

Veepro magazine



Genomics,
a new era



From 20 to 2,000 cows
in Maroc Vert

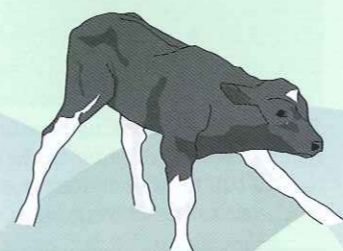


Breeding for
kg fat and protein



Genomics revolution

Genomic selection is the talk of the day in the breeding world. The Netherlands is in the lead. The use of tens of thousands of markers is creating a revolution in breeding. When they are just over 12 months old, young bulls can already be used as proven bulls.



The decoding of the cow's DNA results in a more rapid development in cattle breeding. We are on the verge of radical changes in breeding programs. Markers make it possible to determine the traits that a calf has inherited from its parents very early on. Based on this information, the characteristics of a bull calf can be predicted. Does that bull transmit lots of protein, improve feet & legs, udder?

50,000 markers

The new technique has already made its entrance.

Thanks to genomics young bulls just over 12 months can be used as proven bulls.



Since the beginning of this century, various markers have been discovered that can predict particular traits. Initially, the number was limited. Last year however, there was a breakthrough. Instead of lengthy research for the best ten markers, suddenly in one fell swoop 50,000 markers have become available. They are able to unravel most of the genetic variation. The use of such a large range of markers as predictors is called genomic selection.

That can be done for a low price: 200 Euro. In coming

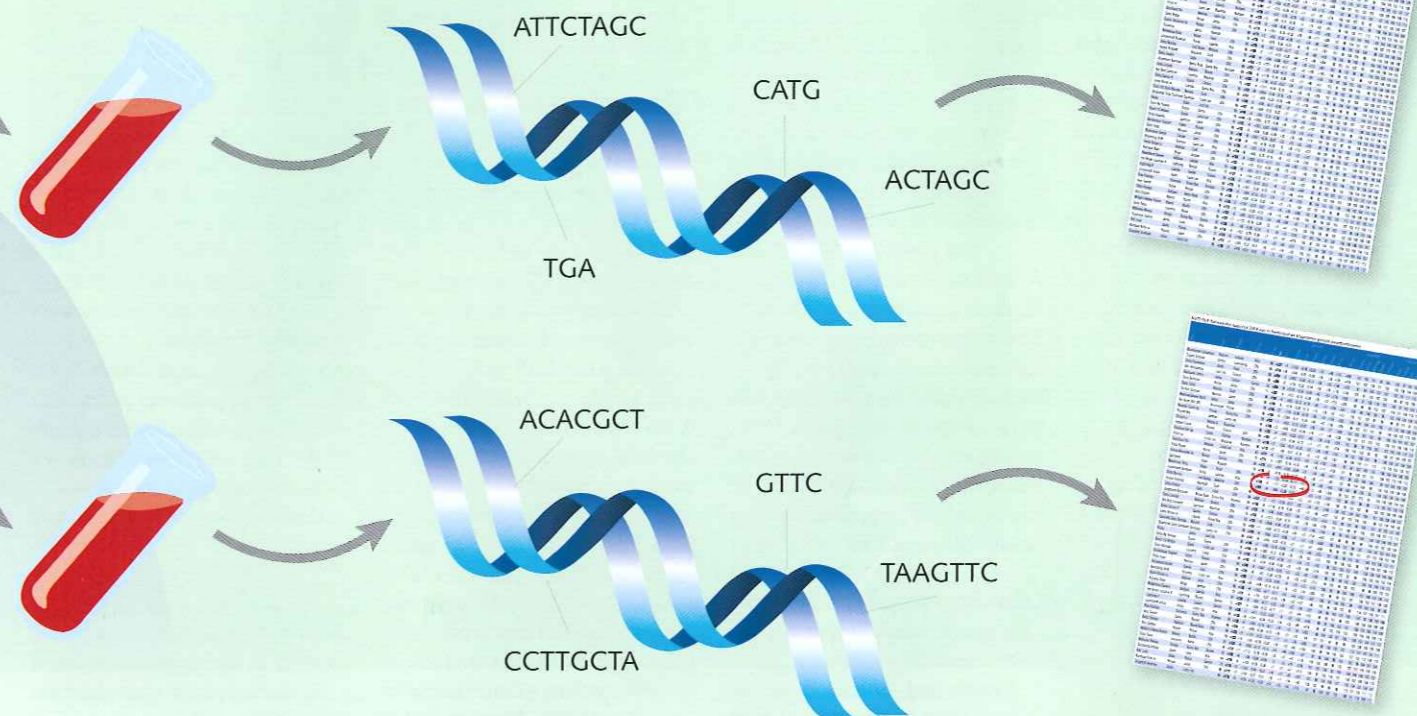
years the price will likely drop further to around 50 Euro. Then it will become interesting to determine not only for bull calves but also for young heifer calves reliable breeding values. This will prevent raising the wrong heifers. In this way, both on the male and the female side, breeding will be able to make a major step forward. At the end of the 1990s, the Animal Sciences Group (ASG) at Wageningen University laid the basis for this genomic selection. Together with the breeding organizations CRV and Hendrix Genetics (pork and poultry), ASG is now working on a further introduction, but also the rest of the international breeding world is not sitting still. One of the most significant changes will be that marker selection will replace progeny testing. However, we are not there yet. In order to reach that point, the reliability of genomic selection needs to further increase.

