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Abstract
PIT1, a member of the POU-domain family of genes, is a positive regulatory factor of growth hormone, prolactin, and thyrotroph-stimulating hormone beta in several mammals. Therefore, PIT1 was chosen as a candidate gene to investigate its association with growth and carcass traits in pigs. The five Iowa State University reference/resource three-generation families consisting of crosses of Meishan x Duroc, Meishan x Hampshire, Meishan x Landrace, Minzhu x Hampshire, and Minzhu x Landrace were used. The three PIT1 polymorphisms were based on two RFLP using a PIT1 POU-domain cDNA probe and the restriction enzymes BamHI and MspI and a PCR/RFLP using RsaI. Birth, 21-d, and 42-d weights, average daily gain, several backfat measurements, longissimus muscle area, muscle color, marbling, and firmness scores were evaluated for their association with the three PIT1 polymorphisms. Mixed-animal-model analyses were used with the informative family data in which the PIT1 polymorphisms were segregating. Results from mixed-model analyses revealed that pigs with the MspI CC genotype ($P < .01$) were associated with heavier birth weight (.12 kg) than DD genotype pigs. The MspI CC genotype pigs were also significantly associated with greater average backfat (.41 cm, $P < .01$), greater first-rib backfat (.45 cm, $P < .01$), greater last-rib backfat (.32 cm, $P < .07$), and greater last lumbar backfat (.46 cm, $P < .10$) than the DD genotype pigs. The CC genotype represents primarily Chinese alleles and may be useful for future genetic improvement in synthetic lines involving Chinese and American pigs.(ABSTRACT TRUNCATED AT 250 WORDS)

Keywords
Pigs, Genetic Markers, Quantitative Traits, PITs, Chinese Pigs

Comments
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Association of PIT1 Polymorphisms with Growth and Carcass Traits in Pigs[1,2]

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ABSTRACT: PIT1, a member of the POU-domain family of genes, is a positive regulatory factor of growth hormone, prolactin, and thyrotroph-stimulating hormone β in several mammals. Therefore, PIT1 was chosen as a candidate gene to investigate its association with growth and carcass traits in pigs. The five Iowa State University reference/resource three-generation families consisting of crosses of Meishan × Duroc, Meishan × Hampshire, Meishan × Landrace, Minzhu × Hampshire, and Minzhu × Landrace were used. The three PIT1 polymorphisms were based on two RFLP using a PIT1 POU-domain cDNA probe and the restriction enzymes *Bam*HI and *Msp*I and a PCR/RFLP using *Rsa*I. Birth, 21-d, and 42-d weights, average daily gain, several backfat measurements, longissimus muscle area, muscle color, marbling, and firmness scores were evaluated for their association with the three PIT1 polymorphisms. Mixed-animal-model analyses were used with the informative family data in which the PIT1 polymorphisms were segregating. Results from mixed-model analyses revealed that pigs with the *Msp*I CC genotype ($P < .01$) were associated with heavier birth weight (.12 kg) than DD genotype pigs. The *Msp*I CC genotype pigs were also significantly associated with greater average backfat (.41 cm, $P < .01$), greater first-rib backfat (.45 cm, $P < .01$), greater last-rib backfat (.32 cm, $P < .07$), and greater last lumbar backfat (.46 cm, $P < .10$) than the DD genotype pigs. The CC genotype represents primarily Chinese alleles and may be useful for future genetic improvement in synthetic lines involving Chinese and American pigs. Results from this study suggest that PIT1 may be a candidate gene for a quantitative trait locus in pigs.

Key Words: Pigs, Genetic Markers, Quantitative Traits, PITs, Chinese Pigs

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Introduction

Swine breeders have made considerable genetic advancement in some performance traits. Continued improvement may require molecular marker-assisted selection to improve efficiency (Soller and Beckmann, 1982; Rothschild et al., 1990). Molecular marker-assisted selection will first require identification of candidate genes or anonymous genetic markers associated with the traits of interest. Only a few studies (Jung et al., 1989; Rothschild et al., 1990; Clamp et al., 1992; Andersson et al., 1994) have shown associations of genes with quantitative trait loci (**QTL**) in pigs.

