Mapping Genes for Fatness and Growth on Pig Chromosome 13: A Search in the Region Close to the Pig *PIT1* Gene

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Summary and Implications

Previous research has shown that the *PIT1* gene in several pig populations and the chromosomal region near *PIT1* in some pig populations has been significantly associated with fatness and growth on pig chromosome 13. To confirm these previous results and to clarify the role of the *PIT1* gene in controlling pig fatness and growth, this research project was focused on studying the chromosomal region close to the *PIT1* gene. The ISU Chinese x U.S. pig families were used and the traits analyzed were birth weight, 21-day weight, 42-day weight, longissimus muscle area, backfat thickness at several locations, meat color, marbling and firmness on the carcass, and growth rate for selected time periods. The total number of F_2 pigs used ranged from 241 to 330. Significant evidence of a genetic marker for first rib backfat thickness was detected approximately 20 centimorgans (cM) from the *PIT1* gene. Evidence of a genetic marker for birth weight was detected at the estimated *PIT1* position. These results confirmed the previous published research on pig chromosome 13 for the birth weight but suggest that other genes in the region may be partly responsible for the earlier results on the backfat thickness.

Introduction

The *PIT1* gene, which was found on pig chromosome 13, is a regulatory gene of several important hormone (GH, PRL, and thyrotropin β) genes. Because of the biological importance of *PIT1*, the possible association between this gene and several economic traits was studied in different pig families. The *PIT1* gene was significantly associated with pig birth weight and backfat measures in the ISU pig families. In the Scotish Meishian x Large White pig families, *PIT1* was significantly associated with birth weight. The Swedish Wild boar x Large White pig population also has a region near *PIT1* on pig chromosome to be associated with birth weight and early growth. In cooperation with the geneticists in Sweden, *PIT1* was mapped to the chromosomal region, which was shown to be associated with early growth and birth weight in the Swedish pig families.

Although a significant association between *PIT1* and economic traits was shown in previous analyses, this effect may be due either to *PIT1* or to linked genes. The specific objective of this study was to confirm the genetic markers for birth weight, early growth, and backfat on pig chromosome 13 in the ISU F_2 pig families and to clarify the role of the *PIT1* gene.

Materials and Methods

Five three-generation pig families (Meishian x Duroc, Meishian x Hampshire, Meishian x Landrace, Minzhu x Hampshire, and Minzhu x Landrace) were established at Iowa State University (ISU) for identification of genetic markers for economically important traits.

Sixteen traits were measured and analyzed on F_2 animals. Growth traits were birth weight (BWT, kg), 21-day weight (WT21, kg), weaning weight or 42-day weight (WWT, kg), growth rate from birth to 21-day (ADG1, kg/d), from 21-day to weaning (ADG2, kg/d), from birth to weaning (ADG3, kg/d), and from weaning to marketing (ADG4, kg/d). Carcass traits (1) included loin longissimus muscle area (LMA, cm^2), backfat thickness at the first rib (FRIB, cm), last rib (LRIB, cm), lumbar rib (LUMBAR, cm), and 10^{th} rib (TENTH, cm), average backfat thickness (ABF, cm), meat color (C), marbling (M), and firmness (F) scores on the carcass.

Genotyping of *PIT1* and two markers flanking each side of *PIT1* (*Swr1008*, *S0068*, *Sw398*, and *Sw1056*) were done by using standard biotechnology methods (e.g., PCR, restriction enzyme digestion, and automated genotyping software). The *PIT1* gene and the four adjacent markers were linkage mapped between these genetic markers to obtain relative distances between each marker. The linkage mapping information was used in the later statistical analyses. The statistical analyses in this study were divided into two parts; one analyzed the association between each gene marker and economic traits individually (single marker analyses), the other one analyzed the difference between the parental breeds by utilizing the information of linkage mapping and genotyping of all markers (interval mapping analyses).

Results and Discussion

The length of the linkage map of chromosome 13 using the *PIT1* gene and four markers flanking *PIT1* was approximately 49 cM. The linkage map with cM distances in parentheses was *Swr1008*-(9.5)-*S0068*-(11.9)-*PIT1*-(10.9)-*Sw398*-(16.8)-*SW1056*.

