individuals was extracted from blood using a saline precipitation protocol, and DNA from F₁ and F₂ pigs was extracted using a commercial protocol (Boehringer Mannheim). Animals were genotyped for 92 markers (90 microsatellites and 2 PCR-RFLP), which were chosen to be highly informative based on the index of Ron *et al.* (1995). They provided a uniform coverage of the 18

autosomes. PCRs were carried out in an MJ Research Thermal Cycler. The microsatellite PCR products were analysed with Genescan software on capillary electrophoresis equipment with fluorescence detection (ABI PRISM 310 Genetic Analyzer). Genotypes were stored in the Gemma database (Iannuccelli *et al.*, 1996).

(iii) Statistical analyses

Linkage analysis was carried out using the CRI-MAP 2.4 program, using the 'build' option (Green *et al.*, 1990). Marker information contents were obtained following Knott *et al.* (1998). The QTL mapping was performed using a regression model following Haley *et al.* (1994). This model assumes that putative QTL are diallelic with alternative alleles fixed in each parental breed. The following statistical model was used:

$$y_{ijk} = S_i + F_j + C_{ijk}b + c_a a + c_d d + e_{ijk}, \quad (1)$$

where y_{ijk} was the observation ijk for traits, S_i was the fixed effect of sex i (i = male or female), F_j was the fixed effect of full-sib family j (j = 1 to 58 levels), C_{ijk} was the covariate coefficient for sex i , family j and animal k , b was the covariate effect, a was the additive effect, d was the dominance effect and e_{ijk} was the random residual term. The covariate (C_{ijk}) was age at weight for live weight, age of slaughter for carcass

Table 2. Marker positions (Pos) and information content (IC) at marker positions arranged by chromosome (Chr)

Chr	Marker	Pos	IC	
1	SW1515	0.0	0.53	
	CGA	30.1	0.99	
	S0113	46.2	0.57	
	S0155	55.0	0.78	
	SW1828	85.0	0.85	
2	IGF2	0.0	0.70	
	S0141	30.3	0.93	
	SW240	41.8	0.98	
	SW395	64.7	0.95	
	S0226	72.4	0.99	
	S0378	87.0	0.93	
	SWR308	130.1	1.00	
	3	SW72	0.0	1.00
S0206		25.6	0.51	
S0216		55.1	1.00	
S0002		77.5	0.72	
SW349		86.0	0.99	
4	SW2404	0.0	0.80	
	S0301	40.8	0.85	
	S0001	59.5	0.88	
	SW839	72.8	1.00	
	DECR2	78.8	0.18	
	S0214	95.1	1.00	
	SW445	116.8	1.00	
	S0097	134.4	0.84	
	5	SW413	0.0	0.98
		SW2425	66.1	0.50
S0005		81.8	1.00	
IGF1		113.8	0.91	
SWR111		130.9	0.95	
6	S0035	0.0	0.65	
	SW1057	44.3	0.96	
	S0087	57.7	1.00	
	SW316	81.2	0.90	
	S0228	96.0	0.48	
	SW1881	108.7	0.82	
	SW2419	145.3	0.96	
	7	S0025	0.0	0.73
		S0064	40.1	0.76
		TNFB	68.9	0.93
		S0066	87.8	0.99
SW632		111.9	0.94	
S0101		137.7	0.92	
SW764		160.3	0.94	
8		SW2410	0.0	0.98
	SW905	26.0	0.60	
	SWR110	44.7	1.00	
	S0017	66.5	0.98	
	S0225	86.1	0.83	
	SW61	109.1	1.00	
	9	SW983	0.0	0.99
		SW911	31.1	0.71
SW2571		79.5	0.73	
SW2093		109.2	0.99	
SW1349		160.9	0.76	
10	S0038	0.0	0.74	
	S0070	45.5	0.82	
	SW1626	100.5	0.97	
11	S0385	0.0	0.87	
	S0071	43.1	0.75	
	SW703	72.3	1.00	

Table 2 (cont.)

