Understanding the impact of genetics on pork quality

Pork quality is an integral part of a good eating experience. Consumers speak loudly with their money and over the last 35 years, pork consumption has decreased in the United States and Canada. According to the USDA, pork consumption in 1980 was 25.8 kg per capita and in 2014 it dropped to 21 kg per capita. In Canada pork consumption per capita has decreased from 32.2 to 20.6 kg in the same time period.

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One possible reason is the decrease in pork quality with the increased emphasis for leaner pork. In recent years, the demand for better tasting pork has been increasing. Most North American producers do not get paid directly for pork quality, but this may change as consumers demand better pork quality that will result in a consistently good eating experience.

There are many factors that can influence pork quality including stress, diet, fasting prior to slaughter, pre-slaughter handling, stunning methods, and post-slaughter handling. These factors are environmental and can vary across producers and packing plants.

Conversely, genetics plays a significant role in pork quality. One classic example of the effect of genetics on pork quality is the ryanodine receptor 1 (halothane) gene. Animals that contain two copies of the unfavourable allele are more susceptible to Porcine Stress Syndrome, which is associated with pale, soft, and exudative (PSE) pork. Another example is the effect of the Rendlemann Napoleon (RN) gene on pH and cooking loss. Once these mutations were identified genetic tests were developed to quickly remove the undesirable genotypes from swine populations.

Unfortunately, it is not as simple for other pork quality traits including pH, marbling, colour, shear force, and drip loss. These traits are largely polygenic, or controlled by multiple genes.

### Genetics of pork quality

Pork quality traits generally have moderate to high heritability. Therefore, these traits can be improved through genetic selection. Some of the key pork quality traits include shear force (a measure of tenderness), marbling, colour, pH, and drip loss. Many of these traits are associated, or correlated, with carcass composition traits, and with each other, and some of these associations are antagonistic, for example by moving one trait in a favourable direction, another trait tends to move in an unfavourable direction (Table 1).

An example of unfavourably related traits is carcass back fat thickness (BF) and intramuscular fat (IMF). Back fat has a positive genetic correlation with IMF. Back fat is a key component in carcass lean yield and IMF is a key meat quality trait. By selecting for increased carcass lean yield (decreased BF) then IMF is decreased resulting in lower pork quality. Although the above relationship is antagonistic, the correlation is not perfect so that it is possible to increase IMF without increasing BF.

Not all carcass and pork quality traits are unfavourably correlated. Hot carcass weight is negatively correlated with loin colour, which is a favourable correlation. As hot carcass weight increases, loin colour gets darker. Also, in terms of pork quality, shear force and cooking loss are positively and favourably correlated, as shear force decreases (increased tenderness) cooking loss also decreases (moisture is retained in the meat).

Lastly, pH is a good overall measurement of pork quality. The pH of muscle is favourably correlated with colour, cooking loss, and drip loss. Therefore, the better the pH value the darker the meat is and less water is lost from fresh pork and during cooking.

### Genomics of pork quality

Pork quality is one of the areas where genomics can have a large impact on genetic progress. The traits are expensive to measure and are generally recorded post-mortem.

Since the release of the swine genome sequence in 2012, much work has been conducted to identify regions within the genome, known as QTL, that are associated with traits of interest. Of the QTL detected and published, 35% are related to pork quality, followed by carcase, health, production, and reproduction (Fig. 1).

Clearly a lot of research has gone into identifying genomic regions and investigating the genetic architecture for pork quality traits because of the potential impact on genetic progress for traits that are measured post-mortem.

Once a QTL is identified, genes surrounding the QTL are investigated to see if they are directly contributing to the differences in actual measurements between pigs. These genes are called candidate genes. One candidate gene is PRKAG3 and located on chromosome 15.

Different variants of this gene are associated with meat pH, colour and water holding capacity with one specific allele explaining RN. Calpastatin (CAST) located on chromosome 2 is another important gene associated with meat tenderness. However, candidate genes need not be known in order to make genetic improvement. Instead, SNP (single nucleotide polymorphism)
Phisms) information can be incorporated into a breeding program in order to attain greater genetic progress. The current commercially available SNP panel includes 80,000 SNPs per animal genotyped.

Genesus recently concluded a large scale genomic study of pork quality. Table 2 is a summary of the chromosomes identified that contain QTL associated with various pork quality traits. These results demonstrate the complex genomic architecture with at least one QTL found on 13 of the 18 pairs of autosomes (non-sex chromosomes) in the swine genome.

Selection for pork quality

Selection for pork quality is not as simple as selecting for growth. Key pork quality traits such as colour, IMF, pH, shear force, and drip loss cannot be measured directly on the selection candidate.

This information must come from related individuals that have pork quality measurements. Because this information cannot be obtained on the selection candidates, a large dataset of related individuals must be used in order to accurately estimate breeding values of the selection candidates.

In 1998 Genesus Inc established, and now continues to grow, a large database of carcase and pork quality traits. The Genesus carcase and pork quality program provides detailed carcase cutout and measurements collected on over 50 quality traits per animal. To date, over 15,000 animals have been evaluated through this detailed testing procedure.

Carcase and pork quality information from this large dataset together with growth performance, ultrasonic measurements, feed intake and pedigree relationships on selection candidates and harvested animals that contain detailed cutout information are an important resource for selection. Genetic correlations among pork quality and all other important traits need to be considered and can be estimated from this combined set of data.

Utilising the correlations amongst pork quality, carcase, and performance traits, breeding values can be estimated from this resource and used for selection purposes.

A dataset of this size is required in order to achieve the desired accuracy for breeding values.

This accuracy can be further enhanced through the use of genomics. As previously mentioned, detailed measurements on important pork quality traits cannot be measured directly on the selection candidates.

However, selection candidates can be genotyped shortly after birth and that information, along with the pedigree and performance information, can be incorporated into genomic estimated breeding values.

In doing so, the accuracy of the breeding values using genomic information can be 17-77% better than non-genomic based breeding values for pork quality traits. Simply put, that is 17-77% greater genetic improvement per year.

Conclusions

Consumers enjoy tender, flavourful and juicy pork. In order to give the consumer what they want pork quality must be an integral part of a genetics program. However, it is a large investment and requires a substantial amount of data to improve these traits. Pork quality is part of a very complex system and selecting for the ideal pig is challenging, but not impossible. Multiple genes with small effects control many of the key pork quality traits.

Traditional selection methods can accurately identify superior animals, but genomics is an invaluable tool that can greatly increase the rate of genetic improvement in pork quality traits.

Table 2. Chromosomes that contain QTL identified for pork quality traits.

<table>
<thead>
<tr>
<th>Traits</th>
<th>Chromosomes</th>
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<tbody>
<tr>
<td>Fresh loin pH</td>
<td>15</td>
</tr>
<tr>
<td>Peak shear force (tenderness)</td>
<td>2, 17</td>
</tr>
<tr>
<td>Ham colour</td>
<td>1, 2, 5, 6, 9, 13, 14, 15</td>
</tr>
<tr>
<td>Loin colour</td>
<td>1, 2, 5, 8, 9, 10, 13, 15, 17, 18</td>
</tr>
<tr>
<td>Drip loss</td>
<td>13, 14, 15</td>
</tr>
<tr>
<td>Cooking loss</td>
<td>15</td>
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<tr>
<td>Carcase length</td>
<td>2, 5, 6, 7, 13, 17</td>
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References are available on request from the author.