The statistical results (F ratio) for each marker in the single marker analyses are summarized in Table 1. In the early growth stages, weight measurements and growth rate were shown to be significantly associated with most of the markers in the search region. Significant differences (P<.0003) in BWT were associated with the *S0068*, *PIT1*, *Sw398*, and *Sw1056* genotypes. Similar associations with WWT were detected by the same markers. The marker *Swr1008* (P<.011) and *PIT1* gene (P<.05) were shown to be associated with ADG1. Significant associations between ADG2 and the markers *Swr1008* (P<.003), *S0068* (P<.0001), *Sw398* (P<.0005), and the *PIT1* gene (P<.0006)

were found. Differences in ADG3 were detected by the same three markers and the *PIT1* gene. *Sw1056* was the only marker in the search region of chromosome 13 associated with the ADG4 (P<.004). For backfat thickness measurements, *Swr1008* and *PIT1* genotypes detected significant differences in ABF (P<.04) and FRIB (P<.003). The marker *S0068* was associated with LRIB (P<.03). In addition, *Swr1008* was associated with meat firmness (P<.05).

In the interval mapping analysis, there was evidence of a marker for BWT at the estimated map position of *PIT1* with an F ratio of 4.35 (P<.014). Also, at the map position of *Swr1008*, there was evidence of an effect for FRIB (F = 9.17, P<.0001), TENTH (F = 3.57, P<.03) and ABF (F = 4.57, P<.011). The F ratio curves were plotted for early weight, growth rate at different stages and for backfat measurements (Figures 1-3). The genetic effects of the markers, which were mapped in this study, seemed to be mainly dominant. Results indicated that the mean of heterozygous animals for the BWT and backfat markers was significantly smaller and leaner than the mean of the homozygous animals.

Our results for birth weight and early growth are consistent with the expectations based on expression studies of *PIT1* in rodent, human, monkey, and pig. Our results for backfat thickness demonstrate that *PIT1* is not the gene responsible for backfat thickness. An extended study will be helpful to map the backfat thickness gene more precisely.

Acknowledgments

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Reference

1. Yu, T.-P.; Tuggle, C. K.; Schmitz, C. B.; Rothschild, M. F., 1995: Association of *PIT1* polymorphisms with growth and carcass traits in pigs. J. Anim. Sci. 73: 1282-1288.

Table 1. Summary of F ratios for each marker of single marker analyses on chromosome 13.

Trait[a]	*Swr1008*	*S0068*(10)[b]	*PIT1*(21)	*Sw398*(32)	*Sw1056*(49)
BWT	0.75	2.61***[c]	3.62***	2.72***	2.88***
WT21	1.19	0.91	1.77	1.21	1.49
WWT	1.43	2.45***	3.34***	1.69*[c]	1.67*
ADG1	1.84*	0.85	1.92*	1.18	1.17
ADG2	2.07**[c]	3.32***	3.37***	2.55***	1.26
ADG3	1.76*	2.15**	3.32***	1.80*	0.98
ADG4	1.29	0.64	1.15	0.92	2.26**
ABF	1.67*	1.36	2.17*	1.09	0.52
FRIB	2.25**	1.57	2.96**	0.96	0.63
LRIB	1.25	1.74*	1.72	0.92	0.60
LUMBAR	1.37	0.83	0.96	1.07	0.73
TENTH	1.37	0.97	1.27	1.09	0.68
LMA	1.53	1.00	1.37	1.31	1.58
C	1.14	0.73	0.55	0.92	0.91
M	0.85	1.13	1.12	0.93	0.82
F	1.63*	0.50	0.44	0.51	1.09

[a]BWT: Birth weight (kg), WT21: 21-day weight (kg), WWT: 42-day weight (weaning weight) (kg), ADG1: growth rate from birth to 21 days (kg/d), ADG2: growth rate from 21 days to weaning (kg/d), ADG3: growth rate from birth to weaning (kg/d), ADG4: growth rate from weaning to slaughter (kg/d), ABF: Average back fat thickness (cm), FRIB: First rib back fat thickness (cm), LRIB: Last rib back fat thickness (cm), LUMBAR: Lumbar rib fat thickness (cm), TENTH: Tenth rib fat thickness (cm), LMA: longissimus muscle area (cm^2), C: Meat color (score, 1-5), M: Meat marbling (score, 1-5) and F: Meat firmness (score, 1-5).
[b]The map position is estimated in cM from the proximal end marker (*Swr1008*) to the investigated marker.
[c]*P<.05, **P<.01, ***P<.001.