Chr	Marker	Pos	IC
12	S0143	0.0	0.78
	GH	31.4	0.71
	SW874	48.6	0.98
	S0106	81.7	0.79
13	S0219	0.0	0.57
	SW935	30.9	0.54
	SWR100	64.0	0.97
	SW398	81.4	0.96
	SW1056	91.2	0.41
14	SW769	121.5	0.58
	SW857	0.0	0.89
	SW1125	18.8	0.92
	SW210	42.2	0.82
	S0007	55.8	0.87
	SW1557	90.8	0.43
	SW2515	114.0	0.75
	15	SW919	0.0
SW1111		16.3	0.56
S0149		38.3	1.00
SW936		56.0	0.85
SW1119		79.9	0.45
16	SW742	0.0	0.99
	S0298	18.4	0.44
	SW2517	35.9	1.00
	S0061	69.4	0.37
17	SW24	0.0	1.00
	SW1920	28.3	0.95
	SW2431	72.2	0.51
18	SW1023	0.0	0.85
	SW787	21.5	0.84
	S0120	35.1	1.00

weight and carcass weight for the rest of traits. The coefficients c_a and c_d were calculated as

$$c_a = pr(QQ) - pr(qq) \quad \text{and} \quad c_d = pr(Qq),$$

where $pr(QQ)$ was the probability of being homozygous of Iberian origin, $pr(qq)$ was the probability of being homozygous of Landrace origin and $pr(Qq)$ was the probability of being heterozygous. The analysis was performed every centimorgan for each of 18 autosomes, by means of an F -test comparing the models with and without the QTL coefficients (a and d).

Genomewide and chromosomewide levels of significance were calculated using permutation techniques (Churchill & Doerge, 1994). A total of 20000 permutations within family and sex were calculated for each testing point along the 18 autosomes. Confidence intervals for QTL location were calculated using the χ^2 drop approximation (Mangin *et al.*, 1994), although Visscher *et al.* (1996) found that this procedure underestimates the confidence interval. The 95% confidence interval limits were obtained at chromosome locations where the F -statistics decreased 1.92 units starting in both directions (Mangin *et al.*, 1994).

Furthermore, a two-QTL analysis was performed with two different models. The first model included the effects of both QTL from two different locations but did not allow for interaction between them. The statistical model was:

$$y_{ijk} = S_i + F_j + C_{ijk}b + c_{a1}a_1 + c_{d1}d_1 + c_{a2}a_2 + c_{d2}d_2 + e_{ijk}, \quad (2)$$

where a_1 and a_2 were the additive effects and d_1 and d_2 were dominance effects for both QTL. The coefficients c_{a1} , c_{d1} , c_{a2} and c_{d2} were calculated in the following way:

$$c_{a1} = pr_1(QQ) - pr_1(qq),$$

$$c_{d1} = pr_1(Qq),$$

$$c_{a2} = pr_2(QQ) - pr_2(qq),$$

$$c_{d2} = pr_2(Qq).$$

where pr_1 and pr_2 were the probabilities for genetic configurations QQ , Qq and qq in locations 1 and 2, respectively.

The second model allowed for epistasis:

$$y_{ijk} = S_i + F_j + C_{ijk}b + c_{a1}a_1 + c_{d1}d_1 + c_{a2}a_2 + c_{d2}d_2 + c_{axa}I_{axa} + c_{axd}I_{axd} + c_{dxa}I_{dxa} + c_{dxd}I_{dxd} + e_{ijk}, \quad (3)$$

where I_{axa} , I_{axd} , I_{dxa} , I_{dxd} were the additive \times additive, additive \times dominance, dominance \times additive and dominance \times dominance epistatic interaction effects, respectively. Moreover, c_{axa} , c_{axd} , c_{dxa} and c_{dxd} were the regression coefficients calculated as follows:

$$c_{axa} = pr_1(QQ)pr_2(QQ) - pr_1(QQ)pr_2(qq) - pr_1(qq)pr_2(QQ) + pr_1(qq)pr_2(qq),$$

$$c_{axd} = pr_1(QQ)pr_2(Qq) - pr_1(qq)pr_2(Qq),$$

$$c_{dxa} = pr_1(Qq)pr_2(QQ) - pr_1(Qq)pr_2(qq),$$

$$c_{dxd} = pr_1(Qq)pr_2(Qq).$$

following the Cockerham (1954) model for epistatic interactions.

