

An Overview of QTL Research for Growth and Body Composition in a Meishan Cross Population at the Meat Animal Research Center

Gary Alan Rohrer

US Meat Animal Research Center
USDA-Agricultural Research Service
Clay Center, NE 68933

Justification

The Meishan pig was imported from China because they excelled in female prolificacy (Young, 1994). The Chinese pigs were also quite useful for genomic analyses as they were phenotypically different from occidental pigs in virtually every trait of importance. Furthermore, due to limited exchange of germplasm between Chinese breeds and other breeds for nearly one thousand years, considerable genetic diversity exists.

The dramatic phenotypic and genetic diversity made crosses between Meishan and occidental pigs the ideal quantitative trait locus (QTL) mapping populations for numerous production traits. Due to the poor growth rate and lean percentage of Meishan pigs, they currently have had little impact on commercial swine production in the US. However, QTL mapping with these pigs has greatly increased our knowledge about the inheritance of quantitative traits and has provided the markers necessary to improve the body composition of composite populations containing Meishan pigs.

Population Structure and Data Collection

The resource population was developed by reciprocally crossing Meishan pigs with a four breed composite population (WC; Chester White, Landrace, Large White and Yorkshire). The F1 females produced were either mated to Meishan or WC boars to produce over 700 backcross progeny. The progeny were weighed every four weeks beginning at birth and backfat depths were estimated every four weeks beginning at 3 to 3.5 months of age.

Half of the females and about 40 boars were retained for breeding the next generation of the population. These animals and their descendents were evaluated for reproductive traits. The remaining 540 progeny were slaughtered at approximately 100 kg live weight. Standard carcass composition measurements such as backfat depth, loin eye area and carcass length were recorded. In addition, the weight of each primal cut was recorded before and after trimming to less than 6 mm of subcutaneous fat (excluding the belly) of one side of each carcass.

Published Results

The carcass data results were published by Rohrer and Keele (1998 a,b) and the information collected on the live animals were reported in Rohrer (2000). The published

analyses assumed that the Meishan founders were homozygous for a different allele than the WC founders at each QTL. The line cross analyses have more power than other analyses when the assumption is correct, but have less power when the assumption is not valid. Breed of sire was fitted as a covariate since there were $\frac{1}{4}$ Meishan $\frac{3}{4}$ WC and $\frac{3}{4}$ Meishan and $\frac{1}{4}$ WC animals present in the population. It was not possible to test for parent of origin effects on alternate heterozygotes due to the population structure. Only measurements from the live animals that were recorded at developmentally significant timepoints were analyzed to avoid analyzing numerous genetically similar traits. The timepoints selected for weight were birth, weaning, 8 weeks, 26 weeks, average daily gain from 8 to 18 weeks and from 18 to 26 weeks of age. The ultrasound measures of backfat at 14 and 26 weeks of age were analyzed.

From all of these analyses, only three genomic regions reached genome-wide significance for presence of QTL. Each of these regions also presented multiple associations with body composition traits and all were highly significant for average carcass backfat and all measures of backfat at 26 weeks of age. The three regions were located at the end of the long arm of chromosome 1 (1qter), and near the centromeres of chromosomes 7 (7cen) and X (Xcen). The effect of all three of these QTL on fat deposition were subsequently confirmed by other groups in Meishan cross populations (for a summary see Bidanel and Rothschild, 2002).

The QTL at 1qter was highly significant for carcass backfat over the last rib and last lumbar vertebra. This region had the most significant associations with loin eye area and trimmed wholesale product. From the measurements on the live animals, it became clear that the most important effects of this QTL were early in life. This region significantly affected weight at 8 and 26 weeks of age, average daily gain from 8 to 18 weeks of age and fat thickness at both 14 and 26 weeks of age. The most significant association detected for this QTL was with 14 week fat depth over the first rib. In addition, a QTL affecting age at puberty in females in this region was later detected (Rohrer et al., 1999).

