

Genomics – it would be

We have the

Dutch AI company CRV uses a lot of genomic selection, or selection on the basis of markers.

Because the subject still provokes many questions, we explain the truth and dispel the myths in relation to genomic selection.

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Until relatively recently, geneticists could only determine the expected value of young bulls without daughter information. The specific genes the offspring had received from its parents, in other words what a bull had actually inherited, was unknown.

But now thanks to genomic selection, which is also referred to as marker selection, they can determine this information at a very early age and with a reasonably significant degree of reliability.

Two full brothers or sisters may have a totally different inheritance. A calf gets half of its genes from its father and the other half from its mother. That is how the expected genetic value is calculated, and this has a reliability coefficient of around 30%. This is because not every offspring of a specific pair of parents receives the same genes from its parents, even though their expected value is the same.

An example of two full brothers with a totally different inheritance can be seen in Slogan and Addison. While Slogan, with -262kg of milk, $+0.22\%$ fat, and $+0.11\%$ protein, is a real high contents bull, Addison is a tremendous milk yield bull with $+1,937\text{kg}$ of milk, -0.82% fat, and -0.27% protein. Slogan scores 99 for udder health and 104 for fertility, while Addison scores 108 and 93, respectively, for these two traits.

Additional tool

Genomic selection can be used at an early stage to identify which specific genes a young animal has received from its two parents. The Dutch AI company CRV is, therefore, much better able to determine which of the full brothers or half brothers have the best genes.

“Genomic selection is, in addition to expected value, an extra tool for selection,” says CRV’s head of breeding technology Pieter van Goor. In a previous role he was responsible for the Delta Nucleus programme and the selection of bull mothers. He witnessed Kian, Paramount, and Fidelity, among



a shame not to use it

technology



others, right from the beginning. “Thanks to genomic selection we can say, with a reliability coefficient of 60%, what specific genes an offspring has received from its parents,” explains Mr van Goor. “It would therefore be a shame if CRV did not make use of selection on the basis of markers.”

At the beginning of the 1990s, the genes were discovered that are responsible for hair colour, red factor, and genetic defects such as BLAD and CVM. Hair colour and genetic defects are determined by a specific gene, but there are also characteristics that are determined by several genes, such as milk inheritance.

Finding these specific genes is a difficult process, which is why markers have been developed. These are small, identifiable pieces of DNA that reside close by the gene. A marker provides information about that gene and the genetic tendencies of the animal. A marker test is a pretty good way of predicting what the animal has inherited.

This is nothing more than a total of positive and negative markers of the DNA that the animal has received from its parents. This technology has developed enormously over time.

It started with the recognition of one marker, and now we have as many as 55,000 markers at our disposal. The mystery of DNA is being increasingly unravelled in this way. “Through collaboration between various European participants in Euro-Genomics, we now have a reference population of more than 25,000 reliable breeding bulls,” says Mr van Goor. “Each of these bulls has a large number of daughters active on dairy units. The number ranges from a few hundred to more than 100,000 daughters, such as in the case of Kian.

“The breeding values of the bulls from this reference population are therefore extremely reliable. Consequently, we have an enormous repository of information concerning a total of between 20 and 25 million dairy cows.”

DNA research

All bulls in the reference populations, such as those that inherit high milk yield or high contents potential or are udder improvers, provide information. “We use this information to estimate the genomic breeding values of the bull and heifer calves that do not yet have their own daughters milking in a herd,” says Mr van Goor.

The reliability of the genomic breeding value for NVI is now 60% and this percentage will increase further in the future. The reliability on the basis of the expected value alone is between 30% and 35%. “During the past 20 years, a lot of gains have been

Genomic and daughter breeding values – what’s the difference?

In practice, the genomic breeding values and the breeding values on the basis of the daughters are closely related. Geneticists know this because, so far, 505 bulls that have a genomic breeding value have now received a daughter-based proof.

Table 1 shows what the differences are for these 505 bulls between the most recent genomic breeding values and their daughter breeding values.

The mean variance from the genomic breeding value is small. The spread of the breeding value life span is 270 days. Figure 1 indicates that changes in NVI may occur between genomic breeding value and the breeding value on the basis of daughters. This is not unusual or unexpected.

These changes are to be expected on the

basis of the 60% reliability. This figure indicates that, in 64% of cases, the difference between the genomic breeding value and the daughter

breeding value deviates by less than 40 NVI points. And only 18% of bulls drop by more than 40 points, and 18% rise by more than 40 points.

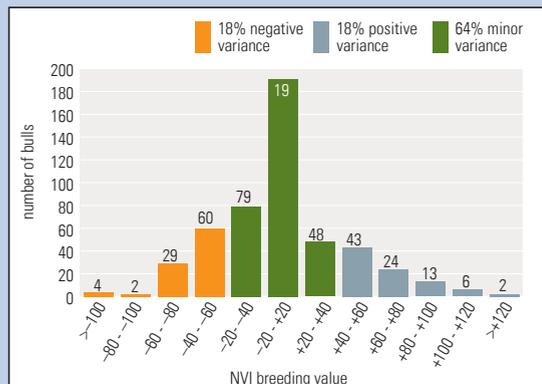


Figure 1: Changes in NVI in the first 505 genomic bulls whose daughters are now being milked

change	(%)
reliability	+23,1
NVI	-2,2
Inet index	+1,0
life span	-18,0
total score	-0,6
udder health	-0,2
fertility	-0,1

Table 1: Difference by feature between the most recent genomic breeding value and the breeding value on the basis of daughters



made in this area – we have learned so much more about DNA.”

Mr van Goor indicates that DNA research also seems to be fully accepted in society. “Just think about human medicine in relation to various forms of cancer.”

CRV switched from test bulls, for which just the expected value was known, to marker-selected bulls. With these ‘InSire’ bulls it is not just the expected value but also the effects of the markers are taken into account.

Since August 2010, the foundation GES

(Genetische Evaluatie Stieren – genetic evaluation of bulls) has been calculating official genomic breeding values for InSire bulls. The genomic breeding value comprises 50% information on the basis of pedigree and 50% marker information. This can vary by breeding value, however. By using marker technology, we can now ascertain, with a reasonable degree of reliability, what an animal will inherit. “We would be really crazy were we not to use this extremely valuable information,” concludes Mr van Goor. |

With his latest genomic breeding value in December 2011, Het Broek Silky (pictured is daughter Liesje 94) scored +837kg milk, +22kg fat, +29kg protein and 182 NVI. Now, with 113 milking daughters, he’s scoring +932kg milk, +15kg fat, +30kg protein and 227 NVI