The candidate gene approach is justified when genes previously identified in the species of interest or other species have functions related to the traits of interest. Pit-1 is a member of the POU-domain family of genes that play important regulatory roles in developmental processes (Herr et al., 1988; Rosenfeld, 1991). The POU-domain was originally identified as a highly conserved region of 150 to 160 amino acids found in three mammalian transcription factors, Pit-1, Oct-1, Oct-2, and also in the product of the nematode gene unc-86 (Herr et al., 1988; Ruvkun and Finney, 1991). Pit-1 is a pituitary-specific transcription factor that regulates growth hormone, prolactin, and thyroid-stimulating hormone β subunit genes (Ingraham et al., 1990a,b; Steinfelder et al., 1992). Dwarf mice and humans with multiple pituitary hormone deficiencies have been found that lack Pit-1 gene activity (Li et al., 1990; Pfaffle et al., 1992; Radovick et al., 1992).

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The purpose of this study was to characterize porcine PIT1 genetic variability in five three-generation reference/resource families of Chinese × American pigs and to determine its association with performance and carcass traits.

Materials and Methods

Experimental Animals

In 1989, 22 female and 10 male Meishan pigs, 8 Fengjing boars, and 10 Minzhu boars were imported to Iowa State University from the People's Republic of China under a cooperative project that involved the USDA/ARS, the University of Illinois, and Iowa State University (Young, 1992). Some of these Chinese pigs were used to develop five three-generation breed-cross families for gene mapping and quantitative trait loci studies at Iowa State University. The five Chinese × American breed-cross families were Meishan × Duroc, Meishan × Hampshire, Meishan × Landrace, Minzhu × Hampshire, and Minzhu × Landrace. The structure of the five reference breed-cross families is shown in Table 1. Matings to produce F_2 offspring included those that were inbred (between brother and sister) and those that avoided inbreeding.

Management and Data Collection

Sows in this study were kept in an outside lot, which had a large shelter during their gestation, and were fed a 15% crude protein diet at a rate of 2 kg/d. Just before farrowing, they were moved to a central farrowing house with solid concrete floors. Pens were bedded with straw and contained a creep area. Three to four days after farrowing, sows were moved to 5.5 m long and 4.8 m wide lactation pens and fed a 16% crude protein diet. The pigs were kept warm in 5.5-m × 1.8-m pens filled with straw. They were fed creep beginning 21 d after birth. Pigs were weaned at 42 d of age and then moved to a 2.4-m × 3.6-m indoor pen with a flush gutter until they reached a market weight of approximately 90 kg. The weaned pigs were fed ad libitum amounts of an 18% crude protein diet until they reached 34 kg. After 34 kg, they were given ad libitum access to a 16% crude protein diet.

The traits involved in these analyses were birth weight (**BWT**), 21-d weight (**WT21**), 42-d weight or weaning weight (**WWT**), average daily gain (**ADG**) (from 42 d to marketing), longissimus muscle area (**LMA**), color (**C**), marbling (**M**), firmness (**F**), first rib backfat (**FRIBBF**), last rib backfat (**LRIBBF**), last lumbar backfat (**LUMBARBF**), 10th rib backfat (**TENTHBF**), and average backfat (**ABF**) of first rib, last rib, and last lumbar. The scores for color, firmness, and marbling were graded on a scale from 1 to 5 and were very pale to very dark for color, very soft to very firm for firmness, and void of marbling to excessively marbled for marbling. These color, firmness, and marbling scores were scored according to the standards outlined previously (Meeker et al., 1991). The weaning weight was adjusted to 42 d by using the formula {adjusted weaning weight = [(WWT/age at weaning) × 42]}. The backfat traits and LMA measured on the carcass were adjusted by using market weight as a covariate in the model.