Both two-QTL analyses were performed for every two locations using a bidimensional genomic scan at 10 cM intervals along the 1900 cM of the 18 pig autosomes. Thus, 17955 regression analyses were carried out for every trait. Models (1), (2) and (3) were nested between them, and partial contrasts of subspaces of the model were carried out using an F -test. Several contrasts were performed. First, the statistical contrast of model (2) versus model (1) was performed for detecting QTL given the effect of a second location in the genome, using an F -test with 2 degrees of freedom in the numerator. Secondly, the statistical contrast of model (3) versus a model without any QTL coefficient was performed for detecting a joint effect of

the two locations in the genome, and their interaction, using an F -test with 8 degrees of freedom in the numerator. Finally, the statistical contrast for evidence of epistasis was carried out between models (3) and (2), by an F -test with 4 degrees of freedom in the numerator.

The nominal F -test significance levels cannot be used due to the large number of tests performed. Thus, genomewide and bi-chromosome levels of significance for two QTL models were calculated using permutation techniques (Churchill & Doerge, 1994). A total of 20000 permutations within family and sex were calculated for each two points tested.

3. Results

Summary statistics of phenotypic records of analysed traits are presented in Table 1. Table 2 shows the linkage map of the markers used in the analysis. The average chromosome length, the order of the markers and the distances between them are similar to published maps (<http://www.genome.iastate.edu/maps/marcmap.html>).

The genomewide F values for level of significance at 5%, 1% and 0.1% were 8.53, 10.39 and 13.07, respectively. Significance values from the permutation test were equivalent to previous studies (Pérez-Enciso *et al.*, 2000). There were no substantial differences in thresholds between chromosomes.

Results of a single-QTL analysis for growth, length of carcass and muscle mass traits are presented in Table 3. Only one genome-wide significant QTL, for length of carcass (LC), was found in SSC4, in the region defined by the *S0001* and *SW839* markers. Other suggestive QTL with chromosome-wise significance were detected on SSC2, SSC4, SSC5, SSC8 and SSC17.

For muscle mass traits (DLO and LDA), there was a genomewide significant QTL on SSC2 in the region close to the markers *SW395*, *S0226* and *S0378*. Another QTL was detected in SSC6, in the region near the markers *S0228* and *SW1881* (Table 3). There was also a suggestive QTL in SSC4.

Results of single-QTL analysis are presented in Table 4 for fat deposition traits. Genome-wide significant QTL were located in SSC4 and SSC6. In SSC4, the QTL mapped to the region near the markers *SW839*, *DECR2* and *S0214*. Another group of QTL was detected in SSC6 for all fat deposition traits, which mapped to the region defined by the markers *SW316*, *S0228* and *SW1881*. There were also suggestive QTL in SSC1, SSC2, SSC7, SSC8 and SSC14.

Results for carcass composition traits are presented in Table 5. Genomewide significant QTL were found in SSC4 and SSC6 at similar locations to the QTL

Table 3. Single-QTL analysis: weight (LW, CW), carcass length (LC) and muscle traits (DLO, FLO, LDA)

