

The first bulls with a genomic breeding index in August 2010 realised index ratings with their daughter information in December

Genomic selection: first results are positive

The scores of the first group of bulls to switch from a genomic breeding value to a breeding value with daughter information have risen by an average of nine NVI points. Of these 64 bulls, 13 had a change in their rating of more than 40 NVI points. And 12 bulls are back in the top 16. Both CRV and the Genetic Evaluation of Sires foundation are pleased with the results.

text **Florus Pellikaan**

The first 'practical' results of genomic selection have been eagerly awaited by converts and sceptics alike. Based on the past two rounds of indexing, analysis is already possible: in August 2010, for the first time, the GES (Genetic Evaluation of Sires) foundation in The Netherlands calculated breeding values in which genomic data were included.

This resulted in, among other things, a new list of young bulls whose breeding values were based on their pedigree index and genomic data. Between August 2010 and December 2010, 64 bulls from this group saw an average of 100 daughters coming into milk and in the December 2010 index run they received an index rating that included daughter information for the first time. The big question is, of course, how do the August genomic breeding values for these bulls compare with the December breeding values with daughter information.

Table 1 shows the average breeding values of bulls in August alongside the average values in December. In terms of NVI scores, the 64 bulls averaged 60 points in August and 68.9 points in December. Rounded up, this represents a small increase of nine NVI points. In addition, for the traits milk and protein, the bulls scored higher due to inclusion of the daughter information compared with the genomic breeding values. The bulls' scores for udders and overall conformation fell slightly. A breakdown

Table 1: Average genomic breeding value without daughter information in August 2010 and average breeding value with daughter information in December 2010

trait	all bulls (total 64)			top 25 % per trait (total 16)		
	genomic value	breeding value with daughter info	difference	genomic value	breeding value with daughter info	difference
NVI	60.0	68.9	9.0	122.6	121.6	-1.0
kg milk	686.3	703.7	17.5	1447.9	1482.7	34.8
kg protein	20.3	22.2	1.8	35.8	39.2	3.4
udder	102.9	102.2	-0.7	106.5	105.6	-0.9
feet & legs	102.0	101.7	-0.3	105.4	104.9	-0.5
total type	103.5	103.0	-0.5	107.4	107.1	-0.3
longevity	148.6	163.7	15.1	400.4	395.1	-5.4
fertility	96.5	97.0	0.5	100.2	100.3	0.1
cell count	100.3	100.7	0.4	105.4	105.5	0.1

