

BREEDING PROGRAMS AND PROGENY TESTING IN THE TIMES OF GENOMIC SELECTION

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Genomic selection will be the next big milestone for the development of breeding programs for dairy and dual purpose cattle. The theoretical work was done during the last 8 years since MEUWISSEN (2001) made the first proposal to use genomic information in cattle breeding programs. During the last years the technology for genotyping our animals were developed rapidly. Now it is possible to get the genome-wide information of our breeding animals for 40000 to 60000 Single nucleotide proteins (SNP) for a price of about 250,00 EURO. Therefore it is important for a breeding association or an A.I. Company to plan how this information can be sampled in an optimal way for a utilization in our breeding programs to increase the genetic standard of our breeds.

Genetic Gain
 Genomic Selection
 0,467 σ_A

Key words: genomic, genetic markers, progeny, selection

1. Advantages of genomic selection

Genomic selection means, that breeding values of animals are derived by the information of 20000 to 60000 loci, which were evaluated by new techniques of detection of genetic markers. Many scientific projects are in progress to estimate breeding values out of this information. In USA, New Zealand and Netherlands systems of genomic selection are in practice since several months. France has announced to start in April 2009 and in Germany July 2009 should be the start of this new technique. All these countries are in strong competition with their Holsteins and therefore the pressure is very high to introduce such a system.

The advantages of genomic selection are that at the age of 12 months a breeding value derived by genomic selection has a reliability of 0,55 to 0,75 for dairy traits. Without genomic selection only a pedigree breeding value with a reliability of about 40% can be derived out of the animal model. If the reliability out of the genomic selection is high enough to use these sires as proofed sires in artificial insemination the generation interval in cattle breeding programs can be reduced drastically. This results then in a much higher genetic progress. L. Shaffer (200) pointed out that the genetic progress will be more than twice in comparative to a progeny testing system, if the reliability of the genomic breeding values is 0,75.

Table 1
 Four pathways of selection, progeny testing

Pathway	Selection %	Accuracy		Generation	
		i	fn	Interval, L	i x fn
Sire of bulls	5	2.06	0.99	6.5	2.04
Sire of cows	20	1.40	0.75	6	1.05
Dams of bulls	2	2.42	0.60	5	1.45
Dams of cows	85	0.27	0.50	4.25	0.14
Total				21.75	4.68

Table 2
 Four pathways of selection, genome-wide strategy

Pathway	Selection %	Accuracy		Generation	
		i	fn	Interval, L	i x fn
Sire of bulls	5	2.06	0.75	6.5	2.04
Sire of cows	20	1.40	0.75	6	1.05
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Dams of cows	85	0.27	0.50	4.25	0.14
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2. Demands for breeding programs

National breeding programs have to take into account the international competition. For traits, which are evaluated and used international by organizations like INTERBULL, this breeding programs have to take into account that the genetic progress in those traits should be on the same level as in the other countries. For national breeding programs dairy traits like milk yield and e.g. somatic cell score are much more important than functional traits like longevity, fertility and calving ease.

In contrast for breeders these functional traits seem to be more important, since the profit of a breeding herd results mostly from the value of the sold products like milk and breeding animals. Breeding animals can only be sold from the farm if more animals are produced than the farmer needs to replace his herd. Therefore longevity and fertility have a very high importance for single breeders.

Since national breeding programs are in international competition and are carried out by breeders which own between 20 and 500 Herd book cows, both parts have to be included in an optimal strategy. From the theoretical approach of quantitative selection a reliability of 60 to 65 % may be enough to select A.I.-bulls and use them to produce 20000 or 30000 progenies in the population. For breeders, especially those with smaller herds below 100 cows, the value of the single animal is too high to believe in a higher increase of the genetic value only on average. These farmers try to make sure that the sires,

which are used in their herd will lead to high quality progenies. The best known strategy for this is a progeny testing program with at least 100 daughters. This may result in lower selection differentials as if only genomic breeding values are used.

3. Impacts on breeding programs

Nearly all specialists in breeding programs want to use genomic information in their breeding programs. Breeds with a high competition between breeding programs in different countries have a much higher pressure to utilize this information. But at this time we do not know about the realized reliability of genomic information and we don't know about the intervals in which the formula for calculating the breeding values out the genomic information should be adapted.

In the dual purpose breed Fleckvieh (Baltata Romaneasca) have not such a high pressure from international competition. Therefore we are thinking on a more evolutionary way to introduce genomic selection in our breeding program.

- Preselection of young test bulls by genomic selection
- More intensive progeny testing of those sires with 500 instead of 100 daughters
- Sampling the information on production traits and functional traits out of this test bulls
- Deriving economic weights under the new situation to optimize the breeding goal

Working with this steps has the big advantage, that the breeders may follow the

elements of the new breeding program. If they learn to work with this genomic information they are much more active in using such techniques in their herds. Since our breeding programs are based on an active work of the farmers, this seems to very important to get a suitable solution for the whole population. This can also be proofed by the inseminations done in our A.I. Station in Germany. About 15 to 20% of our cows are inseminated with sires, which have already many daughters from the second crop and therefore a reliability of 99%. This shows that some milk producers do not trust in our bulls with a reliability of about 80%. It seems to be not reasonable to convince these farmers to use genomic selected bulls. Perhaps it is possible to convince them to use bulls, which were tested with a group of 500 female (dairy) and 500 male (beef) progenies. After introduction of genomic selection some specialized breeding farms may accept genomic breeding values to produce the next generation of test bulls. If both pathways are possible there is a real reduction of the generation interval for our dual purpose breed. This slow strategy gives us the chance to make more evaluations on the development of functional traits with genomic selection. This seems to be very important, because the decision for good and less good breeds will be done in future more on functional traits than on production traits. The discussion about crossbreeding in the Holstein population coming from the USA is mainly based on the fact, that American milk producers are not satisfied with the longevity,

fertility, calving ease and somatic cell count of their cows.

4. Consequences for cattle breeding in Romania

For cattle breeding in Romania the introduction of genomic selection may be a good chance to take part in a cooperation of national breeding programs. In Baltata Romaneasca as well as in Holstein you are working strongly together with the populations in Germany, France and Austria. Since this is done for a longer period the Romanian population has many links to western European populations. Therefore the genomic breeding values for Germany and France can also derived for Romanian animals. This gives Romanian breeders the chance to take part in the German testing program and sell animals as test bulls in these populations. For the foreign populations the population from which the test bulls are selected increases and may then be responsible for a higher genetic gain in Romania and Germany or France respectively. This formulated goal may be a little bit optimistic, but long cooperations between Romanian and German partners in the last 10 years - as we carried out in Targu Mures - give me the motivation to continue this in the future.

In this context, genomic selection is not only a good chance to improve animal breeding but also the cooperations between the German and the Romanian breeding associations and their breeding programs.