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Genomic selection

It is said that the genomic selection of cattle is comparable in its importance for cattle breeding to the successful introduction of the deep freezing of bovine semen and the influence it had on breeding progress.

We would like to inform you in this leaflet of the techniques of genomic selection, differences between alternative selection methods, the advantages, and the possible use for the farmer.

If you have any questions, please do not hesitate to contact our staff at any time.

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1. What is new?

The aim of animal breeding is to change the genetic endowments of the animals and – as a result – improve their traits. However, this is not a matter of the genetic manipulation of the animal itself. So far selection has been carried out on the basis of the phenotypical (recorded) production as an indicator of the congenital production potential. It would be best if the animals’ production predisposition could be extracted directly from their genetic information without going the long way round by using the indirect phenotypical way. Genomic breeding value evaluation and selection is now really close to what was once a dream. Even though the cattle’s genome has now been decrypted, we know very little about the position



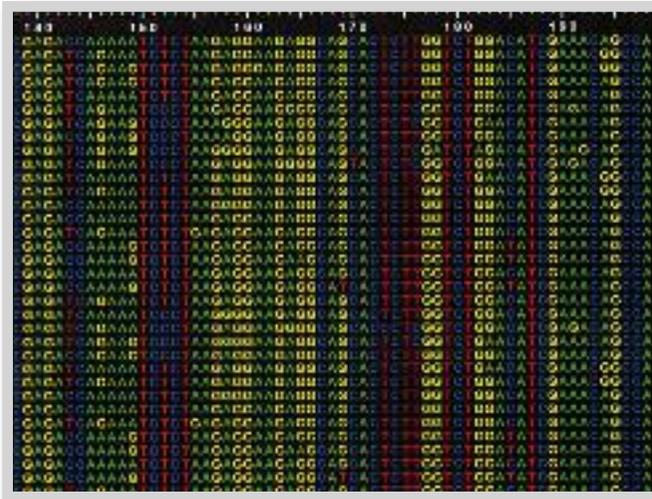
DNA helix (computer simulation)

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and effectiveness of the genes for the majority of the transmission traits. So genomic breeding value evaluation does not work directly on the basis of information about genes, but by using markers. The development of these new methods of genetic analysis and the changes in breeding value evaluation have been developed and were supported by the German Federal Ministry of Research and Technology within the subsidiary program FUGATO.

2. SNP markers

It is so-called SNP (Single Nucleotide Polymorphism) markers that are used. They are composed of only one genetic letter and there are two different models for every marker in the entire population. Every animal has the genetic information in the form of a double chromosome set; one set from the father and one set from the mother. The



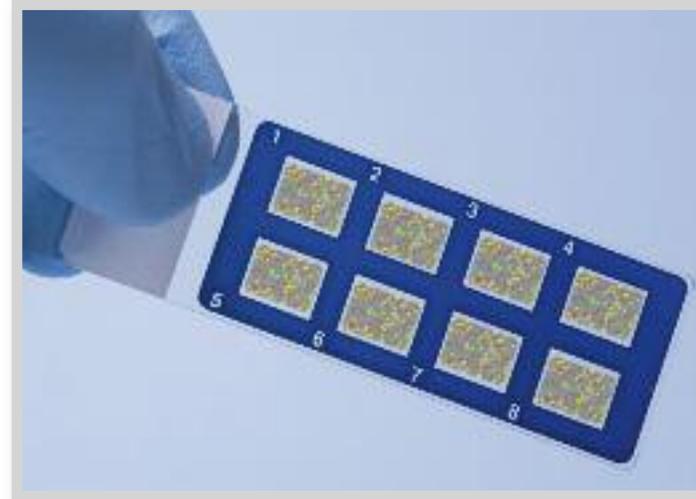
Sequence of bases

Every animal has the genetic information in the form of a double chromosome set; one set from the father and one set from the mother.

result is that every marker for an animal can have three combinations: homozygous option AA, homozygous option BB or heterozygous AB. Heterozygous AB means that the animal received different options from the father and the mother.

3. Marker testing or typing

Many hundreds of thousands of such SNP markers of cattle are known. 54,001 of them are shared equally in the entire genome i.e. all chromosomes can now be extracted through a relatively cheap lab method in a one step process. This process is called "typing".



Analysis chip (Specimen)

The unit used in the laboratory for testing the 54,001 markers is called a chip or 54K chip to indicate the number of markers simultaneously tested. A little of the animal's genetic material is used for the typing. As

54,001 so-called SNP (Single Nucleotide Polymorphism) markers are used on a analysis chip in order to type a bull's genetic layout.



all cells of an animal have genetic material, blood (approx. 2 ml) or semen (approx. 2 doses) can be used. You can also extract enough gene material for the typing from approx. 30 roots of hair. However, the danger of contamination of hair samples with genetic material of other animals is higher and the result could be incorrect. The typing's result is 54,001 times AA or BB or AB.