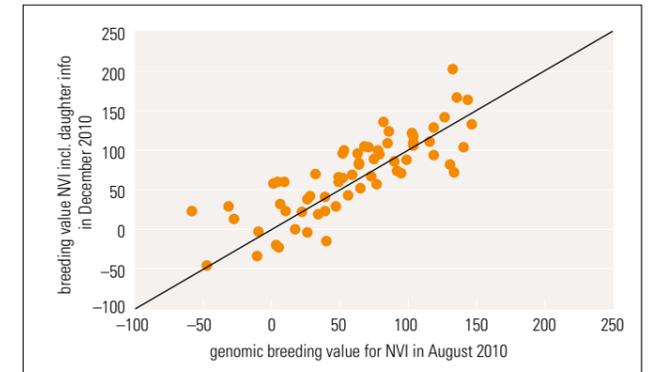
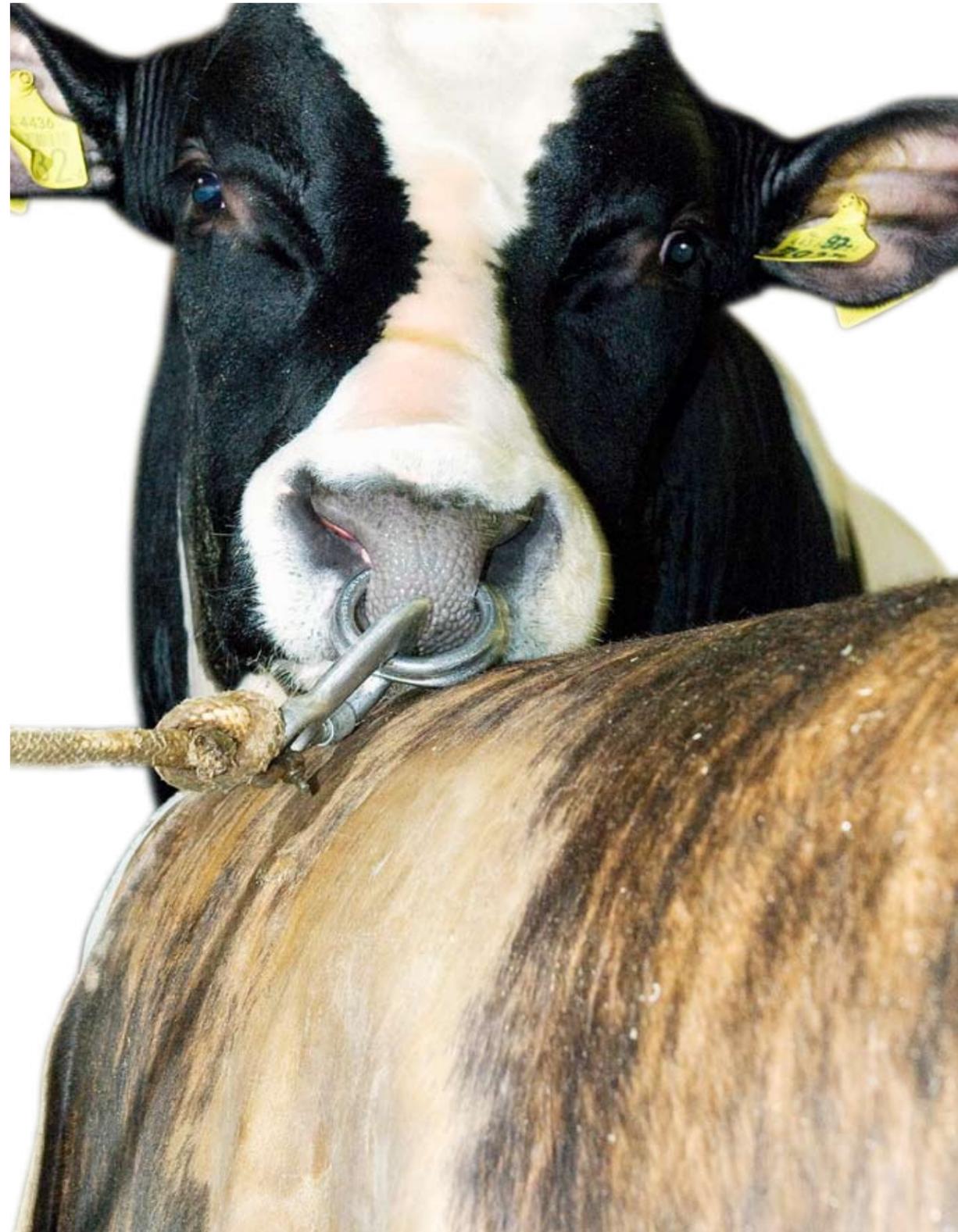


Figure 1: The genomic breeding value for nvi of 64 bulls and their breeding value with daughter information. The closer the point is to the black line, the better the breeding values match

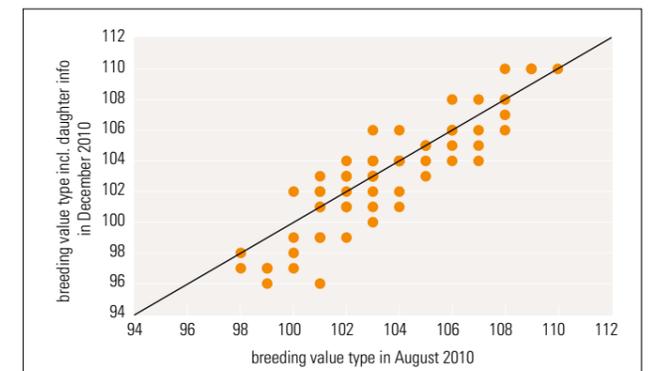


Figure 2: The genomic breeding value of type of 64 bulls and their breeding value with daughter information. The closer the point is to the line, the better the breeding values match

was also given for the top 25% of the bulls, ranked by their genomic breeding value (16 bulls).

Conservative approach

"On average, the breeding values based on daughter information are a good fit with the values we had predicted using genomic data. This applies both to the group as a whole and to the top 16 bulls. And we are very happy with that," says CRV's head of breeding Sander de Roos. "We notice that some people still don't really trust the genomic breeding values. These first analyses are therefore very valuable. All in all, in the NVI breeding value, we have if anything given the bulls a rather low estimated rating based on genomics, but that's because we deliberately opted for a fairly conservative approach."

The differences between the average breeding values in August and those in December are so small that Sander is not seeking any explanations. "In this case we're talking about a limited number of bulls that as yet have relatively small numbers of daughters who are all in their first lactation."