Chr	Trait	Pos (CI)	<i>F</i>	<i>a</i>	<i>d</i>	<i>S_c</i>	<i>S_g</i>	<i>h_Q²</i>
2	LW	70 (51–85)	6.58	3.16 (0.89)	0.34 (1.27)	*		0.05
	CW	78 (48–95)	6.81	2.77 (0.75)	–0.27 (1.09)	*		0.06
	DLO	54 (45–81)	10.36	–2.51 (0.56)	0.99 (0.90)	***	*	0.12
	LDA	68 (61–80)	12.91	–1.84 (0.36)	0.25 (0.52)	***	*	0.11
4	LW	92 (81–106)	7.33	–2.58 (0.89)	2.85 (1.30)	*		0.05
	CW	89 (63–103)	5.96	–2.04 (0.74)	2.10 (1.14)	*		0.05
	LC	69 (61–77)	11.81	–1.03 (0.21)	0.05 (0.33)	***	*	0.09
	DLO	73 (60–106)	6.73	–1.69 (0.46)	–0.04 (0.67)	*		0.05
	LDA	73 (68–100)	8.18	–1.36 (0.34)	–0.44 (0.50)	**	+	0.07
5	LW	130 (120–131)	7.03	–2.84 (0.84)	–1.56 (1.20)	*		0.05
	CW	129 (79–131)	7.17	–2.11 (0.70)	–2.04 (1.02)	*		0.05
6	DLO	111 (101–123)	9.58	–1.79 (0.52)	1.74 (0.75)	**	*	0.08
	LDA	116 (104–124)	16.98	–2.02 (0.43)	1.94 (0.66)	***	***	0.18
8	CW	54 (42–61)	6.49	1.43 (0.79)	3.85 (1.35)	*		0.08
17	LW	18 (2–54)	5.56	–2.46 (1.03)	4.03 (1.68)	*		0.07
	CW	13 (0–23)	6.41	–2.36 (0.81)	3.00 (1.37)	*		0.08
	LC	12 (0–27)	5.82	–0.87 (0.25)	0.10 (0.42)	*		0.04

Chr, Chromosome; Pos, position; CI, confidence interval; *F*, *F* value; *a*, additive effect; *d*, dominance effect; *S_c*, chromosomewise significance level at 95%(*), 99%(**) and 99.9%(***) ; *S_g*, genomewise significance level at 90%(+), 95%(*), 99%(**) and 99.9%(***) ; *h_Q²*, percentage of variance explained by the QTL.

Table 4. Single QTL analysis: fat deposition traits (BF1, BF2, DFAT, FFAT)

Chr	Trait	Pos (CI)	<i>F</i>	<i>a</i>	<i>d</i>	<i>S_c</i>	<i>S_g</i>	<i>h_Q²</i>
1	BF2	29 (11–44)	6.33	0.13 (0.04)	–0.09 (0.06)	*		0.05
2	DFAT	78 (67–95)	6.00	2.06 (0.63)	0.92 (0.90)	*		0.06
4	DFAT	71 (66–88)	25.98	3.71 (0.52)	–0.70 (0.78)	***	***	0.18
	FFAT	90 (81–100)	9.62	1.83 (0.46)	–1.09 (0.70)	**	*	0.08
	BF1	69 (64–76)	16.92	0.27 (0.05)	–0.19 (0.08)	***	***	0.13
	BF2	72 (66–78)	12.43	0.18 (0.04)	0.08 (0.06)	***	**	0.09
6	DFAT	103 (100–107)	35.50	4.49 (0.58)	–2.36 (0.87)	***	***	0.27
	FFAT	88 (71–108)	7.95	1.73 (0.49)	–1.58 (0.81)	**	+	0.08
	BF1	102 (90–108)	19.38	0.34 (0.06)	–0.11 (0.08)	***	***	0.16
	BF2	89 (72–93)	22.89	0.26 (0.04)	–0.18 (0.07)	***	***	0.19
7	DFAT	160 (154–160)	7.43	–1.81 (0.55)	–1.67 (0.79)	*		0.06
	BF2	160 (150–160)	5.44	–0.13 (0.04)	–0.02 (0.06)	*		0.04
8	DFAT	52 (39–64)	5.19	–1.70 (0.64)	1.90 (1.02)	*		0.06
14	BF2	90 (75–114)	5.77	0.15 (0.05)	0.10 (0.09)	*		0.07

Chr, chromosome; Pos, position; CI, confidence interval; *F*, *F* value; *a*, additive effect; *d*, dominance effect; *S_c*, chromosomewise significance level at 95%(*), 99%(**) and 99.9%(***) ; *S_g*, genomewise significance level at 90%(+), 95%(*), 99%(**) and 99.9%(***) ; *h_Q²*, percentage of variance explained by the QTL.

described in the previous paragraph. In both cases, a reduction of weight in RSH, LSH and LLO appears when alleles of Iberian origin are present, and, at the same time, BELL increases. There are also suggestive QTL in SSC6, SSC8, SSC9, SSC13 and SSC16.