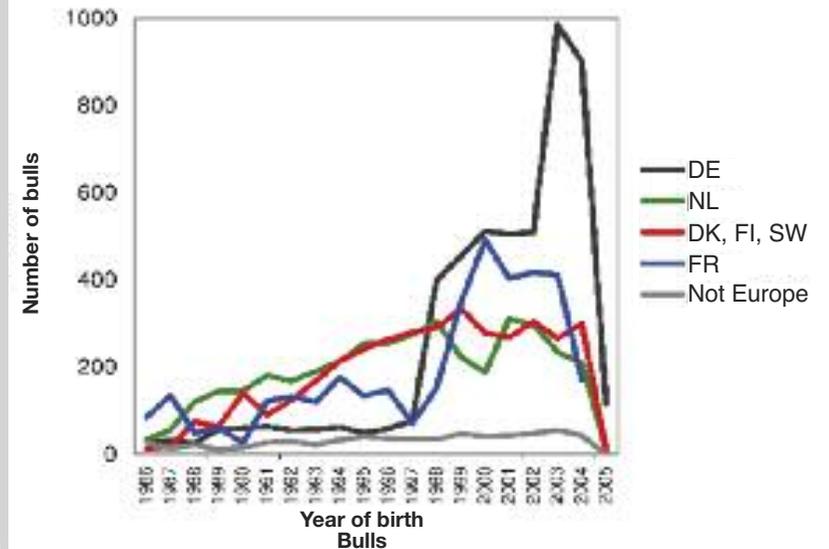
4. From the marker to a genomic breeding value: the training sample

As a result of the equal spread of many markers over the entire genome, it is assumed that close to every gene, which influences the production of one of the transmission traits, is one of the 54,001 markers. This means that the marker is transmitted almost every time, together with the appropriate combination of genes. We do not know, however, the different genes and their effect. In order to be able to evaluate an animal's genomic breeding value using its markers, certain advanced tests are first necessary. To find out which SNPs, i.e.

In the training sample: Laudan – proven by more than 45,000 daughters and known as sire of worldwide reputation.

which markers are connected with which trait, the SNP samples first have to be compared with known (genetic) production traits of selected animals. Animals with known genetic production are daughter proven bulls. From the comparison of the SNP sample with the genetic production of these bulls, it can be determined which SNP has how much influence on the trait, so the genomic evaluation formulas are conveyed that way. The more reliably

Origin of the more than 17,000 Holstein bulls in the German training sample (March 2010). The German training sample is the biggest and the best structured worldwide:



Source: vit

DE= Germany; NL= Netherlands; DK= Denmark; FI= Finland; SW= Sweden; FR= France

As a result of the equal spread of many markers over the entire genome, it is assumed that close to every gene, which influences the production of one of the transmission traits, is one of the 54,001 markers.

Today, more than 25,000 Holstein bulls form the German training sample (August 2013)

proven bulls you have available for this formula, the better you can allocate the SNP to a trait and indicate the extent of the influence. Proven bulls that are included in this analysis are the so-called “training sample”. The genomic evaluation formulas conveyed from the training sample are then used for the calculation of the genomic breeding values of other (usually younger) animals without their own reliable conventional breeding value information.

5. Reliability

The reliability of genomic breeding values mainly depends on the extent and structure of the training sample as well as the reliability of the daughters’ breeding values of the training sample bulls. The complexity and the reliability of the conventional breeding values for all – as well as for all functional traits – are No 1 in the world. The size and structure of the German training sample is also unique worldwide because of the exchange of information with three European partners from France, Scandinavia and The Netherlands. None of the other training samples worldwide is so well-structured, i.e. represents the entire, latest Holstein genetics from Europe and North America. The genomic formulas can only convey reliably the breeding values of younger cows when their genetics (SNP sample) are well-represented via preferably



The reliability of genomic breeding values mainly depends on the extent and structure of the training sample as well as the reliability of the daughters’ breeding values in the training sample bulls which, in Germany, are of unique quality compared to the rest of the world.

many related animals (sire, dam’s sire, paternal half brothers and sisters etc) in the training sample. So the training sample has to be continuously expanded and updated alongside the population development. The reliability of breeding values for younger animals based solely on genomic data (SNP typing) is shown by the figures in the middle column of table 1. The reliability shown is the actual reliability; i.e. it has already been corrected for the overestimation observed in all genomic evaluation methods.

