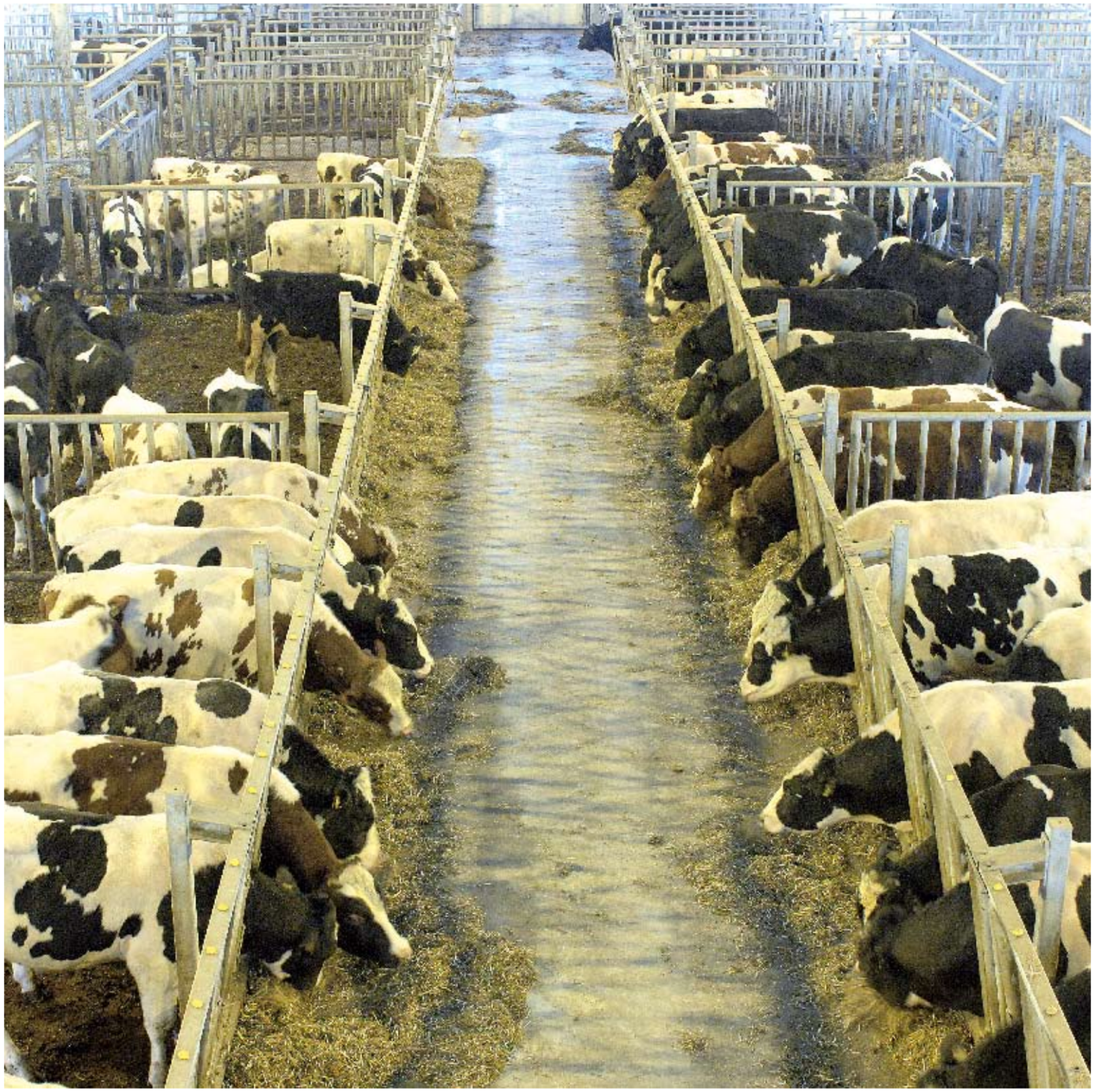
It's all in the genomes

CRV is embracing genomic selection a nd doubling its chances of sire success

CRV has been using genomic selection since 2006 and has invested heavily in selecting sires via genetic markers. As well as the potential to double the chances of test animals succeeding, the organisation is also looking to select test animals from a wider genetic base.



The Dutch/Flemish AI organisation has been investing in research into genes and genetic markers in cattle since 1994. Working with Belgium's University of Liege and the New Zealand AI organisation LIC, it originally looked into how far tracing specific genes could strengthen its breeding programme.

"You can use DNA – the data inherited on the chromosome in cell nuclei – to determine the genetic value of an animal," is how Wiepk Voskamp summarises the research. "Such DNA profiles, with the inherited information, never change and each individual gets one from birth. By ultimately assigning a value to the DNA profile, you get a picture of what an animal has inherited from its ancestors." Miss Voskamp, CRV's research and development manager, and her team have been working with DNA data for years to finally make it usable as a so-called genomic selection breeding value. Researchers Chris Schrooten, Sander de Roos and Erik Mullaart have made major contributions.

Wiepk Voskamp

They started looking for genes, such as the gene for milk production, in 1994. This search was very cumbersome because there is not only one gene, but a number of genes, which are responsible for milk production.

They did eventually find genes, including those that determine hair colour or an inherited variation such as CVM, and even for durability, but those were relatively easily traced.

