



Frequently asked questions

1. What is Genomic Selection (GS)?

Genomic Selection is the selection of animals based on genetic markers. When the markers effects are known and it is known which markers the animal carries, the breeding value of the animal based on these markers can be calculated and can be used for selection.

2. What is a genetic marker?

Genes are situated on the DNA and are responsible for the genetic differences between animals. For traits like milk production, hundreds of genes have an effect on the performance of an animal. It is unknown where exactly the genes that have an effect on specific traits are located and which variants of a gene (good or bad) the animal carries. However, we can follow the heredity of genes by the use of markers. Markers that lie close to a gene have roughly the same heredity as the gene itself. HG has identified 60,000 genetic markers that are being used to enhance the pedigree indexes of young bulls or the cow indexes of potential bull dams, which usually have low reliability. For animals with markers measured, it can be determined if the animal carries good genes or not. Animals that carry the 'good' genes on many locations get a higher 'enhanced' breeding value.

3. What is a genome?

The heritable information of an animal is stored in its DNA. The DNA is divided into chromosomes and all the chromosomes together form the genome. A cow has 29 chromosomes and 30,000 genes. There are two copies of every gene – one from the dam and one from the sire.

4. How do you get from marker information to genomic breeding values

For GS it is essential that genetic marker information and phenotypic information are available in large quantities. For phenotypic information it is most common to use the breeding values (BV) of progeny tested bulls, but it is also possible to use the phenotypic records of cows. With statistical analysis the association between markers and BVs can be estimated. When it is known which markers a young bull carries, his BV based on markers can be estimated.

5. Are markers safe for the animal?

The animals are not genetically manipulated. The use of marker selection has no influence on the genes of an animal. Markers are a tool for selection at an early stage. This is done through blood testing. The integrity of an animal is not questioned with this technique. Natural genetic variation remains the source for genetic improvement.

6. For which traits are markers particularly suitable?

To estimate the breeding value of a bull for milk production, the performance of his daughters is taken into account. Since milk production has a high heritability, a relatively low number of daughters can give a reliable prediction for this trait. The big advantage of using markers is that



these mainly add information to the functional traits with a low heritability like fertility, longevity and udder health. Genomic selection enables higher reliabilities for these traits than previously.

7. Do markers mean a revolution in cattle breeding?

Some expect radical changes in cattle breeding within 10 years. The current expensive system with test sires, lay-off sires and proven sires may then be history. Whether things will change quickly is hard to say although it is obvious that by using genomic selection soon after the birth of a promising young bull it can be determined what the genetic potential of that bull is. And using genomic selection on proven sires to enhance the reliability of their proofs will enable a more accurate choice of the right sires of sons to breed the next generation of bulls. On the female side, a more reliable choice can be made in the selection of bull dams.

8. Since when is CRV studying Genomic Selection?

CRV has been investing in research into genes and genetic markers since 1994. Working with Belgium's University of Liege and the New Zealand AI organization LIC, it originally looked into how far tracing specific genes could strengthen its breeding programme. Following the acquisition of AmBreed, the co-operation with LIC was dissolved. CRV has been using genomic selection since 2006 and has invested heavily in selecting sires via genetic markers.

9. What is the difference between marker selection and genomic selection?

It is the same. In CRV's communications both terms are used. The term *genomic selection* refers to the research method and *marker selection* indicates that the young bulls are selected based on their marker information.

10. What are the reliabilities of genomic selection?

A conventional tested animal's parent average is around the 35% reliability. With genomic selection this can be increased to more than 50%. The GS information roughly adds 15% more reliability to the parent average of the bulls. This 15% extra reliability might increase when the reference population becomes larger or when more markers are available. Marketing GS bulls in a group will increase the reliability. For example, five bulls with a GS breeding value together have a reliability of 90%.

Thanks to genomic selection we know more about traits with a low heritability at an earlier stage, especially the durability and health traits. By using only daughter information, achieving a high reliability takes a long time because we often need to wait until the daughters are culled. Genomic selection, therefore, offers a huge advantage.