Roel Veerkamp: "This is certainly a positive indication"

"For me, as researcher and as someone who is responsible for estimating breeding values, these practical results provide positive justification of our confidence in this technology." This is the initial response of the coordinator of the GES foundation for genetic evaluation of bulls in The Netherlands, Roel Veerkamp.

"The best validation still are practical results. This is a new technology in a very early stage of development, when there are always things that can happen that you don't expect. Now the practical results have confirmed our expectations,



and that's very encouraging. This isn't the final answer, but it's certainly a positive indication."

According to Roel, the analysis gives producers a good insight into the proper

use of genomic selection. "If they want to use genomic bulls with high index scores, they now know that, on average, they will stay high and that they will bear out the genomic breeding values."

"With reliability of 63%, you still need to accept there will be some changes. However, the genomic bulls right now are scoring so highly that they can easily afford a slight adjustment. Therefore the advice remains to use a group of genomic bulls."

The reliability of the NVI breeding value has risen between the two indexing sessions by an average of 13% to a total of more than 76%. "That is still quite limited," says Sander. "It takes a few years to determine the definitive breeding values of bulls. On average, the breeding values will remain at the same level, but the discrepancies with the genomic breeding value for individual bulls may be somewhat greater."

Validation studies

The initial positive results of genomic selection come as no surprise to Sander. "We carry out validation studies many times a year in which we compare breeding values in the same way, but with much larger numbers of bulls including bulls with daughters who have already gone through several lactations. These current results are consistent with what we have seen in our validation studies."

The change between the genomic breeding value in August 2010 and the breeding value with daughter information in December for each individual bull is shown for the characteristics NVI and overall conformation in Figures 1 and 2.

Of the 64 bulls, 10 had an increase of more than 40 NVI points and three dropped more than 40 NVI points. "That is in line with what you might expect with such an increase in reliability. The genomic breeding value is 63% reliable, and then of course absolutely stable genetic values don't yet exist," according to Sander. "In the next round of indexing, if a progeny tested bull has a lot of daughters added and rises or falls 20 NVI points, will anybody look twice? It's the same for the bulls moving from a genomic breeding value to a breeding value with daughter information. If they all fluctuate wildly,

trait	number of bulls again in top 16
NVI	12
total type	13
cell count	12

Table 2: The number of bulls in the top 16 based on genomic breeding values and breeding values with daughter information

then there is something wrong, but these results show that this is not the case."

According to Sander, it is clear from the analysis of the first results of genomic selection exactly what CRV wants to achieve using the technology. "The highest group of bulls, even with daughter information, is still high up on average in terms of breeding value. Suppose that in 2006 we had only used bulls who last August had a genomic breeding value of more than 50 NVI; we wouldn't have missed any good bulls. Of the bulls with a genomic breeding value of less than 50 NVI points, the highest one now has 70 NVI points. In addition, any bull now scoring less than 40 NVI points on the basis of daughter information would not have been used."

Not included

Table 2 lists how many bulls out of the top 25% (sixteen bulls in total) ranked according to their genetic breeding value in August 2010 were still in the top 25% for the breeding value with daughter information in December 2010. For NVI and cell count, the figure was 12, and for overall conformation 13. The top four for overall conformation were exactly the same in August and December, although some bulls had in fact gone up one or two points for overall conformation.

The first Dutch results are distinctly more

positive than the initial experiences from New Zealand and the United States. Sander probably has an explanation for this. "In those countries the bull dam information is taken into account. This has resulted in a great deal of overestimation because of the high production records and high conformation scores on the dams' side. Later, if the bulls have daughters coming into milk, they slump. Even before official publication of the genomic breeding values, we made the decision that we would no longer include bull dam information."

When CRV began using genomic selection in 2008 and announced genomic breeding values for test bulls, this bull dam information was still being used. "At that time it was a logical choice, since the publication of parent averages values for test bulls was generally accepted and this also included bull dam information. When we noticed that it was necessary to remove bull dam information for the sake of unbiasedness of the genomic breeding values, we decided to remove it at once. As a result you saw a sudden one-off drop in bull breeding values."

Sander adds a clear postscript to these first positive results. "Major deviations will certainly occur for individual bulls. That's why we emphasise the importance of using several genomic bulls. The InSire bulls that are available are around the 200 NVI mark. In a few years' time it will be apparent that on average they are still around the 200 NVI mark, but one bull will have 150 points and another 250."

"A producer using several bulls therefore runs very little risk. He'll get a few daughters from an absolute winner and a few from a bull whose score drops a bit. But even then, that bull will still be at the same level as many popular sires." |