



Quantitative trait loci for fatness at growing and reproductive stages in Iberian × Meishan F₂ sows

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Summary

A considerable number of fatness QTL have been identified in growing pigs, but there is a lack of knowledge about the genetic architecture of this trait in gilts and sows. We have performed a genome scan, in 255 Iberian × Meishan F₂ sows, for backfat thickness (BF) at 150 (BF₁₅₀) and 210 (BF₂₁₀) days of age, 30 days after conception (BF₃₀) and 7–10 days before farrowing (BF_{bf}). We have found one BF₁₅₀ QTL in SSC6 (120 cM) that was highly significant ($P < 0.001$) at the chromosome-wide level and suggestive at the genome-wide level ($P < 0.1$). Ten additional chromosome-wide significant QTL were found for sow BF₁₅₀ (SSC1, SSC13), BF₂₁₀ (SSC6, SSC8, SSC15), BF₃₀ (SSC5, SSC6) and BF_{bf} (SSC1, SSC6, SSC13). The location of several of the BF QTL varied depending on the growing and reproductive status of the sow, suggesting that part of these genetic effects may have a temporal pattern of phenotypic expression.

Keywords backfat thickness, quantitative trait locus, reproduction, sow.

The genetic architecture of fatness traits in pigs has been explored in depth in recent decades, allowing us to delineate an array of genomic regions whose variation has quantitative effects on these phenotypes (Rothschild 2004). These studies have been mostly performed in growing pigs, whereas the genetic analysis of fatness in other physiological stages (e.g. pregnancy and lactation) has been poorly studied so far. In this sense, it is worth mentioning the study of Muñoz *et al.* (2009), which was focused specifically on the analysis of SSC6 genetic variation and its influence on growth and fatness traits and identified one QTL affecting backfat thickness (BF) in sows at different stages (at 150 days of age and 1 week before the gilts gave birth to their first litter). From an economic point of view, body condition (i.e. fatness) during gestation is a major determinant of sow productivity as it affects diverse-related traits such as prolificacy, piglet weight at birth and at weaning, number of litters per year, lactation yield and sow longevity (Whittemore 1993). Underfeeding during pregnancy leads to a diminished conception rate and to an increase in the

time needed to return to oestrus (Dourmad *et al.* 1999), whereas an excess of BF is associated with a lower feed intake during lactation, farrowing difficulties and locomotion problems (Dourmad *et al.* 1999). In general, fat deposition in pregnant sows increases during gestation, as a result of both maternal and foetal growth, and diminishes during lactation because of the energy expenditure involved in milk production (Whittemore 1993). Lipid deposition is particularly important in the first three quarters of gestation, whereas some maternal adipose tissue mass might be lost in the last quarter as a consequence of the accelerated foetal growth that takes place from the 85th day of gestation onwards (Whittemore 1993). Backfat thickness in sows displays moderate to high heritabilities ($h^2 = 0.30$ – 0.45 ; Serenius & Stalder 2006), demonstrating that this trait has an important additive genetic component that makes it amenable to genetic selection.

With the aim of gaining new insights into the genetic architecture of fatness traits in adult sows, we have measured BF at 150 (BF₁₅₀) and 210 (BF₂₁₀) days of age, 30 days after conception (BF₃₀) and 7–10 days before farrowing (BF_{bf}; i.e. the day when sows were moved from gestation to farrowing pens) in 255 Iberian × Meishan F₂ sows. Backfat thickness was measured with a Renco apparatus (A-mode equipment; Renco Corp.) as the average of two ultrasonic measurements taken on each side of the spinal column, 5 cm from the mid-dorsal line at the position of the last rib. The detailed

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description of this resource population can be found in the study by Rodríguez *et al.* (2005), and a summary of the phenotypic data set is shown in Table 1.

