

# Creation of a fast track solution to better pork quality

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The QuickSNP set includes over 100 SNPs, associated with mainly pork quality, carcase quality, disease resistance, but also the standard production characteristics like growth, back fat, and muscle depth.

Most of the SNPs on the QuickSNP panel are associated with traits that have not been routinely measured yet, either because the traits are very expensive to measure or have a detrimental effect on the animal. The genotypes derived from the QuickSNP will allow for a more precise selection of those animals that pass on the desired characteristics to their offspring.

## History of genome research

The exponential development of the sciences of genetics and biochemistry combined has resulted in an enormous expansion of the tools and applications that can be used in pig breeding.

Genomics is the word for the science and technology that deals with the code of life, DNA. Starting some 150 years ago with the discovery of the principle of natural and arti-

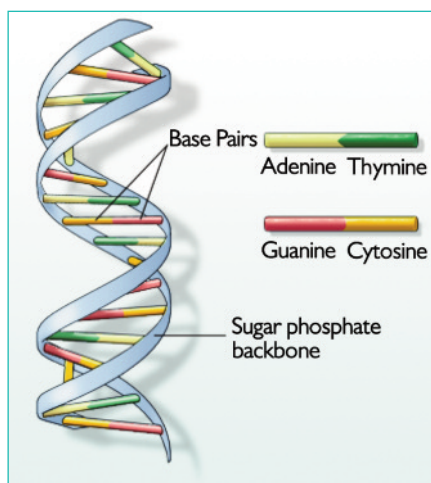


Fig. 1. Schematic representation of a DNA strand.

ficial selection (Darwin), continuing with the discovery of inheritance of simple genetic traits (Mendel) through to the discovery of DNA as the molecular basis of genes by Watson and Crick in 1953, the foundation was laid for the DNA technologies that were largely developed from the 1980s onwards.

These DNA technologies are improving at a massive rate, making the technology more and more accessible.

Today we have the – more or less – full

genome sequence of many species, more than 20 bird and mammal species, including man. Genomes of higher species contain some 20,000 genes.

The pig has only been added to this list towards the end of 2009. Since ultimo 2008 we also have hundreds of thousands of SNPs (Single Nucleotide Polymorphisms) of the pig available. These can be used as easily identifiable markers for locations on the genome of the pig. Until then we only had information on part or whole of the DNA sequence of some hundreds of single genes of the pig.

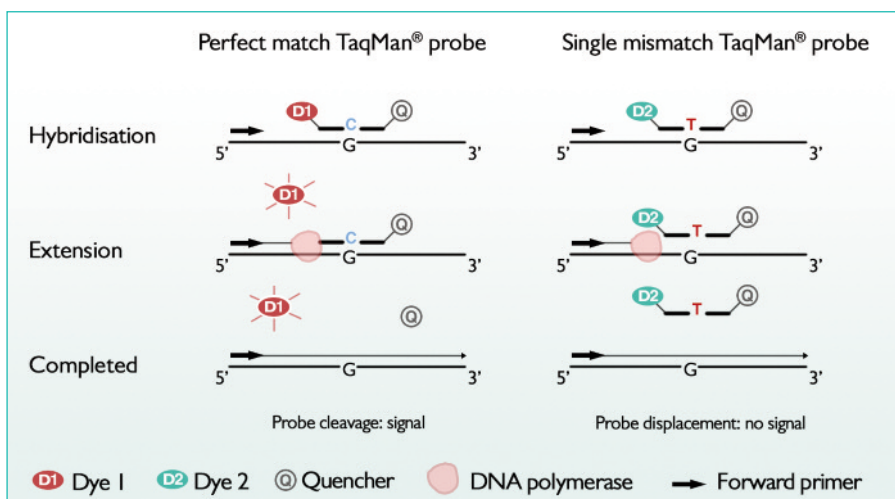
## The pig genome

The genome of the pig consists of roughly three billion base-pairs, three billion different letter combinations (Fig. 1).

Out of these three billion base-pairs only a small percentage shows variation between individual pigs. These are so-called 'single nucleotide polymorphisms' or SNP (pronounced 'snip').

A SNP is any location on a chromosome where a single DNA base (adenine, cytosine, guanine or thymine) can be found in different variants in different homologous chromosomes. The genome of the pig has millions of such SNP locations and SNPs are therefore a rich source of genetic markers.

Fig. 2. Open Array platform genotyping.



## Genetic markers

Genetic markers may have a direct effect on expression of the genome by altering a sequence that codes for protein expression or a sequence that controls the expression of another sequence. However, a SNP may also merely be located closely to and inherit together with another DNA sequence that is responsible for a functional genetic variant. In both cases the SNP variants are reflecting functional genetic variation.

Many of the single gene tests that were developed later were also derived from analogies with the human genome and genome function. The QuickSNP set is a so-called low density SNP chip. The SNP set includes over one hundred SNP. The SNP

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are analysed using the OpenArray platform from Applied Biosystems. This is a real-time detection process; each cycle produces a fluorescent signal proportional to the amount of product present (Fig. 2).