"The genes for CVM or hair colour are actually 'all or nothing' genes," Miss Voskamp says. "If an animal has the gene for CVM, it's a carrier. If an animal doesn't have the gene, it isn't. For most characteristics, however, inheritance is a little more complicated and many genes, sometimes hundreds, determine why and how a characteristic is ultimately expressed. Finding genes is a difficult, time-consuming process. When we thought we weren't getting fast enough, we continued with marker research aimed at genomic selection." (See box)

Alfred de Vries

Marker chip

Marker research has accelerated in recent years as the DNA profiles of more breeds of animals, including cattle, are unravelled by research institutions in different countries. This DNA profile data is in the public domain and CRV's researchers also used this public information. CRV's research team produced the DNA profiles of 1,400 sires of known breeding value, using a computer chip containing 3,000 markers.

"Validating this data was a major first step towards using genomic selection in practice," says Ate Lindeboom, CRV's products director. Mr Lindeboom has been closely involved with all this research for many years. "By learning to use data from 3,000 markers, we could make the step to a DNA chip that could recognise 60,000."

As well as an expected value, CRV has also been giving its test animals genomic selection (GS) breeding values since the end of 2006. This GS breeding value covers data from the pedigree, expected value and added value via genomic selection.

"A test animal's expectation value for production is normally around 35% reliable," explains Alfred de Vries, breeding manager at CRV. "By adding genomic selection data, we can increase this to more than 50%. This increases the test animal's chances of being successful, as we are in a better position to assess what its inheritance pattern will be beforehand. We now expect 10%

Ate Lindeboom

bull name	sire	expectation value	GS expectation value	NVO breeding value
Newhouse Sneeky	Jimtown	5.3	23.7	29.0
Newhouse Ricky	Looking Major	14.2	8.6	7.0

Table 1: Expectation values and breeding values achieved for kg protein

bull name	sire	expectation value	GS expectation value	NVO breeding value
HS Twister	Lightning	105.5	107.0	110.0
Delta Whizzkid	Sinatra	101.0	97.5	93.0

Table 2: Expectation values and breeding values achieved for udder depth

of the test animals we use, ultimately, to be promoted to breeding animals. Thanks to using genomic selection, we expect the percentage success rate to double, at least."

The organisation has been compiling GS breeding values using a DNA chip with 60,000 markers since the end of 2007. Two examples of validating sires using this chip can be found in Table 1. Based on expectation values, via pedigree data, Jimtown's son Newhouse Sneeky had a breeding value for protein of 5.3kg. The GS breeding value indicated 23.7kg, which was much higher. Ultimately, Sneeky achieved 29.0kg protein when his daughters started milking. The expectation value for Sneeky's distant grand-nephew Newhouse Ricky seemed to be overestimated, but the GS breeding value was closer to this, given the breeding value realised ultimately. "These examples show we can estimate hereditary trends better," Mr de Vries explains.

1,000 sires

As far as CRV is concerned, genomic selection not only makes the expected breeding value of test animals more reliable, but also increases it. "We can add another selection step to the breeding programme," says Mr de Vries.

At present, CRV selects 500 young Holstein sires each year (red- and black-and-white), of which around 260 are used. From this year on, this selection must deliver 1,000 young sires in the first selection phase, which are given GS breeding values using genomic selection and pedigree data. Of these 1,000 young sires, 200 are ultimately used each year. "Because we select so broadly at the outset in the first instance, we can work widely on bloodlines," Mr de Vries explains. "Not only that, but we also expect being able to select more widely to give 35% more genetic progress."

Mr Lindeboom adds: "Genomic selection now enables us to segment test animals for different markets. We can use a group of sires with a high GS breeding value for milk for the North American market, but we can also deliberately select a group of sires with higher GS breeding values for secondary characteristics for the European market, for example."

GS breeding values offer prospects mainly for secondary and type characteristics. These characteristics are less reliable than production ones, and genomic selection helps make them more reliable earlier on (see Table 2).

Spreading bloodlines

"We will be using heifers and cows with high GS breeding values more intensively," says Mr de Vries. The Delta nucleus test programme will remain, and of the 200 two year olds tested, 50 are expected to be left over each year, which can be used as donors. The Eurodonor programme (bullmothers contracted from producers) will deliver more young sires. "Thanks to genomic selection, we will now be coming across businesses where we can buy in young sires from new cow families," Mr de Vries forecasts. "If GS breeding values indicate they meet our requirements, we will use these sires too. New cow families mean a wider bloodlines. We are now planning how to deal with these bull dams. If bull dams have high GS breeding values, we will want to get and buy a lot of embryos from those cows."

Mr Lindeboom says that CRV has opted quite consciously to cut the breeding programme down to a limited extent, although it has complete trust in what genomic selection can do.

"Cutting down the test programme is the first gain, because you don't need to test as many sires. But we aim to double the selection pool then select strictly. The aim at CRV is to grow to a world market level, and increasing the percentage success of our breeding animals will help here."

Jaap van der Knaap

Chromosomes, genes and genetic markers

The reasons why individuals look the way they do is due to a combination of inherited characteristics and the environment they live in. Inherited characteristics are fixed by chromosomes in the nucleus of each cell – a kind of recipe for making that individual. Spread over these chromosomes (they come in pairs) are between 20,000 and 30,000 genes. If you know which gene has a favourable effect on protein content, for example, you can use test animals that have that gene and avoid ones that don't.

Finding precisely where genes are is a complex, expensive process. In many cases, a number of genes are responsible for a single characteristic. That's why 'markers' were developed. With markers, you can tell roughly where the gene should be.