11. Can you tell me more about the reference populations?

For CRV, reference populations have been built for the Netherlands (Holstein only) and New Zealand (Holstein and Jersey) and there are plans to also build a reference population for the US. For young Holstein bulls from any country, Genomic Breeding Values (GBVs) on the Dutch and New Zealand scale can be calculated when the bull is genotyped.

For a reference population, genetic markers and BVs are needed for hundreds to a few thousand bulls. The costs for genotyping a reference population are very high and, therefore, reference populations will become available for just a few countries.

12. Is there also a reference population for non-Holstein breeds?

With the tens of thousands of markers that are currently used it is necessary to build up a reference population for every specific breed. Results from Holsteins can not be used for Jerseys, for example. This makes it more difficult to build a reference population for smaller breeds as Fleckvieh, MRIJ and Belgian Blue because these breeds have fewer AI tested bulls and it is more difficult to get a return on such large investments. When more markers or full genome sequences are available, smaller breeds can profit from the reference populations in the larger breeds because the functional mutations will be identified or, in other words, markers that are so close to the mutation that they will work across breeds.

13. Can individual cows be genotyped?

Yes, it is possible to genotype individual cows in the same way, as bulls are genotyped. It is yet unknown if this service will be offered to individual farmers.

14. Could you give me some examples of GS breeding values?

Bull calf A (Paramount x Dustin)			Bull calf B (Paramount x Dustin)		
Marker-effect production			Marker-effect production		
+749 +10kg fat +16kg protein			+156 -6kg fat +4kg protein		
InSire-proof*			InSire-proof*		
+2212 +55kg fat +64kg protein			+1619 +40kg fat +52kg protein		
Marker-effects other traits			Marker-effects other traits		
frame	+2,8	107	frame	-1,4	103
udder	+3,4	111	udder	-1,2	106
feet & legs	+1,2	110	feet & legs	-1,2	107
total score	+3,9	113	total score	-1,3	108
udder depth	+0,6	105	udder depth	-3,9	100
longevity	+46	391	longevity	-44	302

The markers of Paramount son A indicate that he inherits 749 kg of milk more (+2,212) than expected based on his parent average.

Paramount son B inherits feet & legs 1.2 points lower (107) than expected based on his parent average.

Example 2

Expectation values for the two full siblings (Jefferson x Wonderboy) born in 2007

	Milk-kg	Fat %	Protein %	Fat kg	Protein kg
Parent average	+1557	-0.38	-0.14	+31	+40
Genomic Selection					
Delta 2887	+1156	-0.10	+0.06	+36	+42
Delta 2889	+696	+0.08	+0.11	+29	+30



Example 3

Expectation values and breeding values achieved for protein for Newhouse Sneeky and Newhouse Ricky.

	Protein kg (expectation value)	Protein kg (GS- expectation value)	Protein kg (NVO breeding value)
Newhouse Sneeky	5.3	23.7	29.0
Newhouse Ricky	14.2	8.6	7.0

Example 4

Expectation values and breeding values achieved for udder depth for HS Twister and Delta Whizzkid

	Expectation value	GS expectation value	Protein kg (NVO breeding value)
HS Twister	5.3	23.7	29.0
Delta Whizzkid	14.2	8.6	7.0

15. Is the traditional genetic evaluation method still needed when there is already so much information known about the bulls?

The traditional genetic evaluation method is still needed because the estimated breeding values are used to calculate the marker effect on traits. It is also still needed because the breeding values of the bulls selected based on their markers still have to be estimated.





16. What is going to change in HG's breeding programme?

At the moment HG selects around 500 young black-and-white and red Holstein bulls, from which eventually 250 will be progeny tested. In the new situation the HG sire analysts will source around 1,000 young bulls. With this, the variation in pedigrees among the tested bulls will increase and the extra information that genomic selection will provide will highlight the qualities of new cow families more quickly and make it easier to utilise the strengths of these families. Out of these 1,000, with the help of genomic selection, the best 200 will be identified to be progeny tested – a selection intensity of 1:5 compared to 1:2 previously – which leads to more genetic progress.

