

Identifying Genes Of Economic Importance For Pig Production

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Summary and Implications

Traditional quantitative approaches to animal breeding rely upon recording data from phenotypic traits of interest, such as growth rate, loin eye area, and backfat, on a large number of individuals. A battery of statistical methods is applied to these records in order to identify and select the superior individuals, which in turn become the parents of the next generation. This strategy is highly efficient when dealing with traits that are moderately or highly heritable, such as growth rates, and has been used world wide in improving traits of interest. At the same time, there are traits where the parent's phenotype is a poor predictor of their offspring's phenotype, such as reproductive and disease related traits. Furthermore, there are also traits of economic importance to the pig industry, such as meat quality and longevity, whose phenotype is only measured at a time where we can no longer use the animals for breeding purposes. Therefore, in order to tackle these problems, there is a need for other approaches in livestock selection. Recent advances in DNA technology have given researchers the ability to identify genes that control traits important to pig production. These technologies are now being used in our group to find such genes. Eventual discovery of these genes will help in selection of livestock.

Materials and Methods

It is well known that the vast majority of the traits of interest for the pig industry are under control of multiple genes, each gene having a small effect in the genetic regulation of the trait. These traits that are controlled by multiple genes are referred to as quantitative traits. Quantitative trait loci (QTL) refer to the location on the chromosome where they reside. We perform a QTL scan to identify where the gene or genes are located that contribute the most to a certain quantitative trait. In a QTL scan, multiple molecular markers (an identifiable physical location on a chromosome whose inheritance can be monitored) are selected on every chromosome and recorded for every pig as its genotype (genetic makeup) in the population of interest. These genotypes are then analyzed against the phenotypic records for the pig population to identify the chromosome(s) and where along that chromosome(s) a gene lies that is controlling the trait of interest. However, even after we have

identified these regions, we still don't know which gene or genes are controlling the trait, as there could be hundreds of genes that lie in our identified region. Using an approach known as comparative mapping, we can use the location of specific genes in the human genome to predict the location of the same genes in the pig genome. We can then use the incredible amount of information generated by the Human Genome Project to help identify which gene is controlling our trait of interest, due to the fact that humans and pigs are genetically very similar. Instead of using a QTL scan, researchers can also use an approach known as the candidate gene approach to target their gene of interest. This approach involves the researcher selecting a gene that has a known biological action that the researcher believes could contribute to regulate the trait he or she is analyzing. Often researchers combine both methods using the QTL scan first to identify a region and then select candidate genes in that region to analyze.

After the decision is made as to which genes will be studied, a technique called PCR is used to amplify fragments of these genes from many animals representing several different breeds. These fragments are then sequenced to identify the DNA bases that make up the fragment and a comparison is made between them to identify differences or variations in the DNA sequences, known as polymorphisms, between pigs. Genetic tests are developed using the identified polymorphism to determine the genotypes for large populations of pigs, since sequencing large numbers of animals is expensive and time consuming. The resulting genotypes are then analyzed against the phenotypic records of the individual to determine if there is an association between the gene and the trait of interest. Once a gene has been proven to be associated with a trait, pig producers can then use the genetic test to make selections in their herd on a trait that could have otherwise been next to impossible to select using traditional quantitative methods.

Results and Discussion

In our lab, we performed a large QTL scan with over 180 gene markers on a three-generation cross between Berkshire x Yorkshire pigs. This identified over 100 regions of the pig genome that are associated with individual traits. We have also employed candidate gene analyses. From this we have identified several genes that have been associated with traits important to pig production using these techniques. Two such genes that have been identified are *ESR*, which was identified as being associated with litter size and *MC4R*, which was identified as having an effect on loin eye area, back fat, as

well as feed efficiency. These genes were then incorporated into breeding programs to help pig producers realize more economic returns on their investments. From the QTL scan we have identified two genes *PRKAG3* and *CAST*, which are associated with meat quality. Further analysis is now on going for chromosomal regions on chromosomes 1, 5, 6, 7, 12 and 17 for growth, backfat and meat quality traits. With the ongoing advances in DNA technology, it is only a matter of time before additional genes are identified and used in selection programs for pig production.