100 daughters

Every calf receives half of its genes from its sire and half from its dam, but always in a different combination. That makes every descendant unique. The important question is which particular genes a calf has inherited from both parents. To determine this, breeding uses the

50,000 markers are in use. Each marker contains copies of four possible building blocks of DNA: A, C, G and T. On that basis, researchers can determine which genes a calf has inherited. For all markers, the extent to which they explain the differences of a particular trait needs to be determined. For example, animals with an A for a specific marker have an index of 1 kg milk above average, while animals with a C are 1 kg below. Indexes with AA, AC and CC will respectively deviate +2, 0, or -2 kg milk from the average.

young-sire/sire-in-waiting/proven-sire system. Based on approximately 100 daughters of a bull, researchers are able to determine an average performance. With these figures in hand, they can see if a bull has inherited desirable or undesirable traits of his parents. The total value of the obtained genes is expressed in indexes.



In this way, the index of a bull can be determined quite accurately. The greatest disadvantage: It takes almost 5 years before a bull receives his first index (see Figure 1) and farmers can potentially use him. With genomic selection this process can be considerably shortened.

From 30 to 50,000

Genetic markers can already be used in the first months to determine whether a calf has inherited certain desirable genes. In that way, a stricter and more rapid selection of calves is possible. Because the determining of markers was always expensive and

only a few markers were available, research first focussed on finding the best genetic markers. Many markers have been tested. Only the markers with sufficient predictive value have been used regularly in breeding programs. The breeding organizations that

had invested in this, found about 30 markers that led to ten percent extra genetic progress. The price of determining markers has dropped enormously. It is no longer necessary to concentrate on only the best markers. It is now possible to determine all of an animal's markers and to determine the value of these markers each time. With so many markers, the greatest part of the genetic variation between offspring can be predicted. The use of large numbers of markers in this way is called genomic selection.

Breeding programs

The most extreme application of genomic selection (GS) in a breeding program is completely doing away with the young-sire/sire-in-waiting/proven-sire system, and testing young sires only for their markers. After

Figure 1 – The processes and (anticipated) running time of traditional selection and genomic selection.

young-sire/sire-in-waiting/proven-sire system	genomic selection
election of young bulls (age: 0-2 months) on the basis of their parents' achievements	selection of young bulls (age: 0-2 months) on the basis of their parents' achievements
↓	↓
young sires (age 12-14 months) used for young-sire inseminations	determine markers of the young bull calf
↓	↓
first data from daughters (age: ± 49 months)	combine young sires' markers with marker indexes from reference population
↓	↓
reliable sire proofs (age: ± 61 months)	reliable indexes for bull calves (age: 0-2 months)
↓	↓
use as a proven sire (± 61 months)	use as a proven bull (12-14 months)

that, the best of them can immediately be promoted to proven bull status (see Figure 1). That can be done in the span of one year.

In order to get to this step, the GS indexes of young sires need to have a reliability comparable to indexes based on the performance of 100 daughters. Genomic selection has not been able to attain this level of reliability yet. For kg protein the reliability is around 60%, compared to 85% based on the data of 100 daughters. The reliability of GS indexes is expected to increase as the reference population (see text box) increases. Breeding organizations are currently using genomic selection already in the preliminary selection of young sires. From a larger number of bull calves, they can in this way pre-select a group of likely bulls that they will use as young sires. At the same time, the organization can,

50,000 Markers

Currently approx. 50,000 markers are in use, spread over the entire genome (the complete DNA) of the animal. For all 50,000 markers, the extent to which they explain the differences of a particular trait needs to be determined. For example, there are many markers with an effect on kg milk, and each animal has a unique

combination of markers. By determining these effect for each marker compared to the average, and subsequently adding up the effects of all the markers for each animal, the so-called genomic selection indexes (GS indexes) are obtained. Determining the value of each separate marker is very important. This is done

with a so-called reference population, usually includes at least a thousand bulls that have accurate indexes based on daughter information, and from which all 50,000 markers are known. On the basis of a statistical model is determined how these reliable indexes have to be 'distributed' in the effects of all 50,000 markers.

for example, already use the highest ten percent of these bull calves as sires of sons for the next generation. By reducing the number of young sires sampled, or by not using young sires at all anymore (as shown in Figure 1), the cost of the breeding programs can be drastically reduced.

Less chances of inbreeding

This speed can also have a

disadvantage. Greater genetic progress often coincides with increased inbreeding. Sons of a top bull will be used earlier and more often, with a possibility of new top sires being (half-)brothers. On the other hand, with genomic selection there is the possibility to select only the very best sons. That makes it possible to sample sons from a greater variety of sires.

With this, the likelihood of a top bull with an outcross pedigree increases. All in all, genomic selection makes it possible to increase genetic progress, make a new generation of proven bulls available sooner, decrease inbreeding, and lower costs. |

This article was written in conjunction with researchers from ASG (Roel Veerkamp and Mario Calus) and Veeteelt magazine.

Complex rules prohibit exports of heifers

For a brief period of time the Netherlands has been able to export bred heifers again. From the beginning of January to February 15th this was possible if the requirements of the country of destination were met. It is unclear whether exports could continue.

The Netherlands has been shut down due to bluetongue for months. Export of bred heifers was not allowed, even

though their buyers abroad were eagerly awaiting them. Strong regulations prevented any export.

In addition, the Dutch authorities were stricter with exports to countries outside the EU than to its surrounding countries that were also dealing with bluetongue. From those countries however it was possible to export bred heifers. It is all so very complex it is almost impossible to explain, according to Veeopro Holland's director, Johan van den Berg. Foreigners don't understand why regulations can be so different. The countries

outside the EU are very eager to receive Dutch cattle.

Damage to millions

The numbers show how far exports have dropped. In the period from September 2006 to September 2007 almost 50,000 bred heifers were exported from the Netherlands. Demand was even bigger, but there simply were no more heifers available. In the twelve subsequent months the tally stopped at 11,700 head. In the last months of the past