Genotyping at the PIT1 Locus

All pigs in the three-generation pedigrees were bled for PIT1 genotyping. Genomic DNA was isolated from white blood cells using standard techniques (Flanagan et al., 1988). The swine PIT1 POU-domain cDNA fragment (Tuggle et al., 1993) was used as a probe to analyze genomic DNA digested by *Bam*HI and *Msp*I endonucleases as previously described (Tuggle et al., 1993; Yu et al., 1993). An 1746-bp fragment, which was amplified within the last three exons of PIT1, was used in PCR-RFLP analyses with *Rsa*I endonuclease (Yu et al., 1994).

The alleles designated for the polymorphisms detected by using the PIT1 POU domain cDNA and *Bam*HI (denoted PIT1 *Bam*HI) were A (5.8 kb) and B (3.9 kb). The alleles designated for the polymorphisms detected by using the PIT1 POU domain cDNA and *Msp*I (denoted PIT1 *Msp*I) were C (4.5 kb) and D (3.75 kb). The alleles designated for the polymorphisms detected by using the PCR test with *Rsa*I (denoted PIT1 *Rsa*I) were E (710 bp) and F (388/322 bp). All additional *Rsa*I fragments were monomorphic.

Table 1. The number of pigs and structure of the five reference families

	ME[a] × D[b]			ME × H			ME × L			MZ × H			MZ × L		
Generation	M[c]	F[d]	Li[e]	M	F	Li	M	F	Li	M	F	Li	M	F	Li
F_0	2	2	0	2	2	0	2	2	0	2	2	0	2	2	0
F_1	2	7	2	3	5	2	2	4	2	2	4	2	2	4	2
F_2	46	50	13	37	39	9	18	27	6	25	19	7	9	19	5

[a]ME: Meishan; MZ: Minzhu; D: Duroc; H: Hampshire; L: Landrace.
[b]ME and MZ served as sires; D, H, and L served as dams. Two F_0 matings per family to produce F_1 pigs.
[c]Males.
[d]Females.
[e]Number of litters. F_2 pigs may be inbred. Several litters were produced by repeat matings.

Table 2. The allelic frequency of the F_0 pigs in the ISU reference breed-cross families used in the three swine PIT1 analyses

Breed[b]	No. of animals	Allelic frequency					
		PIT1 *Bam*HI[a]		PIT1 *Msp*I		PIT1 *Rsa*I	
		A	B	C	D	E	F
ME	5	.50	.50	.60	.40	1.00	0
MZ	3	.67	.33	.50	.50	1.00	0
D	2	1.00	0	0	1.00	.50	.50
H	4	1.00	0	0	1.00	.38	.62
L	4	1.00	0	0	1.00	.88	.12

[a]PIT1 *Bam*HI, PIT1 *Msp*I: The PIT1 genotypes were deterrmined by using the *Bam*HI and *Msp*I restriction endonucleases, individually, and the swine PIT1 POU domain cDNA in the RFLP analyses. PIT1 *Rsa*I: The PIT1 genotype were deterrmined by using the *Rsa*I restriction endonuclease and the 3′ region of the swine PIT1 genomic DNA in the PCR-RFLP analysis.
[b]ME: Meishan; MZ: Minzhu; D: Duroc; H: Hampshire; L: Landrace.

The frequencies of the alleles for each marker for the original F_0 pigs are given in Table 2, and frequencies of the genotypes in the F_2 pigs are listed in Table 3.

Association Analyses

The association between the genotypes defined by the three PIT1 polymorphism patterns and the traits measured in the pigs was analyzed by using an animal (mixed) model in the PEST program (Groeneveld, 1990). Only F_2 pigs from informative F_1 matings in which the F_1 parents produced F_2 progeny of more than one genotype were used. The general linear model used for the mixed-model analyses was assumed to be as follows:

$$Y_{ijklmn} = \mu + YRS_i + BC_j + Animal_{k(ij)} + Sex_l + PIT1\ Genotype_m + e_{ijklmn}$$