In the bidimensional genomic scan, results from the test of model (2) versus model (1) were similar to the single-QTL analyses. Significant QTL appear at the same locations observed in the single-QTL analysis, and with a similar level of significance. Only in three cases did suggestive QTL in the single-QTL analysis,

affecting LC (SSC17), BF2 (SSC1) and LHAM (SSC13), reach the genomewise significance level at 5%, as calculated in the single-QTL analysis. In the first case, the QTL for LC was located in the region defined by *SW24* and *SW1920* in the SSC17. The test had an *F* value of 9.15, conditioned on the additive and dominance effects of location 67 in SSC4. In the second case, the QTL for BF2 was located at the region defined by *SW1515* and *CGA* in the SSC1, with an *F* value of 8.85, conditioned on the QTL coefficients associated with location 109 in SSC6. Finally, the

Table 5. *Single-QTL analysis: carcass composition traits (RHAM, LHAM, RSH, LSH, RLO, LLO, RRIB, LRIB, BELL)*

Chr	Trait	Pos (CI)	<i>F</i>	<i>a</i>	<i>D</i>	<i>S_c</i>	<i>S_g</i>	<i>h_Q²</i>
4	RSH	72 (62–103)	9.02	−0.12 (0.03)	−0.02 (0.04)	**	*	0.07
	LSH	66 (54–94)	10.41	−0.15 (0.04)	0.06 (0.06)	***	**	0.08
	LLO	67 (61–86)	11.83	−0.22 (0.05)	0.15 (0.08)	***	**	0.08
	BELL	75 (69–89)	14.96	0.24 (0.04)	−0.06 (0.06)	***	***	0.11
6	LHAM	86 (68–101)	5.42	−0.15 (0.05)	−0.07 (0.08)	*		0.05
	RSH	93 (88–100)	18.06	−0.17 (0.03)	0.11 (0.05)	***	***	0.16
	LSH	95 (90–101)	16.98	−0.19 (0.04)	0.14 (0.06)	***	***	0.14
	RLO	87 (67–99)	5.64	−0.02 (0.05)	−0.28 (0.08)	*		0.06
	LLO	113 (89–123)	8.50	−0.13 (0.06)	0.27 (0.08)	**	*	0.08
	RRIB	96 (87–104)	7.60	0.22 (0.06)	−0.05 (0.09)	*	+	0.07
BELL	100 (89–105)	18.46	0.24 (0.05)	−0.20 (0.07)	***	***	0.16	
7	RRIB	160 (154–160)	6.10	−0.19 (0.06)	0.03 (0.08)	*		0.05
	LRIB	150 (141–159)	7.56	−0.22 (0.06)	−0.17 (0.10)	*	+	0.09
8	LSH	21 (0–40)	5.51	0.13 (0.04)	0.03 (0.07)	*		0.06
9	LSH	104 (82–122)	5.56	−0.12 (0.04)	−0.06 (0.06)	*		0.06
13	RHAM	40 (10–59)	5.60	−0.20 (0.06)	0.10 (0.11)	*		0.08
	LHAM	42 (11–58)	7.41	−0.23 (0.06)	0.13 (0.11)	*		0.10
16	RHAM	55 (20–72)	5.50	−0.17 (0.06)	0.17 (0.11)	*		0.08

Chr, chromosome; Pos, position; CI, confidence interval; *F*, *F* value; *a*, additive effect; *d*, dominance effect; *S_c*, chromosomewise significance level at 95%(*), 99%(**) and 99.9%(***) ; *S_g*, genomewise significance level at 90%(+), 95%(*), 99%(**) and 99.9%(***) ; *h_Q²*, percentage of variance explained by the QTL.

QTL for LHAM was located in SSC13, in the region near the markers *SW935* and *SWR100*, with an *F* value of 8.73, after including in the model the QTL coefficients of location 81 of the SSC5.

Genomewise levels of significance of model (3) versus the model without QTL coefficients at 0.1%, 1% and 5% were 6.56, 5.56 and 5.00, respectively. Furthermore, genomewise levels of significance for model (3) versus model (2) at 0.1%, 1% and 5% of significance were 10.74, 9.11 and 8.16, respectively. For the same contrast, bi-chromosomewise levels of significance were also calculated between models (3) and (2). The average values among the 153 two chromosome combinations were 7.56, 5.96 and 4.86 at 0.1%, 1% and 5%, respectively.

