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Development of a High Resolution Map of a Putative Quantitive Trait Locus for Average Daily Gain in Pigs

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Story in Brief

The availability of microsatellite markers located throughout the porcine genome has facilitated genome scans for loci affecting quantitative production traits (Quantitative Trait Loci or QTL). One such scan was completed in a resource family originating from lines divergently selected for average daily gain (ADG) and differing substantially in daily feed intake. The objective of the present study is to produce a high resolution map of a region of chromosome 3 containing a putative QTL for ADG. Thus far, two additional microsatellite markers in the region have been identified that are informative in the resource family. Effects associated with the markers (approximately .03 to .04 kg/d in ADG) supported the hypothesis that a QTL is segregating. Information for these markers will be added to an interval analysis to more precisely determine the location of the QTL, and available markers in the region will continue to be screened for informativeness in this family. Much of the difference in ADG between the lines used to produce this resource family is due to a difference in appetite. Thus, additional knowledge regarding the location and identity of the QTL on chromosome 3 may be applied toward more effective genetic regulation of feed intake in pigs.

(Key Words: Pigs, Genome, Growth, Selection.)

Introduction

Traits such as feed intake, growth, body composition and meat quality are quantitative in nature and each affected by a large number of genes. The identity, location and allelic forms of these genes are largely unknown. This knowledge could enhance genetic improvement, especially for traits that are difficult or expensive to improve with traditional methods. The relatively recent completion of genetic maps of easily identifiable DNA markers throughout the porcine genome (Archibald et al., 1995; Rohrer et al., 1994) provides the opportunity to scan the genome for these loci (quantitative trait loci or QTL). Some of the available markers are in functional genes, but many simply mark a specific "anonymous" point on a chromosome and allow the inheritance of that point on the chromosome to be tracked. Most of these anonymous markers are a type called "microsatellites".

To effectively conduct a scan, a resource family must be available in which QTL alleles and marker alleles are segregating. By detecting the association of marker allele segregation to a phenotypic trait of interest, regions of chromosomes containing QTL can be identified. Such segregation can be achieved by using Grandparental stock from lines or strains that are greatly different in phenotype (e.g., Wild Boar x domestic breed).

A scan for QTL affecting postweaning average daily gain (ADG) in a resource family produced from divergent lines of pigs selected 10 generations for either fast or slow growth rate was reported by Casas et al. (1997). The scan revealed several chromosomal regions containing putative QTL effects, the most significant of which was located on chromosome 3 and accounted for 5% of the phenotypic variation in ADG. The objective of the present study was to type additional markers on this region of chromosome 3 in the same resource family to produce a map with greater resolution of the putative QTL.

Materials and Methods

Animals and Phenotypes. Lines of pigs were established at Oklahoma State University in 1981 to evaluate responses to divergent selection for postweaning ADG. Ten generations of single-trait divergent selection was completed for either fast (Line F) or slow (Line S) ADG. After generation 10, pigs from F consumed ~36% more feed per day, grew ~47% faster and had ~13%

more backfat than pigs from S (Clutter et al., 1998).

The F and S lines were crossed to produce a resource family for the present study. Two F1 (F x S) sires were mated to a total of 29 unrelated dams to produce two half-sib families (124 and 115 offspring from sires 1 and 2, respectively) in which alleles that differ between the F and S lines are expected to be segregating. All progeny were weighed at weaning (28 d) and just before slaughter (approximately 105 kg) to determine postweaning ADG.

Genotyping. In the initial genome scan (Casas et al., 1997), a microsatellite marker on chromosome 3 (Sw251, see Figure 1) was significantly associated with average daily gain in the family of sire 2. Subsequent interval analysis suggested that a region bracketed by microsatellite markers Sw2429 and Sw251 contained a QTL for ADG. In the present analysis, additional microsatellite markers within the region were for selected for genotyping to more precisely determine the location of the putative QTL. Of the markers screened, only two (Sw72 and S0206) were heterozygous in sire 2 and, thus, informative in the half-sib progeny. All progeny of sire 2 were genotyped for Sw72 and S0206 alleles.