These fluorescent signals are then read to declare which allele of the SNP is present in the analysed sample.

## Available SNP

The SNP set was originally developed by the Universitat Autònoma de Barcelona (UAB) to determine the potential utility in individual pig identification and pedigree testing. Over the last years the SNP set has been further developed to include SNP that have an effect on meat and carcass quality traits.

Due to the flexibility of the used genotyping technology it is relatively easy to discard and include SNP. In recent months the set has been upgraded to also include SNP with a potential impact on reproduction and disease resistance traits.

## Pig breeding application

Collecting DNA samples from our pigs has been routine in our nucleus facilities for quite some time now. The routine sampling, shipping and processing of pig tissue samples has been professionalised through the use of standard DNA sample tags that catch an ear notch sample in a small tube.

All samples are shipped and processed at the Hendrix Genetics genomics laboratory. The Genomics Laboratory is a central hub for global molecular DNA work for all Hendrix Genetics divisions. Blood and tissue samples are taken from the pig, poultry and aquaculture divisions, and also from customers' stocks.

Samples are then transported to the genomics laboratory, where DNA is extracted and stored in a BioBank. After in-house analysis and genotyping (Fig. 3),

geneticists of Hendrix Genetics use these to develop breeding programs for the divisions or directly into customer breeding programs.

Currently all replacement animals in the Hypor nucleus facilities are being tested with the QuickSNP.

This is done for several reasons:

- Routine quality check.
- Pedigree check.
- To monitor allele frequencies.

All Hypor replacement animals are checked for a number of SNP markers, if the replacement animals do not meet certain quality criteria, i.e. if they do not show the right genotype, animals will not be used as replacement animals.

Those animals will not enter the central AI station and will not be used as replacement sows. Secondly, all replacement animals have their pedigree checked by means of the QuickSNP genotypes (Fig. 4).

If a parent offspring combination is showing too much discrepancy, for example if the sire has genotype AA and the offspring has genotype CC for a number of markers, then the animals are marked as having a wrong pedigree (more than a certain percentage of deviating genotypes).

The reason why the check has to fail for a number of SNP markers is that the genotyping technology is not 100% accurate.

## Other applications

There is a wide variety of SNP on the QuickSNP panel, i.e. SNP associated with pork quality, carcass quality, disease resistance, but also the standard production characteristics like growth, back fat, and muscle depth.

This variation allows producers to identify the right (breeding) animal for each production environment more accurately. Some of the SNP are explaining large proportions of the genetic differences between animals.

Most of the SNP that explain large amounts of variance for the traits we have

been selecting on for quite some time now have been fixed in the genetic lines, depending on the genetic direction of the line.

The SNP might have been fixed at a certain opposite genotype if one compares different lines, but within a line the SNP with large effects have all been fixed.

However, most of the SNP on the QuickSNP panel are associated with traits we have not been routinely measuring, either because the traits are very expensive to measure or have a detrimental effect on the animal, for example if one has to kill an animal to measure carcass traits, or one has to infect an animal with a pathogen to measure disease resistance or resilience, then this animal cannot be used for breeding anymore. The genotypes derived from the QuickSNP will allow for a more precise selection of those animals that pass on the desired characteristics to their offspring.

## Conclusion

The exponential development of the sciences of genetics and biochemistry combined has resulted in an enormous expansion of the tools and applications that can be used in pig breeding.

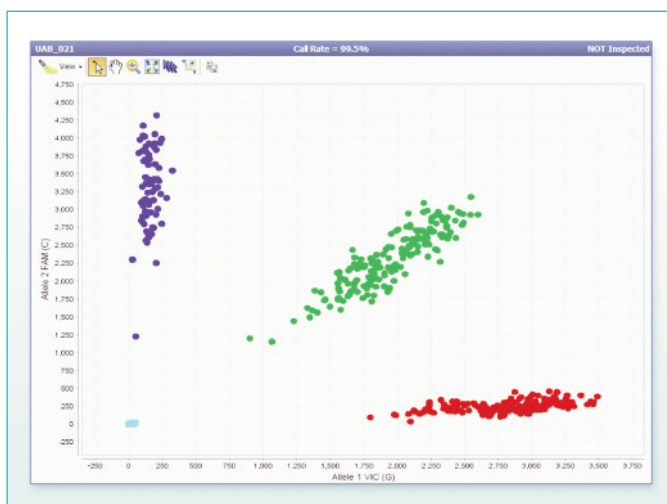
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The SNP set includes over 100 SNP, associated with pork quality, carcass quality, disease resistance, but also the standard production characteristics like growth, back fat, and muscle depth.

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**Fig. 3. Example of SNP genotype assignment, three colours represent the three possible SNP genotypes.**



**Fig. 4. Overview of pedigree checks over time.**