The contrast of model (3) against the no-QTL model had a large number of locations with a joint significant effect. However, most of them are related to QTL previously detected in the single-QTL analysis. Only in one case was the joint analysis for LW significant at 5% genomewise (*F* = 5.04), and both locations show a chromosomewise significance only in the single-QTL analysis. The regions involved were located at SSC2 and SSC17, defined by the markers *SW395*, *S0226* and *S0378*, and *SW24* and *SW1920*, respectively. At SSC2, the additive and dominance effects were 5.12 ± 1.33 and 5.71 ± 1.94 , respectively. At SSC17, the additive effect was -1.32 ± 1.37 and the dominance effect 7.98 ± 1.96 . Additive \times additive, additive \times dominance, dominance \times additive and

dominance \times dominance effects were -2.18 ± 1.62 , -2.67 ± 1.72 , 0.25 ± 1.87 and -10.18 ± 2.68 , respectively.

Finally, results from the test of model (3) versus model (2) did not provide significant results at the genomewise significant level. However, cases of bi-chromosomewise significance are reported in almost all traits. In total, 12 cases showed significance at 1%, even fewer cases than expected by chance (see Table 6).

4. Discussion

In the single-QTL analysis, three QTL regions with genomewise significance at SSC2, SSC4 and SSC6 were identified. These QTL have alleles with effects on different traits that are genetically related.

The QTL that we described in SSC2 plays a role in the development of muscle mass in loin (LDA and DLO), and it has a minor secondary effect on DFAT. In SSC2, there are some QTL described in the literature for muscle mass on the distal region, close to the location of IGF-II (Andersson-Eklund *et al.*, 1998; Jeon *et al.*, 1999; Nezer *et al.*, 1999) or in a more proximal region (De Koning *et al.*, 1999). The QTL that we found in our experiment maps to the region defined by the markers *SW395*, *S0226* and *S0378*, which is closer to the paternally imprinted QTL described by Rattink *et al.* (2000) than to the IGF-II region. However, this QTL did not show any

Table 6. Two-QTL analyses: bi-chromosomewise significant epistatic effects at 1%

Trait	Pos ₁	Chr ₁	Pos ₂	Chr ₂	F ₁	F ₂	a ₁	d ₁	a ₂	d ₂	I _{axa}	I _{axd}	I _{dxa}	I _{dxd}
BF2	40	6	26	13	6.87	6.39	0.04 (0.08)	-0.44 (0.12)	0.00 (0.08)	-0.54 (0.13)	-0.13 (0.10)	0.33 (0.13)	0.00 (0.12)	0.79 (0.19)
RHAM	22	3	6	4	6.02	3.91	0.09 (0.09)	-0.57 (0.16)	-0.04 (0.10)	-0.23(0.16)	0.26 (0.12)	-0.38 (0.15)	-0.28 (0.16)	0.79 (0.26)
RLO	60	1	83	8	6.79	3.79	0.12 (0.09)	-0.39 (0.15)	0.13 (0.09)	-0.50 (0.16)	-0.39 (0.12)	-0.27 (0.15)	-0.39 (0.14)	0.71 (0.23)
	110	6	36	18	6.74	4.03	-0.04 (0.08)	0.05 (0.11)	0.11 (0.09)	0.11 (0.12)	-0.50 (0.11)	0.09 (0.12)	-0.06 (0.13)	-0.25 (0.16)
RRIB	8	12	113	14	6.48	3.61	-0.04 (0.12)	-0.60 (0.21)	0.02 (0.12)	-0.34 (0.19)	0.49 (0.15)	-0.10 (0.19)	0.34 (0.21)	1.24 (0.32)
	113	2	8	17	6.44	3.81	-0.19 (0.13)	-0.95 (0.24)	0.15 (0.14)	-0.81 (0.23)	0.43 (0.16)	0.05 (0.20)	-0.38 (0.23)	1.42 (0.40)
LSH	112	7	49	16	6.46	3.40	-0.08 (0.06)	-0.30 (0.09)	0.05 (0.06)	-0.37 (0.09)	0.22 (0.07)	0.10 (0.09)	-0.10 (0.08)	0.57 (0.14)
	13	2	99	6	6.40	7.76	-0.05 (0.08)	0.17 (0.14)	-0.50 (0.08)	0.22 (0.12)	0.17 (0.10)	-0.03 (0.11)	0.57 (0.13)	-0.14 (0.20)
DLO	63	14	8	16	7.08	3.75	6.02 (1.48)	0.46 (2.40)	-2.66 (1.29)	-4.99 (2.39)	-7.75 (1.62)	-8.38 (2.43)	-0.47 (1.99)	2.17 (4.08)
	53	7	42	10	6.31	3.62	-1.46 (1.50)	-1.32 (2.50)	-7.04 (1.47)	-0.92 (2.61)	2.98 (1.64)	0.33 (2.53)	10.94 (2.23)	-0.89 (4.33)
DFAT	79	6	86	13	6.51	7.89	3.24 (1.19)	7.99 (2.00)	0.74 (1.15)	6.55 (2.12)	-3.30 (1.52)	0.59 (2.08)	-3.05 (1.87)	-15.07 (3.39)
LW	71	11	58	12	6.14	3.89	0.34 (1.52)	7.94 (2.55)	4.48 (1.52)	9.19 (2.85)	-8.19 (1.98)	-1.73 (2.60)	-4.24 (2.27)	-12.46 (4.05)