The QTL at Xcen was highly significant for most measures of carcass backfat and all live measures of backfat and trimmed wholesale product. This region presented suggestive evidence for QTL affecting carcass length and loin eye area. Similar to 1qter, the most significant association of Xcen was with 14 week fat depth over the first rib. Subsequent analyses determined that this region has a dramatic effect on pubertal plasma FSH in boars and mature testes size (Rohrer et al., 2001).

The QTL at 7cen was unique in many ways. While it was highly significant for measures of subcutaneous fat depth at slaughter and at 26 weeks of age, there was no apparent effect detectable at 14 weeks of age. In plots of the F-ratios for this region on backfat traits a characteristic bimodal peak was observed, which may indicate that two genes are actually causing the observed effect. And the most striking observation about this QTL is that the Meishan breed contributed the allele for reduced backfat. This region was also highly significant for carcass weight, carcass length average daily gain from 18 to 26 weeks of age and 26 week weight. There was suggestive evidence for an affect on leaf fat.

Principle Component Analyses

After these initial publications, the data were analyzed using procedures similar to the infinite-dimensional approach recommended by Kirkpatrick (1997). The approach first implemented a principle component analysis of all of the data measured on live animals. Then the solutions for each animal for the most important principle components were analyzed as phenotypes. The first three principle components explained over 80% of the variation in the data and were the only ones included in the QTL analyses. The "biological" descriptions of these components (PCs) are as follows. PC1 basically emphasized all measures of weight and backfat similarly (overall size) and represented 60.1% of the variation. PC2 contrasted weight versus backfat (composition) and represented 15.5% of the variation. PC3 contrasted early weight and fat to later weight and fat (early versus late growth) and represented 6.5% of the variation.

The results of these analyses did not reveal any new QTL regions but did help define the identified regions better. For PC1, overall size, *lqter* and *Xcen* were highly significant. PC2, composition, indicated that both *Xcen* and *7cen* possessed significant effects where the most likely position the *7cen* QTL was at 60 cM (slightly below the centromere on the long arm). Somewhat unexpected, *Xcen* was also significant for PC3, early versus late growth, while *7cen* was approaching genome wide significance ($p = .121$). The most likely position of the *7cen* QTL was at position 40 cM for PC3. Also of importance is that the F-ratio curves of *7cen* for PC2 and PC3 were smooth curves with only a single peak.

The principle component analysis has possibly separated the affects from *7cen* into two different QTL that may help determine the causative gene(s) for each peak. Unexpectedly, the principle component analysis did not effectively separate out the effects of the QTL at *Xcen*, or else three individual genes, each with a slightly unique effect on fat deposition and growth, exist at this particular region of the genome.

Fine Mapping

From comparative mapping (Goureau et al., 1996) the human chromosome that contains the gene causing each observed effect can be determined. For the QTL at *lqter*, the gene in human resides on chromosome 9, most likely towards the end of the long arm. The QTL, or QTLs, at *7cen* likely reside on the short arm of human chromosome 6 near the major histocompatibility complex, but if the QTL actually is below the centromere then the gene could possibly reside on human chromosome 15.

The QTL at *Xcen* has been studied in more detail at MARC because of its association with male fertility. The gene in the human genome definitely resides on the X chromosome and presumably quite close to the centromere. Several genes in this region have been evaluated, but the causative polymorphism has not been discovered. The first gene extensively studied was androgen receptor. However, there were no differences between Meishan and WC pigs in the coding region that would alter the amino acid

composition of the protein. A polymorphism in another positional candidate gene for testes size is currently being evaluated and this gene could possibly affect fat deposition.

Conclusions

The Meishan cross population has been extremely useful for identifying genomic regions affecting body composition and growth rate. To date, no causative polymorphisms have been found but the results could still be used in a marker-assisted selection program. The effects of the 3 QTL for backfat could reduce average backfat in a composite Meishan population by 1.8 cm based on the estimated effects from the QTL analyses. Since there were no QTL affecting reproduction rate associated with these genomic regions, marker-assisted selection in a composite population could easily reduce the amount of backfat while maintaining superior litter size performance.

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