Genomic DNA was extracted from frozen blood or tail tissue using commercial protocols. The Iberian \times Meishan population was genotyped for 115 molecular markers. More specifically, genotypes were obtained for 109 microsatellites and six single-nucleotide polymorphisms as reported in the study by Noguera *et al.* (2009). Genome scans were performed with the Qxpack software (Pérez-Enciso & Misztal 2004) and assuming the following operational animal models:

- For BF₁₅₀ and BF₂₁₀:

$$BF_{150,ijk}, BF_{210,ijk} = a_i + Age_i + Weight_i + Batch_j + [P_i(II) - P_i(MM)]\alpha + P_i(IM)\delta + e_{ijk}$$

- For BF₃₀ and BF_{bf}:

$$BF_{30,ijkl}, BF_{bf,ijkl} = a_i + p_i + Weight_i + Batch_j + PN_k + [P_i(II) - P_i(MM)]\alpha + P_i(IM)\delta + e_{ijk}$$

where a_i and p_i were the infinitesimal additive genetic and permanent environmental random effects associated with i th sow, respectively. Systematic effects accounted for two linear covariates. These were age (Age_i , mean age at 150 days was 148.98 ± 0.24 days and mean age at 210 days was 210.48 ± 1.04 days) and live weight ($Weight_i$, mean weight at 150 days was 70.94 ± 0.77 kg and mean weight at 210 days was 103.86 ± 1.15 kg) of the sow. Systematic effects also accounted for two discrete effects: batch ($Batch_j$, $j = 1-7$) and parturition number of the sow (PN_k , $k = 1-4$). In addition, these models accounted for the additive (α) and dominant (δ) QTL effects. Coefficients $P_i(II)$, $P_i(MM)$ and $P_i(IM)$ defined the probabilities for the i th individual having inherited Iberian (I) or Meishan (M) alleles at a specific genomic location (Pérez-Enciso & Misztal 2004). Genome-wide and chromosome-wide significance thresholds were assessed according to Nezer *et al.* (2002).

Results of the genome scan using a single-QTL model for sow BF traits are summarized in Table 2. Most of the observed QTL effects are additive, agreeing well with heritability estimates and previous QTL reported for these traits in growing pigs (Johnson & Nugent 2003). We did not

Table 1 Phenotypic summary for backfat thickness (BF, mm) traits in the Iberian \times Meishan F₂ sow population.

Traits ¹	N ²	Records	Mean (SE)
BF ₁₅₀	207	207	22.49 (0.29)
BF ₂₁₀	255	255	28.51 (0.32)
BF ₃₀	222	377	29.30 (0.22)
BF _{bf}	223	348	32.63 (0.29)

¹BF₁₅₀, backfat at 150 days of age; BF₂₁₀, backfat at 210 days of age; BF₃₀, backfat 30 days after conception; BF_{bf}, backfat 7–10 days before farrowing. Repeated measurements were obtained for BF₃₀ and BF_{bf} (1.56 and 1.70 phenotypic records per sow, respectively).

²N = number of analysed sows.

find any genome-wide QTL, a feature that might be explained by the limited sample size and reduced allelic effects for these traits. At the chromosome-wide level, we found several QTL displaying positional concordance with fatness QTL previously reported in other pig populations, e.g. BF₁₅₀ and BF₂₁₀ at SSC1, SSC5 and SSC6 (Rohrer 2000; Bidanel *et al.* 2001). It is worth emphasizing that chromosome-wide QTL at SSC6 showed highly significant associations ($P < 0.01$) with almost all fatness traits, in agreement with previous estimates obtained from the same population (Muñoz *et al.* 2009). Interestingly, novel QTL positions were found for BF₁₅₀ at SSC13 and for BF₂₁₀ at SSC8 and SSC15. In addition, we identified QTL for two traits that have been poorly studied so far: BF at 30 days of gestation (SSC5 and SSC6) and before farrowing (SSC1, SSC6 and SSC13). Almost half of the QTL for BF reported in this work had a favourable effect coming from the allele of Meishan origin. This feature could be a reflection of the different genetic regulation of adipose growth patterns in Iberian and Meishan sows.

As previously mentioned, the SSC6 QTL for BF was consistently detected irrespective of the time point under consideration (Table 2). This result indicates that genetic variants harboured in this chromosomal region exert a key role in the regulation of BF in pigs and that, most importantly, their effects remain constant along time. The *leptin receptor* (*LEPR*) gene, a key regulator of fat homeostasis (Unger *et al.* 1999), maps to this SSC6 region (Óvilo *et al.* 2002). *LEPR* has been pinpointed as a strong positional and functional candidate gene, as several polymorphisms of this gene have been consistently associated with pig body composition by several authors (Óvilo *et al.* 2002, 2005; Chen *et al.* 2004; Mackowski *et al.* 2005), including in our population (Muñoz *et al.* 2009). Leptin and its receptor constitute an essential hormonal signal linking metabolic status and neuroendocrine control of reproduction (Barb *et al.* 2005). Functional analyses are underway to look for causality of *LEPR* polymorphisms with respect to the fatness QTL detected in different experimental populations.