Pos₁, position, in centimorgans, of the first location; Chr₁, chromosome of the first location; Pos₂, position, in centimorgans, of the second location; Chr₂, chromosome of the second location; F₁, F values of model (3) versus model (2); F₂, F value of model (3) versus the no-QTL model; a₁, additive value of the first location; d₁, dominance value of the first location; a₂, additive value of the second location; d₂, dominance value of the second location; I_{axa}, additive × additive effect; I_{axd}, additive × dominance effect; I_{dxa}, dominance × additive effect; I_{dxd}, dominance × dominance effect.

significant result when tested for imprinting (Varona *et al.*, 2001). The confidence interval of the QTL includes the calpastatin locus (CAST) as a candidate gene. Calpastatin is an enzyme that has been hypothesized to play an important role in the difference of muscular development of callipyge lambs (Lorenzen *et al.*, 2000), although it is not the causal mutation of the callipyge genotype.

The Iberian allele of the QTL in SSC4 increases DFAT, FFAT, BF1, BF2 and BELL and reduces RSH, LSH, LLO and LC. It must be noted that LSH, RSH and LLO are weighted after elimination of covering fat, which increases when the Iberian alleles are present, causing a reduction in the weight of these pieces. As BELL consists predominantly of fat, the detected QTL is strongly related to fat deposition and, as suggested by previous studies (Pérez-Enciso *et al.*, 2000), with fatty acid composition. This result agrees with the effect of the FAT1 locus described by Andersson *et al.* (1994) and Marklund *et al.* (1999). Among the possible candidate genes located in the same region, the 2,4-dienoyl-CoA-reductase (DECR) may play a role in fat deposition metabolism, and it maps into the QTL confidence interval in our experiment (Clöp *et al.*, 2002).

Another QTL is detected at SSC6 for fat deposition, with pleiotropic effects on muscle mass and carcass composition traits. This is consistent with the results of Gerbens *et al.* (2000), and Ovilo *et al.* (2000a) for a subset of this population. Gerbens *et al.* (2000) postulated the H-FABP gene as a positional candidate gene. However, in our population the H-FABP gene maps at the 84 cM position of SSC6 (Ovilo *et al.*, 2000b) and only the confidence intervals for FFAT and BF2 include the location for H-FABP. Moreover, Ovilo *et al.* (2000b) and Gerbens *et al.* (2001) did not find any conclusive association between mutations of H-FABP and fat metabolism. In the SSC6, and closer to the QTL, the LEPR gene (Ernst *et al.*, 1997) has been suggested to have an effect on fatness variation (Hardge *et al.*, 2000), and maps near to the mapped QTL in SSC6.