where Y_{ijklmn} = trait measured on each of the ijklmnth animal, μ = population mean of the measurements, YRS_i = fixed effect due to the ith year season, BC_j = fixed effect associated with the jth breed-cross type, $Animal_{k(ij)}$ = random effect due to the k(ij)th animal with expectation mean zero and variance σ_a^2, Sex_l = fixed effect due to the lth sex, PIT1 $genotype_m$ = fixed effect associated with the mth PIT1 genotype, and e_{ijklmn} = random error effect of the ijklmnth animal with expectation mean zero and variance σ_e^2. For BWT, total born was added as a covariate. For WT21 and WWT, total born alive was added as a covariate. For the backfat and LMA traits, market weight was included as a covariate. This general model was used with the analyses involving the informative litters with the individual segregating PIT1 polymorphisms.

The complete relationship matrix was computed. To estimate the ratio of error (σ_e^2) to genetic variance (σ_a^2) the following procedures were used. The error variances were estimated from the mean square error from the least squares analyses involving the

Table 3. The F_2 genotypic frequency of the informative families for each PIT1 genotype

Breed-cross[a]	Genotype					
	PIT1 *Bam*HI		PIT1 *Msp*I		PIT1 *Rsa*I	
MED	AA	.58	CC	.07	EE	.55
	AB	.42	CD	.54	EF	.25
	BB	0	DD	.39	FF	.20
MEH	AA	.53	CC	0	EE	.63
	AB	.47	CD	.40	EF	.29
	BB	0	DD	.60	FF	.08
MEL	AA	.24	CC	.07	EE	.59
	AB	.64	CD	.43	EF	.31
	BB	.12	DD	.50	FF	.10
MZH	AA	.33	CC	.18	EE	.41
	AB	.67	CD	.43	EF	.52
	BB	0	DD	.39	FF	.07

[a]MED: Meishan-Duroc breed cross; MEH: Meishan-Hampshire breed cross; MEL: Meishan-Landrace breed cross; MZH: Minzhu-Landrace breed cross. The MZL, Minzhu-Landrace, pigs were not informative for the individual PIT1 RFLP analyses.

informative data. Because heritability (h^2) estimates were not available for pigs of these breed-crosses and data were not large enough to estimate heritability, they were assumed to be as follows: birth weight, .25; 21-d weight, .2; weaning weight, .2; average daily gain, .3; backfat thickness, .4; LMA, .4; color, .15; marbling, .25; and firmness, .25 (taken from Young [1990]). The genetic variances were then estimated by using the formula $h^2 = \sigma_a^2/(\sigma_a^2 + \sigma_e^2)$. Interaction effects for genotype × breed-cross were tested in the preliminary analyses and were not significant ($P > .10$), so they were excluded from final models. Tests of significance for the PIT1 individual genotypes were *F*-tests, with the residual mean square used as the denominator. The total number of pigs for each trait and the number of pigs used for the informative analyses are given in Table 4.

Results

Individual PIT1 Markers

The animal-model analyses for each individual PIT1 marker based on the data from the informative litters are shown in Table 5. W ith the PIT1 *Bam*HI polymorphisms, heavier birth weight was significantly associated with the BB genotype. Differences approached significance ($P < .10$) for ABF, FRIBBF, and LRIBBF. However, the number of pigs with the BB genotype was very small, and conclusions regarding BB genotype animals should be made with extreme caution.

Differences among pigs with the PIT1 *Msp*I genotypes were highly significant ($P < .01$). The CC pigs were the heaviest at birth. There were consistent differences among pigs with the PIT1 *Msp*I genotypes for the different fat measurements. The CC pigs were the fattest. Significant differences among the genotypes were seen for ABF ($P < .01$) and FRIBBF ($P < .01$), whereas for LRIBBF and LUMBARBF differences were close to significance ($P < .10$). On average, pigs with the CC genotype were approximately .4 to .5 cm fatter than pigs with the CD or DD genotypes. No other differences were detected for the other growth and carcass traits.

With the PIT1 *Rsa*I polymorphisms, no significant differences were seen for any of the traits except ADG ($P < .1$) and LMA ($P < .05$). The pigs with EE and EF genotypes had 3.9 cm^2 more LMA.

