Mapping and Use of QTL for Marker-Assisted Improvement of Meat Quality in Pigs

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Pork is the major source of red meat worldwide (43%). The quality of meat comprises a set of key quality and processing characteristics that are important for the future profitability and competitiveness of the swine industry. But improving meat quality with standard selection methods is extremely difficult because animals must be slaughtered to obtain their performance data, which removes them as potential breeding stock. Selection is, however, possible if the chromosomal regions or genes that are responsible for differences in meat quality traits or growth and composition are mapped.

Background on our research and some expectations:

Techniques of molecular biology and molecular genetics have rapidly progressed. New methods, coupled with advances in human genetics, have opened interesting vistas for investigators wishing to identify genes that control quantitative traits (quantitative trait loci or QTL) such as meat quality and growth and composition. The general use of genes and genetic markers makes it possible to localize the QTL responsible for traits of interest.

Several recent studies identified QTL for meat quality or growth and composition but these were based on crosses that involved at least on non-commercial breed, such as the Meishan or the Wild Boar. Results from these studies are of limited practical use. Our study was based on a cross between two commercial breeds, the Berkshire and the Yorkshire. These breeds were chosen on the basis of results from the NPPC Genetic Evaluation Program (Goodwin, 1995) which revealed that considerable differences in meat quality exist between breeds and that the Berkshire breed, in particular, has very positive meat quality traits.

Set up of the program

The overall goal of this research was to identify specific chromosomal regions associated with meat quality, as well as traits for growth and composition, in a Berkshire x Yorkshire cross.

Specific Objectives

1. Collect muscle quality data on 527 F animals from the Berkshire x Yorkshire muscle quality F2 resource family.

2. Perform a total genome scan using 158 anonymous genetic markers.

3. Perform statistical QTL analyses to determine chromosomal regions associated with muscle quality traits.

Family structure:

Two Berkshire boars (chosen with NPPC guidance) and 9 Yorkshire females were used to produce 9 useful F1 litters. Semen from boar studs was used and sows mated at the ISU Swine Breeding Farm. From the F1 litters, 8 boars and 26 females were chosen to produce 65 litters of 527 animals for genetic and meat trait analysis.

Traits measured:

Performance data collected included birth weight, 16d weight, ADG from birth to 16 days of age and ADG from weaning to slaughter. Pigs were weighed at weekly intervals and sent to market at approximately 108 kg. After slaughter, carcass traits were evaluated according to National Pork Producers Council procedures (NPPC, 1991). These data included carcass weight, visual scores for loin muscle marbling, color and firmness in the

plant cooler and in Ames, ultimate pH, Minolta reflectance and Hunter L. color scores for ham and loin. Water holding capacity was measured using a piece of filter paper (higher weight is less water holding capacity) and drip loss was calculated using two separate cubes of meat and by collecting the drip over 72 hrs. In addition, a loin chop was taken from each carcass and samples from it were used to evaluate lipid content. Also measured was Star Probe tenderness and sensory taste panel evaluations for tenderness, chewiness, juiciness, flavor and off flavor of the cooked loin were collected. In total 28 traits for meat quality and 12 traits for growth and body composition were measured in the F_2 animals.

DNA isolation and genotyping:

Blood samples were collected from all F2 animals, parents and grandparents and DNA samples collected. After testing parentage animals with no clear results were excluded from further analysis.

Genotyping was done by a sub-contracted commercial laboratory (GeneSeek Inc, Lincoln NE). About 180 markers were tested on the F0 and F1 animals. All animals were initially genotyped for 125 markers across the genome. Because the objective of this study was to extend this scan by genotyping for another 33 markers in special regions of interest, additional markers were genotyped. New marker linkage maps were derived for all autosomes and the X chromosome using CriMap and they were used in the QTL analysis based on line cross least squares regression interval mapping.

QTL analyses:

QTL were identified for the 18 autosomes and the X chromosome using the least squared regression interval mapping program developed by Haley and Knott (1994). The models used included sex and year-season and the covariable live weight for carcass traits and the covariable litter size for birth and 16 day weight and for ADG from birth to 16 days. For meat quality and sensory traits the effect of year-season was removed and the effect for slaughter date was added

Significance levels were calculated using the permutation test developed by Churchill and Doerge (1994). This was computed for both the individual chromosome and the genome wise level based on 10,000 random permutations of the data.

Results of our research

A total of 49 QTL were discovered for growth and composition traits, of which 10 were significant at a 1% genome-wise level and another 5 were significant at the 5% genome-wise level. QTL for growth and composition traits were located on the chromosomes 1, 2, 4, 5, 7, and 9. For meat quality traits 73 QTL were detected, of which 5 were significant at a 1% genome-wise level and 14 were significant at the 5% genome-wise level. QTL for meat quality were detected on chromosomes 1, 2, 6, 7, 10, 14, 15, and 18. Results from this study were in good agreement with findings from the initial analyses. But the increase of markers in regions of interest discovered about 20 new QTL at the 5% chromosome-wise level, of which at least one QTL was significant at a genome-wise level of 5%. Twelve of the original QTL were not significant at the 5% chromosome-wise level anymore. These findings confirm the segregation of important QTL for growth and meat quality traits between the Berkshire and Yorkshire breeds.

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