QTL have been reported for fat deposition traits in SSC1 (Rohrer & Keele, 1998; Rohrer, 2000; Bidanel *et al.*, 2001), although in a different region from the suggestive QTL that we found in this study, SSC7 (De Koning *et al.*, 1999; Rohrer, 2000; Wada *et al.*, 2000; Bidanel *et al.*, 2001) and SSC8 (Knott *et al.*, 1998) and SSC14 (Knott *et al.*, 1998) that may correspond to the suggestive QTL detected in this experiment.

The results on suggestive QTL for growth and length of carcass agree with published results indicating evidence of QTL for growth traits in SSC2 (De Koning *et al.*, 1999; Rattink *et al.*, 2000; Rohrer, 2000), SSC4 (Wang *et al.*, 1998; Knott *et al.*, 1998; Walling *et al.*, 2000; Bidanel *et al.*, 2001) and SSC5 (Casas-Carrillo *et al.*, 1997). However, our results had

a lower significance than reported by other authors. A possible explanation for these differences is that, in some of these studies, earlier stages of growth have been analysed and these QTL can have greater effects in those stages. Another possibility is that the alleles were not fixed within the parental breeds, causing a loss of power in the regression analysis (Alfonso & Haley, 1998). Moreover, two suggestive QTL were detected in SSC8 (CW) and SSC17 (CW, LW and LC). To our knowledge, there are no QTL described for growth in these chromosomes in the literature. QTL for growth traits have also been described in SSC1 (Paszek *et al.*, 1999; Rohrer, 2000; Bidanel *et al.*, 2001), SSC6 (Rohrer, 2000; Bidanel *et al.*, 2001), SSC7 (Rohrer, 2000; Bidanel *et al.*, 2001), SSC9 (Wada *et al.*, 2000), SSC10 (Knott *et al.*, 1998; Wada *et al.*, 2000), SSC12 (Rohrer, 2000) and SSC13 (Knott *et al.*, 1998), which are not detected in our population.

When the bidimensional analysis was performed, the statistical contrast of model (2) versus model (1) did not change substantially with respect to the single-QTL analysis, suggesting that the single-QTL analysis is adequate. Cofactors or two-QTL analyses did not improve the statistical analysis substantially. Only in three cases did the suggestive QTL reach the genome-wide significance level when additive and dominance effects of other location in the genome were included in the model. The number of tests performed was very large, and genomewide levels of significance were perhaps not appropriate. In our opinion, these QTL must also be considered as suggestive.

In the statistical contrast of model (3) versus the no-QTL model, it is noticeable that the joint action of two locations of the genome in SSC2 and SSC17 reach a genomewide significant level at 5% for LW, when both locations have been detected as of chromosome-wise significant in the single QTL analysis, and the test for epistatic effects leads to a nominal significant value at 0.1% ($F = 4.26$), but it does not reach the bi-chromosomewise or genomewide levels of significance obtained by two-dimensional permutation. The combination of both QTL and epistatic effects reaches the genomewide level of significance in the joint analysis. As mentioned before, the effect of QTL in SSC2 for growth is well known (De Koning *et al.*, 1999; Rattink *et al.*, 2000; Rohrer, 2000). However, to our knowledge this is the first report of a significant QTL in SSC17 for growth in pigs.

In the statistical test between models (3) and (2) to detect epistatic effects, the number of significant results at the nominal value was huge. Even at the bi-chromosomewise significance level, 12 locations were detected as significant at 1%. However, there is no combination that reaches the genomewide significance level calculated with a bidimensional permutation test. As a consequence, no relevant results of epistasis can be reported. This fact can be explained in two

different ways: either epistasis is not relevant in the traits analysed or there is not enough statistical power with the available data to detect epistasis effects. Under the structure of this population, to reach the genomewide level of significance at 5% (8.16), the percentage of variance that the four epistatic effects should explain was 12.5%, approximately. Thus, in our population, we were not able to detect any epistatic interaction effect of that magnitude. However, further research in calculation of statistical power to detect epistatic effects with the same or alternative designs is warranted.

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