Delta Nucleus Program	Eurodonor	Bulls
<ul style="list-style-type: none"> • Strong pre-selection in heifers via marker - selection • Use maiden heifers stronger for OPU/ET • Higher value of embryos 	<ul style="list-style-type: none"> • Expansion of selection pool • Pre-screening bull dams via marker - selection • More calves per bull dam 	<ul style="list-style-type: none"> • Young bulls at a higher level • Pass rate of bulls much higher • Broader offer: more segmentation • Marker -selection of all calves

17. What are the noticeable changes due to genomic selection?

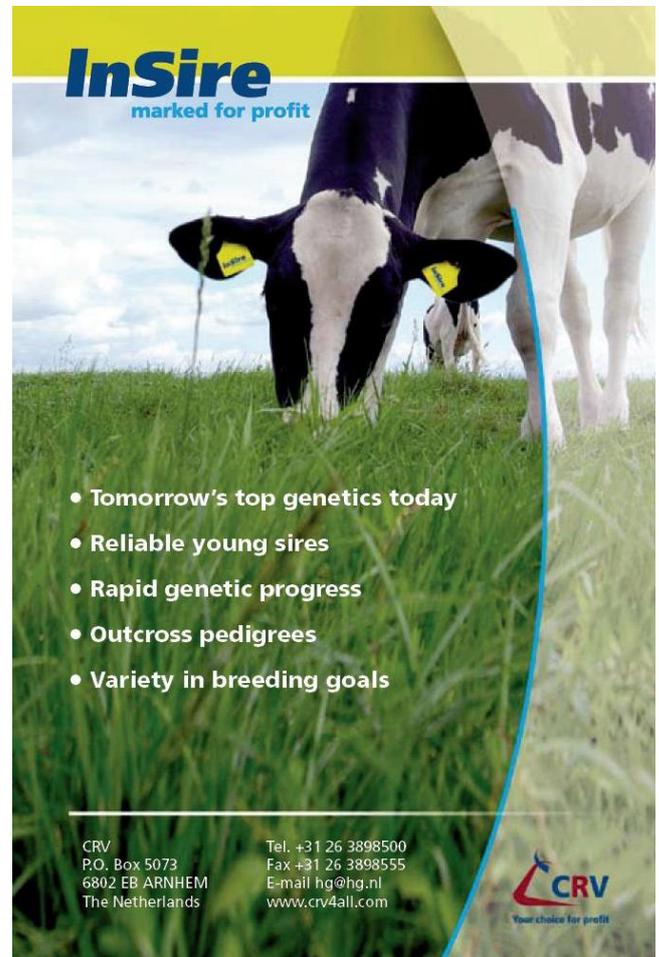
- A higher percentage of young bulls will become breeding bulls. The young bulls will generally score better and there will be fewer disappointments.
- Breeding organisations can use sire of sons at a younger age. After all, by the use of genomic selection, we can find out much quicker which bulls are the most successful.
- With GS, CRV can anticipate changes and demands in the market (for example milk composition) more quickly.
- Genomic selection makes product differentiation much easier. CRV can anticipate and meet the demands of different market segments. With GS, a wider product range can be achieved.

18. What is the advantage for the dairy producer?

Markers give extra information, which is also available earlier. In the future, the breeding values of a bull will not only be based on the performance of his daughters but also on marker information. The breeding value estimation of bulls – particularly for the low heritability traits – will, therefore, be more reliable as more markers will be found. This is a clear advantage for dairy producers. HG will also target its breeding programme towards different market segments. With genomic selection it is possible to predict – at a very young age – whether a bull will transmit the qualities desired by different markets. You can get tomorrow's genetics today!

19. When will marker selected young bulls be available on the international market?

CRV plans to introduce genomic selection to the market in September 2008. Not all countries are allowed to use 'unproven' semen and for the time being these countries cannot use marker selected semen. During the All Holland Dairy Show (NRM), a seminar will be organised to inform you about the actualities around genomic selection.



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