

Selection at DNA level

Genomic selection signals revolution in cattle breeding

Ten years ago it was still a futuristic dream. Today, genomic selection is the hot topic in the world of animal breeding. But what precisely does it involve? Dutch researchers outline the background to this new technology.

Genomic selection is being hailed one of the most significant developments in cattle breeding since the introduction of 'breeding value' assessment. The principle of genomic selection was developed in the late 1990s at Animal Science Group (ASG) in Lelystad and at that time it was just a futuristic dream, impossible due to the high costs of measuring the markers. But 2008 saw a breakthrough. And now 50,000 markers, with the ability to explain the majority of genetic variation, can now be measured for the same amount of money previously required for 100 markers – about £180. So what is the potential impact for dairy cattle breeding and what are the possible applications in individual dairy cattle businesses?

Top bulls

A bull calf receives half of its genes from its father and half from its mother. The offspring do not all receive the same half from their parents. An important question is which specific genes the offspring receive from both parents. This is why, in dairy breeding, the progeny testing system involving three types of bull (the 'test bull', the 'waiting bull' and the 'breeding bull') has been introduced. In this system, the average yield from about 100 offspring of one bull are used to determine whether or not this bull has inherited the right genes from its parents. The total value of the genes obtained is expressed in the form of 'breeding values'.

During the past 10 years, a great deal of research

has been done into the use of genetic markers. The aim of this was to be able to assess, at an early age, whether a calf has inherited certain desirable genes from his or her parents. By doing this, more stringent selection of calves is possible and, as a result, a larger proportion of the test bulls are promoted to breeding bulls and a larger proportion of the selected cows become bull dams.

The best genetic markers

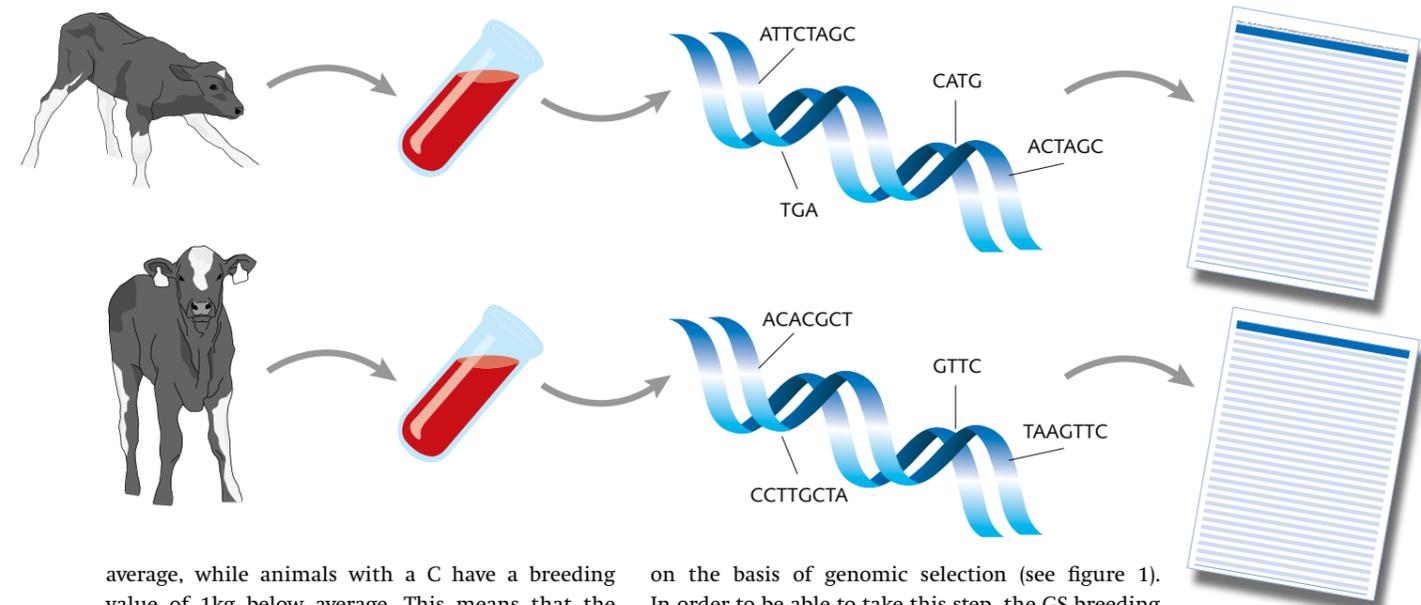
Since the measuring of markers has always been difficult, and because few markers were available, research has been focused on finding the best genetic markers. Many markers were tested, but only the markers that had a sufficiently predictive value were routinely used in the breeding programme. The breeding organisations that had invested in this therefore found about 30 markers that led to a genetic improvement of about 10%.

