

# The Changing World of Genomics and its Impact on the Pork Chain

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## ■ Summary

The increasing availability of genomic information, illustrated by the publication of the complete sequence of the human genome, offers new options for animal improvement. It will no longer be necessary to rely solely on phenotype to predict genetic merit. Instead, variation in individual genes can be identified and exploited. Genes and DNA markers have already been identified that impact growth and backfat, litter size, disease resistance, lean percentage and meat quality. In addition, DNA “fingerprints” provide the means to verify traceability from the plate to the farm. This new information will provide the means to better influence traits beyond the cost of production providing benefits throughout the pork chain. Genomics should help the industry respond more rapidly to the changing demands of consumers.

## ■ Introduction

The pig industry has made remarkable progress in the last 40 years: each sow produces 50% more pigs per year, and her pigs eat one third less feed in order to produce 33% more lean meat. Genetics has played a significant role in this industry improvement, delivering year on year gains in efficiency. The majority of this genetic improvement was accomplished using approaches that Robert Bakewell would have recognized: the measurement of performance and “cross the best with the best”. The application of quantitative genetics (albeit in sophisticated form nowadays) leads to the selection of the best variants (alleles) from genes and combinations of genes for the traits that can be measured. The models used assume that there are a very large number of genes, each with a very small allelic effect. However, this is not always the case, clearly some genes, or more correctly alleles of these genes, have a

relatively large impact. For example, in 1991 Canadian scientists identified a single base pair change in the “Halothane” gene (Fujii et al. 1991) that was responsible for porcine stress syndrome and associated effects on growth, muscling and meat quality. An animal inheriting two copies of the “mutant” variant – differing at 1 of the 3 billion base pairs in the genome – would react to the Halothane gas test, was susceptible to stress and if taken to market would yield poor quality meat described as “pale, soft and exudative” (PSE). More importantly, knowledge of this change allowed breeders to easily identify carriers of the gene, which were otherwise undetectable using the gas test. The pork industry could demand “Halothane-free” breeding stock to reduce the incidence of PSE (at least the component due to this major gene effect).

The ability to determine the specific genotype of an animal provides a number of advantages, especially where the trait of interest is difficult or costly to measure, expressed in only one sex or appears late in life. Disease resistance, litter size and meat quality are all traits that can benefit from the application of genomics and examples can now be provided for each of these traits. As more information is obtained using DNA sequence information or post-genomic analysis of gene expression then we can expect to see more traits yielding to this approach enabling the industry to better respond to the ever increasing and changing demands of the chain and the consumer.

## ■ Results

Two basic approaches are most commonly used to find the “genes” explaining variation in the trait of interests: genome mapping or the “candidate gene approach”. The first utilizes specific genetic designs (for example three generation families based on divergent breed crosses such as Chinese Meishan or Wild Boar and Large White) to find the location of Quantitative Trait Loci (QTL) on the genetic map. This is a powerful design to find regions of the genome explaining the large phenotypic differences between the breeds used in the cross. The breeds are expected to be fixed for different alleles of the genes of interest. All of the projects that have been undertaken have been successful at identifying QTL (Bidanel and Rothschild 2002). Unfortunately, although some of these QTL have now been shown to be relevant to commercial breeds (Evans et al. 2002), they are difficult to apply in a commercial situation. This is primarily due to the limitation of the design, meaning that recombination is necessarily limited and the regions housing the QTL are very large and contain many genes. However, it is likely that QTL results will have increasing value as our genomic tool kits develop. Indeed, the RN<sup>-</sup> mutation (responsible for the ham cooking losses associated with the Hampshire breed), identified initially by a mapping approach was then elucidated using positional cloning and a “BAC contig” constructed for that region of the genome (a physical representation of the DNA sequence from the

QTL region). Interestingly, the “RN” gene had not been identified in other species (Milan et al 2000).

The second method, the candidate gene approach (Rothschild and Soller 1997), has been much more successful in generating tools that can be applied rapidly in marker assisted selection. Information on the biochemical function and DNA sequence of genes (and increasingly position e.g. from QTL studies), accumulated from different species, is utilized to find variants in the target species. These variants are then tested for association with the trait of interest using large numbers of animals from within a breed or genetic line. Importantly, the gene markers are tested for across population (rather than within family) associations that can then be applied directly in the population.

The MC4R (melanocortin receptor 4) gene is a good recent example of the power of this approach. This gene had been shown to be involved in the control of appetite in mice (using a gene knockout approach). The pig gene was isolated and the sequence determined for a number of individuals in order to identify polymorphisms within the gene. A variant was identified in a region of the gene that is highly conserved between animal species and then used to test whether this variation was associated with variation in growth and fatness of a sample of more than 1,700 pigs (Kim et al 2002). More recently we have extended these results to commercial genotypes as well as in breeding lines (see Trial 2 in **Table 1**). In a situation where achieving backfat targets is essential in order to maintain profitability (e.g. in the UK where pigs are fed ad lib in relatively high health conditions) then changing to boars of genotype 11 immediately improves the proportion of animals meeting the performance target of the abattoirs.

**Table 1: Association between MC4R genotype and growth and fatness**

<b>Trial</b>	<b>Genotype</b>	<b>Number of pigs</b>	<b>Backfat (mm)</b>	<b>Days to 110kg</b>	<b>Lean %</b>
<b>1</b>	11 vs 22	2934	-1.5	+2.0	
	P-value		<0.0001	<0.0001	
<b>2</b>	11 vs 22	3867	-1.4		+0.6
	P-value		<0.001		<0.001

Similar results have been obtained for markers impacting litter size and meat quality (e.g. ultimate pH and colour). New results suggest that it will also be possible to select for improved eating quality using DNA markers. One of the most promising areas for the application of genomics is animal health and welfare. An understanding of the genes involved in the development of disease

beginning with the initial interaction between the host and pathogen may provide us with new tools to control disease. Already it is possible to select for pigs that are genetically resistant to post weaning scours and edema disease caused by *E. coli F18*. Pigs that inherit two copies of the “resistant” allele of the FUT1 gene do not bind *E. coli F18*, so that the toxins produced in susceptible animals are never made in sufficient quantities or at the site where they can cause the disease (Meijerink et al. 2000). It may be possible in the future to select specific vaccination or treatment regimes for specific genotypes to improve animal health.

Finally, DNA sequence variation provides an individual with a unique “bar code” from birth all the way through to the plate. It provides, therefore, the perfect method to certify the production chain from farm to consumption. This has already been achieved successfully for beef in some countries (for example Superquinn’s Traceback scheme [www.superquinn.ie](http://www.superquinn.ie)). Such systems can now be envisaged for pigs, providing the ability to track back to farm of origin, even to individual pigs where this is required. It is already possible to verify the breed origin of meat using a simple set of DNA markers and this is particularly valuable where the breed is associated with premium products such as the Berkshire and Kuro-Buta in Japan. As more and more use is made of genetic markers we can envisage that product specifications will include specific genotypes, so that these will be built into the verification systems required to satisfy the chain through to the consumer.

## ■ Conclusion

Quantitative genetics will continue to be the engine for genetic improvement. However, the incorporation of more and new information, such as that which can be provided by genomics (and the many post-genomic technologies) will mean that we can provide more specific products for the different markets that will arise in the future. This will lead to benefits for the producer and through the marketing chain to the consumer.

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