6. Combined genomic breeding values

The direct genomic values (dGW) are calculated from the typings (SNP samples) for all traits. There is also more conventional breeding value in-

Table 1:

Reliabilities of genomic breeding values compared to the reliability of the pedigree’s breeding values:

Trait	Rel. V-P.I.	Rel. dGW	Rel. gZW
RZM	33%	72%	75%
RZS	31%	73%	75%
RZE	30%	63%	69%
RZN	27%	48%	53%
RZR	28%	45%	48%
CEp	33%	41%	45%
CEm	28%	40%	43%
RZD	28%	65%	70%

Abbreviations:

Rel. V-P.I. - Reliability of the pedigree index
 Rel. dGW - Reliability of direct genomic values
 Rel. gZW - Reliability of the genomic breeding value
 RZM - Relative breeding value milk production
 RZS - Relative breeding value somatic cell score
 RZE - Relative breeding value for total conformation

RZN - Relative breeding value functional herd life
 RZR - Relative breeding value reproduction
 CEp - Paternal calving ease
 CEm - Maternal calving ease
 RZD - Relative breeding value milking speed

Source: vit

Genomic breeding values improve the quality of information compared to the pedigree index.

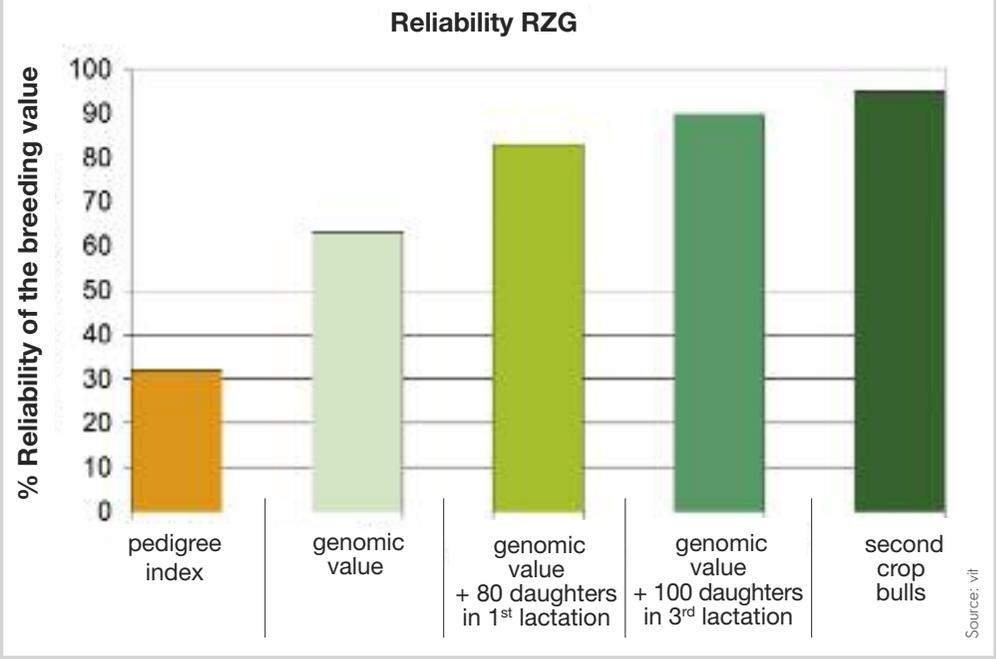
formation for all animals with known pedigree, namely the pedigree's breeding value. In order that every animal has only one breeding value with maximum information and reliability at a particular time, the direct genomic value is not published but the genomically improved breeding value (gZW) which is a combination of the direct genomic value and the conventional breeding value is given. The weighting is done on the basis of the reliability of both values; i.e. for young animals with only a pedigree breeding value, the direct genomic value counts the most and the unreliable pedigree breeding value can increase the reliability of the genomically improved breeding value ([ZW] gZW) by only approx. 3-5% (please see right column of the table 1). Once the conventional breeding value is clearly more reliable from daughter information than from the direct genomic value, it has a higher weighting in the combined gZW. So the combined gZW of daughter proven bulls is usually little different from the purely conventional breeding value.

7. What are genomic breeding values able to do?

The actual reliability of genomically improved breeding values of young bulls – approx. 75% for the milk yield traits and 50% for daughter fertility – is clearly higher than the reliability of the current pedigree breeding value of test bulls. So young bulls with their official gZW qualify formally as sires, and there are no longer test bulls as they were previously known. The comparison of the reliabilities of daughter proven sires (chart 1) shows however, that even bulls with only test daughters in first lactation have higher breed-

ing value reliabilities for high heritability and important traits like production, conformation and udder health. Even though German genomic breeding values are the most reliable when compared internationally, because they have the biggest training sample with more than 25,000 bulls (August 2013). The genomic breeding values are more unreliable than those of the daughter proven sires. With stronger emphasis on the functional traits, the significance of sires with thousands of second crop daughters has increased over the past years because they also offer high reliability for traits like longevity and daughter fertility. The actual reliability of genomic breeding values for those functional traits is still limited to approx. 50%. So if you

Chart 1: Reliabilities of genomically improved breeding values (gZW) of young bulls compared to the reliability of daughter proven bulls.