The PIT1 *Bam*HI, PIT1 *Msp*I, and the PIT1 *Rsa*I individual genotypes are closely linked though we saw one recombinant. This may be a true recombinant or an error in pig identification. That pig was retested and showed the same RFLP pattern, and thus there was no genotyping error for that sample.

Discussion

The study of candidate genes is one method to determine whether specific genes are significantly associated with performance traits in livestock. For obvious reasons, several researchers have investigated growth hormone effects in cattle and pigs (Nielsen and Larsen, 1992; Rocha et al., 1992). Pit-1 is a

Table 4. The total number of pigs for all traits and the number of pigs from segregating litters for each genotype and trait

Trait[a]	Overall	PIT1 *Bam*HI	PIT1 *Msp*I	PIT1 *Rsa*I
BWT	289[b]	115[c]	243[d]	151[e]
WT21	288	115	242	151
WWT	288	115	242	151
ADG	248	100	204	126
ABF	220	90	184	114
FRIBBF	220	90	184	114
LRIBBF	220	90	184	114
LUMBARBF	220	90	184	114
TENTHBF	220	90	184	114
LMA	220	90	184	114
C	220	90	184	114
M	220	90	184	114
F	220	90	184	114

[a]BWT: birth weight, WT21: 21-d weight, WWT: weaning weight, ADG: average daily gain, ABF: average backfat, FRIBBF: first rib backfat, LRIBBF: last rib backfat, LUMBARBF: last lumbar backfat, TENTHBF: 10th rib backfat, LMA: longissimus muscle area, C: color score of the loin, M: marbling score of the loin, F: firmness score of the loin.
[b]Total number of pigs in the five breed-crosses with records of performance for each trait.
[c]Number of pigs from informative PIT1 *Bam*HI litters (16 litters).
[d]Number of pigs from informative PIT1 *Msp*I litters (33 litters).
[e]Number of pigs from informative PIT1 *Rsa*I litters (22 litters).

Table 5. The association between the PIT1 genotypes and economic traits[a]

Trait[b]	PIT1 *Bam*HI				PIT1 *Msp*I				PIT1 *Rsa*I			
	AA	AB	BB	*P*[c]	CC	CD	DD	*P*	EE	EF	FF	*P*
Animals[d]	34–47	52–65	4–5		12–19	96–123	76–107		71–88	33–48	10–15	
BWT	1.25 ± .05	1.20 ± .05	1.46 ± .12	*	1.43 ± .06	1.25 ± .03	1.31 ± .03	**	1.31 ± .04	1.33 ± .04	1.33 ± .07	NS
WT21	5.00 ± .20	4.72 ± .19	4.66 ± .48	NS	5.41 ± .06	4.97 ± .14	5.01 ± .14	NS	5.25 ± .15	5.11 ± .16	5.28 ± .26	NS
WWT	10.17 ± .36	9.60 ± .34	9.43 ± .87	NS	10.42 ± .51	9.58 ± .27	9.61 ± .28	NS	10.08 ± .31	9.99 ± .33	9.92 ± .54	NS
ADG	.50 ± .02	.50 ± .05	.50 ± .05	NS	.47 ± .03	.51 ± .02	.49 ± .02	NS	.55 ± .02	.51 ± .02	.51 ± .03	†
ABF	4.03 ± .17	4.04 ± .16	4.85 ± .38	†	4.65 ± .22	4.07 ± .12	4.24 ± .12	**	4.25 ± .14	4.18 ± .15	4.16 ± .25	NS
FRIBBF	5.16 ± .20	5.06 ± .18	5.95 ± .44	†	5.83 ± .25	5.11 ± .14	5.38 ± .14	**	5.37 ± .17	5.29 ± .18	5.23 ± .30	NS
LRIBBF	3.26 ± .18	3.33 ± .17	4.23 ± .40	†	3.86 ± .26	3.37 ± .14	3.54 ± .14	†	3.44 ± .16	3.48 ± .17	3.53 ± .28	NS
LUMBARBF	3.66 ± .18	3.73 ± .17	4.38 ± .41	NS	4.26 ± .24	3.74 ± .13	3.80 ± .14	†	3.96 ± .15	3.77 ± .16	3.72 ± .26	NS
TENTHBF	3.40 ± .02	3.51 ± .19	3.83 ± .45	NS	3.95 ± .27	3.55 ± .15	3.68 ± .15	NS	3.67 ± .17	3.59 ± .18	3.72 ± .29	NS
LMA	24.1 ± 1.0	24.3 ± .9	25.1 ± 2.2	NS	25.8 ± 1.5	23.8 ± .8	24.1 ± .8	NS	24.8 ± .8	24.9 ± .9	20.9 ± 1.5	*
C	3.09 ± .08	3.06 ± .07	3.18 ± .21	NS	3.10 ± .09	3.07 ± .04	3.10 ± .04	NS	3.11 ± .05	3.13 ± .06	3.02 ± .10	NS
M	3.00 ± .18	3.02 ± .18	3.34 ± .34	NS	3.14 ± .17	2.93 ± .08	3.03 ± .09	NS	2.95 ± .08	2.90 ± .09	3.11 ± .16	NS
F	3.11 ± .09	3.98 ± .08	2.89 ± .21	NS	3.00 ± .11	2.96 ± .05	3.03 ± .05	NS	3.01 ± .06	3.02 ± .06	2.98 ± .11	NS

