

## **Molecular and Quantitative Genetic Approaches to Swine Improvement**

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A comprehensive, ongoing project combining molecular and quantitative genetic approaches to the improvement of economically important traits in swine has looked at meat and carcass quality and composition, sow productivity and piglet survival. Multiple research objectives were pursued including QTL detection, comparative mapping for location of candidate genes, development of new measurement and evaluation systems such as piglet survival and economic analyses to determine optimum combinations of traits for different production systems.

### **Comparative Mapping**

Based on the published linkage maps, cytogenetic maps and radiation hybrid (RH) maps, we identified 764 genes and gene family clusters for swine as orthologous to those found in the human genome. The relative linear locations of these genes on the human chromosome sequence map were used as "rulers" to annotate the porcine genome. Based on mapping information for these markers in the human and porcine genomes, 50 conserved syntenies and 95 marker linkage groups were identified between human and porcine autosomes. These 764 markers can correlate 74% of the human-porcine genomes. The resulting comparative map is shown in Figure 1 below.

Based on the comparative map between human and porcine genomes described above, orthologous genes were selected at an average of 3 Mb intervals on the human sequence maps in order to construct high resolution RH maps of SSC3 and SSC6. These results provide us with the tools necessary for better identification of potential candidate genes for further QTL detection work with the porcine genome.

### **Piglet Survival**

The Ontario swine improvement databases were used to study improvements in modeling sow productivity traits and to estimate genetic and phenotypic parameters of existing traits. A collaborative study was undertaken with the Canadian Centre for Swine Improvement to identify new sow productivity traits and to compute the necessary parameters to design and implement genetic evaluations. Genetic aspects of peri-natal piglet survival as a function of the sow was studied in additional detail. Through this activity peri-natal piglet survival was identified as the most important trait after litter size for sow productivity. Peri-natal mortality is an especially important trait when average litter size increased past 11-12 piglets and the importance increases non-linearly as litter size increases. Although total born and peri-natal survival both have a low heritability, the genetic correlation between the two traits is 0.5. Peri-natal mortality has been adopted as a new trait to add to sow productivity evaluations in the national swine evaluation program.

### **Development of Candidate Genes for Meat and Carcass Quality**

Candidate genes were selected on the basis of their involvement or expected involvement in physiological pathways associated with the growth, carcass and meat quality traits of interest; four fatty acid binding protein (FABP) and six histone deacetylase (HDAC) candidate genes were selected. Two FABP candidate genes were selected on the basis of results found by other studies to serve as a reference point. Eight additional candidate genes were selected to represent new exploration for QTL. Fatty acid binding proteins are involved in the transport of fat across cell membranes. The most likely and representative suite of these FABP genes was developed for this study. Histone deacetylases are involved in the regulation of transcription of DNA into mRNA which is a fundamental step in the activation of any gene to create the product it codes for. The human genome project has revealed that a variety of HDAC genes are present with varying degrees of tissue specificity. Regulatory genes are particularly promising as candidate genes for QTL detection since they control the level of activity of other genes which can lead to differences in the expression of things like growth hormone production that create genetic differences for economically important traits. Primers were developed and the parents and grandparents were genotyped looking for polymorphisms. Of the original ten candidate genes, eight revealed polymorphisms that were suitable for genotyping and that were segregating in the resource population. These eight usable candidate genes then form the basis of the procedure for detecting an

association with the variety of performance, carcass and meat quality traits measured in the resource population. All 429 pigs with samples suitable for DNA extraction, along with the 40 sows, 5 F1 sires and 12 grandparents have been genotyped for all eight candidate genes for a total of 3,888 genotypes. With 103 traits measured per pig, this study involved 824 association tests.

The findings of our study have increased our understanding of the potential role and association of *FABP* and *HDAC* candidate genes with growth, carcass and meat quality traits in swine. Evidence was found for associations between polymorphisms in *FABP3*, 4 and 5 and *HDAC* 1, 3 and 5 and various of these traits. Polymorphic DNA markers in *FABP5*, *HDAC1*, *HDAC3* and *HDAC5* were reported for the first time in this study. Associations of the *FABP3-HaeIII* locus with backfat and IMF, and of the *FABP3-MspI* locus with bodyweight, first reported by Gerbens et al (1999) were confirmed here, although the evidence was not always strong.

**Figure 1 Porcine - Human Comparative Map**