Due the huge reduction in the cost of measuring the markers, the entire process can be carried out more efficiently. It is no longer necessary to look for the best markers. We are now measuring the markers of all animals, and on each occasion we reassess the value of these markers. The additional advantage is that with so many markers we are also able to predict the majority of the genetic differences between progeny. Using large numbers of markers in this way is called genomic selection.

Breeding values

Each animal has two copies of each of the 50,000 markers. The possible copies are A, C, G and T – the building blocks of DNA. Usually just two of the four above-mentioned copies are present for each marker, for example A and C. For these markers, animals can be AA, AC or CC. The combination of markers over the entire genome is unique for each animal. The large number of markers and the fact that they are spread throughout the genome ensures that for all genes at least one marker is in close proximity. In this way, the markers 'mark' the genes, without the genes themselves or their location on the genome being known.

Each of the 50,000 markers is subsequently assessed to measure the extent to which it explains the differences in a specific characteristic. So, for example, animals with an A for a specific marker may have a breeding value of 1kg of milk above



average, while animals with a C have a breeding value of 1kg below average. This means that the breeding values of animals with AA, AC and CC deviate by +2, 0 or -1 respectively from the average. There are many markers affecting kilograms of milk and each animal has a unique combination of markers. In order to assess the effect of each marker in relation to the average, and subsequently to add up the cumulative effects of all these markers, values known as genomic selection values (GS values) are obtained.

An important stage in the application of genomic selection is the measurement of the value of each separate marker. This is done using what is termed a reference population. Generally this population consists of at least 1,000 bulls, for which accurate breeding values are available (based on information from their daughters) and for which all 50,000 markers are known. A statistical model is used to measure how these reliable breeding values can be 'divided up' in the effects of all 50,000 markers.

Breeding programmes

Traditionally, breeding organisations select test bulls on the basis of the average breeding values of their parents. The most extreme application of genomic selection in dairy cattle breeding involves dispensing completely with the test bull/waiting bull/breeding bull system and instead only testing young bulls for their markers. As a result of this, the best of them can be promoted to breeding bulls

on the basis of genomic selection (see figure 1). In order to be able to take this step, the GS breeding values for young bulls must possess a reliability that is comparable with that of the breeding values based on 100 daughters. At the present time, such levels of reliability have not yet been achieved. For example, using genomic selection, test bulls have achieved approximately 60% reliability for kilograms of protein compared with a reliability of 85% based on the data from 100 daughters. The reliability of the GS breeding value is however rather better than the reliability of 35% based solely on the breeding values of the grandparents. The reliability of GS breeding values is expected to increase as the reference population becomes larger.

Generation gap

Breeding organisations are currently employing genomic selection in the preliminary selection of test bulls. In this way, a number of bulls are finally selected from a large number of bull calves and are subsequently used as test bulls. At the same time, for example, the best 10% of bulls (based on GS breeding values) can already be used to sire the next generation. By reducing the number of test bulls, or even eliminating the use of any test bulls at all, as in figure 1, the costs of the breeding programme can be drastically reduced. Trialling test bulls and keeping 'waiting bulls' is always a major component in the total costs of the breeding programme. Genomic selection has the potential to radically