In addition, we have detected a number of BF QTL whose effects vary depending on the age or the reproductive stage of the sow. For instance, consistent effects were detected at SSC1 and SSC13 for BF₁₅₀ and BF_{bf}, but not for the remaining time points. Similarly, QTL for BF₂₁₀ and BF₃₀ were detected on SSC5 and SSC8. In growing pigs, time-dependent QTL for BF have been reported by Rohrer (2000) and Bidanel *et al.* (2001). These studies described the existence of three QTL on chromosomes SSC1, SSC7 and SSCX that have permanent effects, while other QTL were only detectable at young ages. Similarly, the performance of a genome scan for cholesterol, triglyceride and lipoprotein serum levels in 45- and 190-day-old pigs showed marked differences in QTL locations at these two time points (Gallardo *et al.* 2008). Age-specific QTL have also been detected in many other species, such as *Drosophila* (Khazaali *et al.* 2005), mouse (Morris *et al.* 1999) and human (Beck

Table 2 Chromosome-wide significant QTL for fatness traits in sows.

Trait ¹	cM	Nearest marker	LR ²	QTL effects ^{2,3}	
				Additive (SE)	Dominant (SE)
SSC1					
BF ₁₅₀	116	SW1828	9.31*	-2.13** (0.72)	-1.87 (1.10)
BF _{bf}	117	SW1828	8.69*	-4.53** (1.38)	-1.61 (2.16)
SSC5					
BF ₂₁₀	70	S0005	7.67†	-2.44* (0.96)	2.37 (1.62)
BF ₃₀	68	S0005	10.60*	-4.54** (1.22)	-1.05 (1.66)
SSC6					
BF ₁₅₀	120	SW1881	16.25***	1.36** (0.35)	-0.82 (0.48)
BF ₂₁₀	121	SW1881	9.39*	1.20** (0.40)	-0.70 (0.59)
BF ₃₀	131	SW1881-SW1328	8.13*	2.97** (1.39)	3.22* (1.65)
BF _{bf}	132	SW1881-SW1328	8.25*	3.52** (1.52)	3.83* (1.92)
SSC8					
BF ₂₁₀	103	S0225-SW61	7.82*	3.93** (1.33)	1.85 (1.91)
BF ₃₀	111	SW61	7.23†	3.07** (1.15)	-2.05 (1.38)
SSC13					
BF ₁₅₀	38	SWR1008-SW398	8.68*	0.14 (1.17)	4.58** (1.45)
BF _{bf}	48	SW398	10.14*	5.73** (1.80)	4.52 (2.41)
SSC15					
BF ₂₁₀	84	SW936-SW1119	12.31**	-2.72* (1.04)	6.73** (2.21)

¹SSC, Porcine (*Sus scrofa*) chromosome; BF₁₅₀, backfat at 150 days of age; BF₂₁₀, backfat at 210 days of age; BF₃₀, backfat 30 days after conception; BF_{bf}, backfat 7–10 days before farrowing.

²LR, likelihood ratio. Chromosome-wide significance thresholds were calculated according to Nezer *et al.* (2002). ****P* < 0.001, ***P* < 0.01, **P* < 0.05, †*P* < 0.1.

³Minus indicates that the MS allele is associated with a higher fatness than its Iberian counterpart.

et al. 2003), reflecting the existence of environmental cues with transient effects on QTL expression. Regarding this, it is well known that pig reproductive and hormonal status have profound effects on lipogenesis and the pattern of fat deposition and vice versa (Zafon 2007). Sex steroid hormones are deeply involved in the metabolism, storage and distribution of adipose tissue as well as in the modulation of food consumption and energy expenditure (Mayes & Watson 2004). In this way, receptors for estrogens, androgens and progesterone are present at adipose tissue, regulating the expression of lipid metabolism genes such as the leptin and lipoprotein lipase loci (Mayes & Watson 2004). In the light of this, we might hypothesize that the endocrine status of the sow might be an important factor regulating the temporal expression of backfat QTL. From an applied perspective, the identification of QTL associated with fat deposition in sows might be a valuable contribution in the implementation of genetic strategies aimed at maximizing piglet productivity without compromising maternal body condition.

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