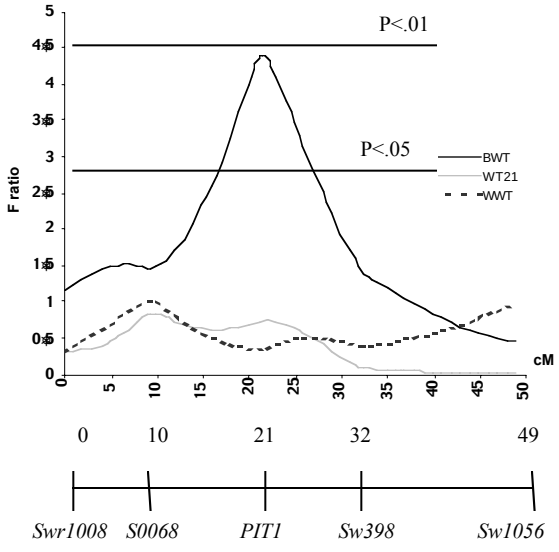

Figure 1. Interval mapping results of early weight measurements by using pooled data. BWT, birth weight; WT21, 21-day weight; WWT, weaning (42-day) weight.

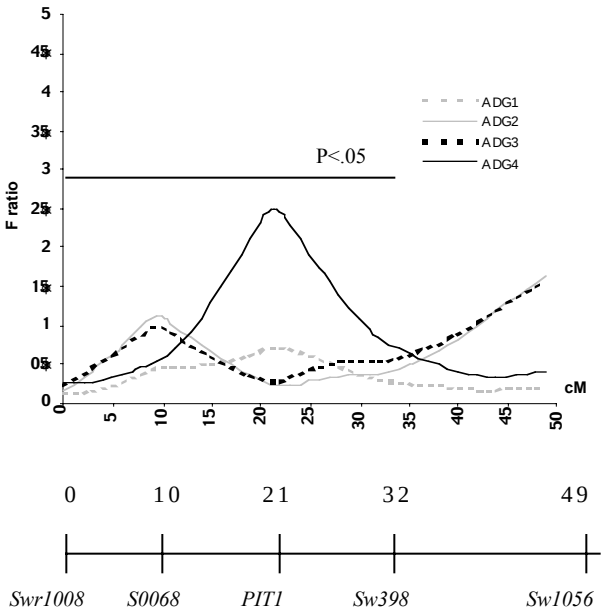

Figure 2. Interval mapping results of growth rate at several different stages by using pooled data. ADG1, Average daily gain from birth to 21 days; ADG2, Average daily gain from 21 days to weaning; ADG3, Average daily gain from birth to weaning; ADG4, Average daily gain from weaning to slaughter.

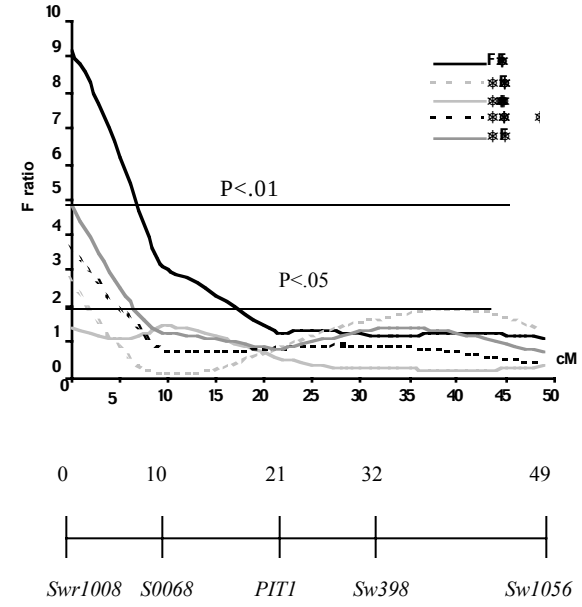

Figure 3. Interval mapping results of backfat measurements by using pooled data. FRIB, first rib backfat thickness; LRIB, last rib backfat thickness; LUMBAR, lumbar rib fat thickness; TENTH, tenth rib backfat thickness.