The researchers

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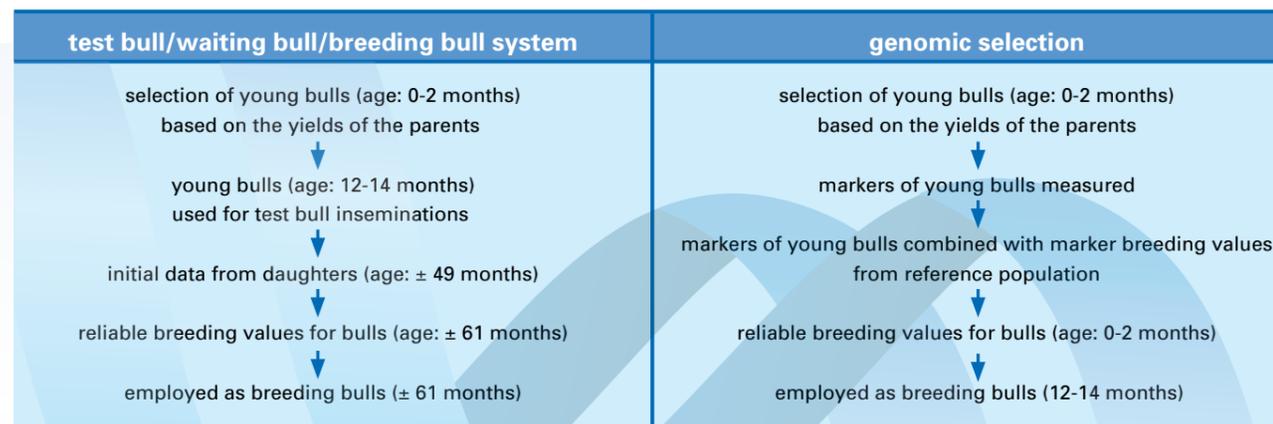


Figure 1: The processes and (predicted) duration of traditional selection and genomic selection

change global breeding programmes and further accelerate genetic advances. By switching completely to genomic selection, the lifetime of breeding bulls can be reduced from five years to one year (see figure 1).

Greater genetic advances are often accompanied by greater inbreeding. One of the reasons for this is that for greater genetic improvement, more zones from a top breeding bull are used than from a test bull, significantly increasing the chance of two new top bulls being brothers or half brothers. With the aid of genomic selection, it is possible to select the best from a large group of progeny of this top bull at an early stage. The total number of zones used from a specific father can therefore be reduced.

In addition, using genomic selection, it is possible to test zones of a larger number of different fathers relatively cheaply. The chance of a new top bull with an outcross lineage thus increases. So genomic selection has the potential to increase genetic advancement in breeding programmes, to shorten the interval between generations, to reduce costs and to reduce inbreeding.

In addition to the impact via breeding programmes

for AI organisations, genomic selection may in future also have direct application in individual dairy herds. In just the same way that breeding values of bulls can be accurately predicted with a large number of markers, the same information can be used to assess breeding values for heifer calves. The interesting thing is that these breeding values are equivalent in terms of reliability to the GS breeding values of bulls.

Heifer calves

We can see two remaining obstacles to the practical application in dairy herds: firstly the availability of the information and the knowledge to be able to estimate GS breeding values. These are still in the hands of the AI organisations who have developed the expertise. Secondly, the costs of measuring the markers, which at about £180 is still on the high side for some cows. These costs should, however, fall in the future. Over a number of years it may be possible to obtain reliable breeding values for about £45. This remains a fixed investment, but it's considerably cheaper than progeny testing or breeding from the 'wrong' heifers.

IGENITY adds more power to its genetic profile panel

Additional genetic markers have been added to Merial's IGENITY profile, making it more powerful and offering producers more 'inside information' than ever before.

Breeding values for marbling, retail meat yield, carcass weight, fat thickness and rib eye area have been enhanced as part of the panel upgrade, making the tool even more valuable for beef producers looking to evaluate these economically important traits.

IGENITY also offers multiple marker analyses for traits such as tenderness, heifer pregnancy rate, longevity, calving ease, docility, coat colour, breed-specific horned/pollled, multi-sire parentage and an optional diagnostic test for

persistent infections (PI) of the BVD virus. And it's also cost effective, at just £30 animal tested for the complete panel – and less than £30 per head if samples from more than 50 individual cattle are sent for analysis.

Adding new markers to the profile means that the amount of genetic variation accounted for in each analysis is much greater. The spread between a score of 1 and a score of 10 is now larger in most cases and, for the additional carcass traits, this means that producers can use the genetic profiling tool to pinpoint an animal's potential – early in each stage of production – more accurately.

For example, the difference in a score of 1 and a score of 10 for rib eye area is

more than 16 square centimetres. And the analysis for marbling represents a difference of 161.4 marbling points when comparing an animal with a score of 1 with an animal with a score of 10.

And because it's comprehensive, producers can use the genetic profile to help evaluate multiple traits that directly affect their bottom line – all from a single DNA sample.

The range of traits analysed by IGENITY make it the most comprehensive DNA profile tool available to the beef industry. And Merial is committed to its genetic research and will continue to add to IGENITY's already broad range of analyses.