[a]Data used from informative litters only.
[b]BWT: birth weight (kilograms), WT21: 21-d weight (kilograms), WWT: weaning weight (kilograms), ADG: average daily gain (kilograms/day), ABF: average backfat thickness (centimeters), FRIBBF: first rib backfat (centimeters), LRIBBF: last rib backfat (centimeters), LUMBARBF: last lumbar backfat (centimeters), TENTHBF: 10th rib backfat (centimeters), LMA: longissimus muscle area (square centimeters), C: the color score of the loin, M: marbling score of the loin, F: the firmness score of loin.
[c]Probability of *F*-test for genotype effect. NS: no significance, †$P < 0.1$, *$P < .05$, **$P < .01$.
[d]Range of number of pigs per genotype.

pituitary-specific activator of the growth hormone gene (Castrillo et al., 1989; Mangalam et al., 1989). Pit-1 can activate the prolactin gene in cell culture (Ingraham et al., 1990a,b), and Pit-1 is involved in thyroid stimulating hormone (TSH-β, thyrotropin) expression (Steinfelder et al., 1992). Pit-1 gene mutations have been identified as the cause of genetic disorders resulting from multiple hormonal deficiencies in both rodents and humans (Li et al., 1990; Pfaffle et al., 1992; Radovick et al., 1992). Given the role that PIT1 plays in growth, it may be a potential candidate gene for marker-assisted selection programs.

We have investigated the genetic variability at the porcine PIT1 locus. Previous research has revealed polymorphisms by using a PIT1 POU domain probe and the restriction enzymes *Bam*HI and *Msp*I (Tuggle et al., 1993; Yu et al., 1993). In the grandparental generation of the ISU gene mapping families, all B and C alleles detected by PIT1 *Bam*HI and PIT1 *Msp*I were seen only in the Chinese grandparents and not the U.S. grandparents. Therefore the B and C alleles can be thought of as the "Chinese alleles" in this population. Further cloning and sequencing of the PIT1 genomic region was performed to find additional variability at PIT1, especially in American breeds. PIT1 *Rsa*I polymorphisms were detected in all five American breeds tested, including the sire breeds Duroc and Hampshire (Yu et al., 1994). We believed that, with these polymorphisms and the genetic differences observed between the breeds, we would be able to detect whether there were significant associations between the PIT1 gene and growth and carcass traits in our swine reference/resource families.