● Daughter information further increases the reliability of the breeding value – up to 99% for second crop bulls

normally think that the reliability of the firstly published daughter breeding values of new sires are too low, young bulls, only genomically tested, may not be an option for you. On the other hand the young generation of genomically tested bulls provides a new breeding opportunity. When using those young genomic bulls, you should always be aware of the limited reliability, so the risk should be spread by using several such bulls. The reliability calculations and data for genomic breeding values are not yet standardized internationally. The data of the German genomic breeding values are realistic however, and the quality of the German genomic breeding values is the best internationally. For correct evaluation of the German breeding values, as well as reliability expressed in percentages, the number of daughters with production information will still be given. This means that everybody is able – on an impartial basis – to select a suitable sire with a choice between a young genomically tested bull or the latest, proven bull with test daughters or even a proven second crop sire.

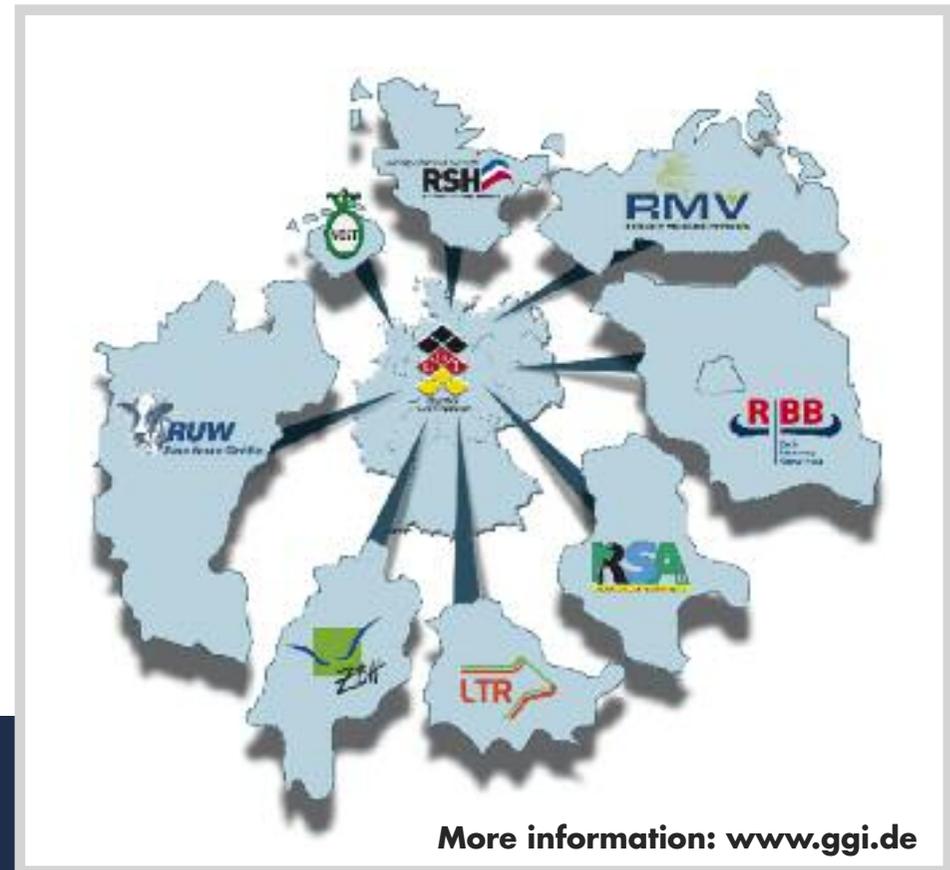
8. GGI

GGI, the German Genetics International GmbH, is the international export marketing body representing nine leading German breeding organizations which provide mainly Holstein and Red Holstein genetics. We offer breeders from all over the world a direct and easy access to the best bulls from the German breeding programs. All sires offered are tested with high reliability and accuracy based on the world-wide leading estimation model for breeding values and stand out for having wide spread proofs and deep pedigrees. The genetic potential of GGI bulls clearly reflects the German breeding philosophy: High milk performance, good conformation, excellent feet and legs, functional and healthy

udders, fertility and longevity.

Furthermore, GGI is a reliable partner regarding all questions concerning cattle breeding and management. Please contact GGI or our international partners, because you are always on the right track with the best GGI sires!

Map of the GGI members in Germany



More information: www.ggi.de

Questions? Do not hesitate to contact us!

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