Statistical Analysis. For each marker, one sire allele was arbitrarily designated as "1" and the alternative allele as "2". Paternal allele inheritance was coded as the probability of receiving allele "1" from the sire. The following model was used to detect effects associated with alternative marker alleles by regressing ADG on the probability of receiving the designated allele:

$$Y_{ij} = m + L_i + S_j + b_{wwt} X_{wwt} + b_{marker} X_{marker} + e_{ijk}$$

where Y_{ij} = j^{th} ADG observation from the I^{th} litter, m = the population mean, L_i = effect of the I^{th} litter, S_j = effect of the j^{th} sex, b_{wwt} = regression coefficient of ADG on weaning weight, X_{wwt} = weaning weight used as a covariate, b_{marker} = regression on the probability of inheriting marker allele 1 from the sire, X_{marker} = probability of inheriting marker allele 1 from the sire, and e_{ijk} = random error.

Results and Discussion

Results for the analyses of Sw72 and S0206 are summarized in Table 1, along with the previous results for Sw251. Regressions of ADG on inheritance of Sw72 and S0206 alleles were similar in significance ($P < .01$) and magnitude (approximately .03 to .04 kg/d in ADG) to the regression on Sw251. These results support the hypothesis that a QTL for ADG is contained in this chromosomal region. Genotypes for these microsatellites will be added to an interval analysis as described by Casas et al. (1997) to obtain a more precise location of the QTL.

As discussed by Casas et al. (1997), the effect indicated by these regression coefficients is equivalent to more than one generation of the average response achieved in the experiment that produced the F and S lines. Previous studies of feed intake in the F and S lines (e.g., Clutter et al., 1998) have revealed that much of the difference in ADG between the lines is due to a difference in appetite. Thus, additional knowledge regarding the location and identity of the QTL on chromosome 3 may be applied toward more effective genetic regulation of feed intake in pigs. To obtain a map of the chromosomal region with enough resolution for this goal to be achieved, the family must be genotyped for additional markers within the region. Most of the available markers in this interval reside on the borders (i.e., near Sw2429 or Sw251), but SwR1637 is near the middle. Our next step is to determine if the F1 sire in question is heterozygous for SwR1637 alleles.

Literature Cited

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Table 1. Relationships of microsatellite markers on chromosome 3 to ADG.

Microsatellite marker	Probability of a Type I error [a]	b-value (kg/d)[b]	Standard Error
Sw251	.0036	.033	.009
Sw72	.0052	.028	.010
S0206	.0021	.040	.013

[a] **Error rates unadjusted for number of comparisons.**
[b] **Regression of ADG on the probability of receiving designated paternal allele.**

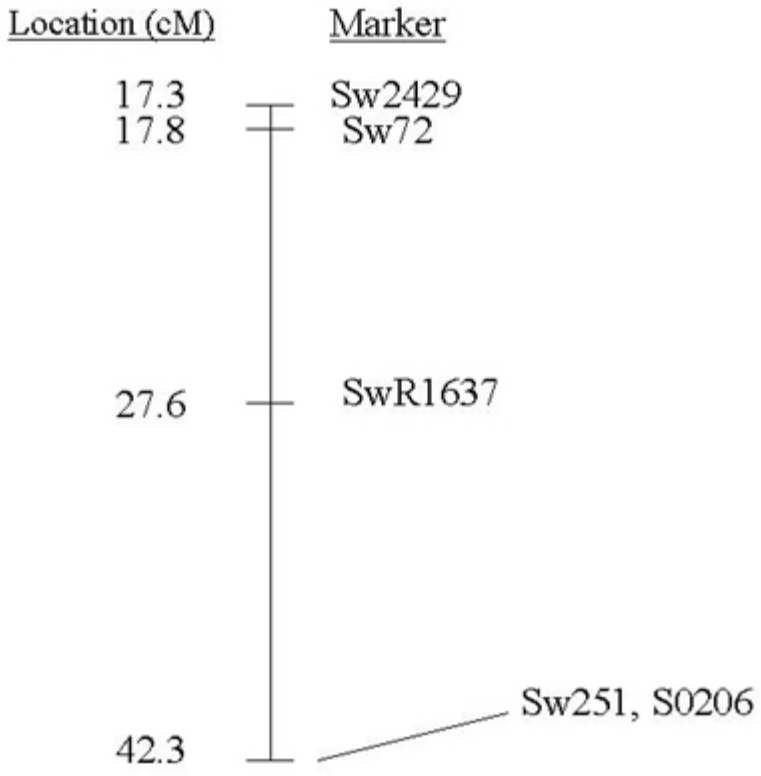

Figure 1. Map position in centimorgans (cM) of microsatellites in the region of porcine chromosome 3 containing the putative QTL for ADG. Positions are based on the USDA chromosome maps (http://sol.marc.usda.gov/).

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