When PIT1 *Msp*I genotypes were tested, the pigs that were homozygous for the "Chinese" PIT1 C alleles had the heaviest birth weights and were the fattest at market weight compared with all other genotypes. The average difference between CC and DD genotypes was .4 cm for ABF. Excessive fatness is a typical feature of the Chinese breeds (Young, 1992). The results here point to the possible identification of PIT1 as a candidate gene of QTL useful for selecting to reduce backfat in the development of synthetic lines of pigs involving Chinese germplasm. There were no significant differences seen between the heterozygous AB and AA genotypes and between CD and DD genotypes in most of the traits. Although larger birth weights are not generally characteristic of Chinese pigs, it seems that PIT1 may have an influence on birth weights. Because larger birth weights are generally thought to be associated with greater neonatal survival, this could be another advantage for the use of PIT1 genotype in selection. Unfortunately, those genotypes that are heaviest at birth were fattest at market weight.

Considering PIT1 as a candidate gene, we assume all D alleles, from either the Chinese or American

breeds, have the same effect on pig performance in our analyses. If PIT1 is thought not to be a QTL itself but a genetic marker for QTL, then it would be important to determine whether the alleles (chromosome pieces) came from the American or Chinese breeds. Obviously the C allele comes from the Chinese breeds only (Table 2). Because the D allele was seen in both American and Chinese breeds, it is difficult in our situation to determine the origin of the D allele. Consider the following problem. If both F_1 parental genotypes are CD, then all D alleles of the F_2 must come from the American breeds. But if the F_1 parental genotypes are CD and DD, then the possible genotypes of the F_2 offspring are $CD_{(A)}$, $CD_{(C)}$, $D_{(A)}D_{(C)}$ and $D_{(A)}D_{(A)}$ [where the $_{(A)}$ is American and the $_{(C)}$ is Chinese]. In our study, approximately two-thirds of the F_1 matings were CD × DD. Thus we are not able to trace the origin of the D alleles in the F_2 generation and analyze the data by the origin of the alleles. However, our analysis would tend to underestimate C allele effects even if D alleles are linked to QTL with different effects in the American and Chinese breeds. For example, the D allele in the Chinese breed may be linked to the same beneficial effect as the C allele and the D allele in the American breed may not be linked to the beneficial effect. Our analysis of combining all the CD genotypes and all the DD genotypes (regardless of the origin of the D alleles) would actually dilute the effect associated with the D allele and lessen the probability of significant differences among CC, CD, and DD genotype animals. However, as stated previously, we believe PIT1 to be a candidate gene rather than linked to a QTL.

Recently QTL have been found in resource families produced by crosses of wild boar and Swedish Yorkshire pigs (Andersson et al., 1994). A growth QTL had been shown to be on chromosome 13. We have recently mapped (Archibald et al., 1994) PIT1 to the region near the chromosome 13 QTL described by Andersson et al. (1994). Our results may suggest that PIT1 is the QTL seen by Andersson et al. (1994).

This study is the first to investigate the role of PIT1 in growth and carcass traits in pigs. Although data sets for some of the individual PIT1 genotypes were limited, these results suggest that PIT1 or a closely linked gene to PIT1 may be important in birth weight and carcass fat traits in swine. Additional populations will be required to repeat these analyses to confirm our results.

Implications

The ultimate goal of gene mapping in livestock is to identify and map genes that affect traits of economic performance. This study reports the association of PIT1, which is a pituitary-specific transcription factor that regulates growth hormone, prolactin, and thyrotropin β subunit genes, with pig growth and carcass traits. Results suggest that, in synthetic lines involving Chinese germplasm, PIT1 polymorphisms may be useful for marker-assisted selection to reduce fat in the carcass. Because no association was seen between alleles found in high frequency in American breeds and growth and carcass traits, then its use in breeding programs using only American breeds may be limited. Further analyses using different restriction enzymes to identify other PIT1 alleles in U.S. breeds of pigs could be useful. Additional studies to identify the relationship of both microsatellite markers and candidate genes with growth and carcass traits in pigs will be needed if marker-assisted selection programs are to become a reality for swine.

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