

Comparing Conventional and Genomic Breeding Programs with ZPLAN+

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Abstract

Genomic enhanced breeding values have been established in practical breeding programs. The results are already integrated in the practical work. Based on these new techniques, today's breeding programs will be structured differently in the near future. Aim of this study was a comparison of three alternative breeding programs using the new software ZPLAN+. The first program was a progeny test system, as already used in conventional breeding programs (CS). The second alternative was a system strictly based on genomic information without proposed progeny tests (GS). The third system was a mixture of genomic information and partial progeny tests (MS). Following parameters were calculated and compared: generation intervals, genetic gain, total return of the breeding program, breeding costs and profit. Generation intervals were 5.02, 3.44 and 4.64 years (CS, GS and MS). The discounted return per year was 49.1 €(CS), 155.25 €(GS) and 88.53 €(MS). Regarding breeding costs (8.42 €, 1.13 € and 4.30 €) per realisation unit (1 cow) remaining profit of 47.46 €(CS), 155.26 €(GS) and 87.59 €(MS) per realisation unit and year could be obtained. The classical system was clearly inferior compared to systems based on genomic selection. The system using genomic information only was superior to the combined system and it is assumed that these systems will be implemented regarding long term cattle breeding.

Keywords: Holsteins, breeding programs, genomic selection, ZPLAN+

Introduction

The development of genomic enhanced breeding values offers new strategies in animal breeding. In conventional breeding programs selection decisions were made after several years of performance tests, using genomic breeding values they can be made very early. This new situation must be adopted by breeding programs as soon as possible to optimize genetic gain on the one hand and to minimize breeding costs on the other hand. The development of new techniques to estimate genomic enhanced breeding values is world wide established and accepted in practical breeding programs. The consequent use of genomics and how breeding programs must be restructured is the new task to stay on the market for each separate breeding program. For this reason the new software ZPLAN+ has been developed within the German FUGATO+Brain project. The new software, developed by *vit* in cooperation with German universities, is based on modern programming technologies using a web-based GUI, is able to mimic new developments in animal breeding and is easy to use compared to existing software packages.

In this study we compared three cattle breeding programs using ZPLAN+ in terms of breeding cost, return and profit.

Material and Methods

The cattle breeding programs were modeled using the new software ZPLAN+ (Täubert *et al.*, 2010). This deterministic software allows a biological design of breeding structures. Different breeds with its genetic parameters using selection groups as smallest structures can be defined. The program combines the discounted gene flow-method (Hill, 1974) and selection index theory (Hazel *et al.*, 1949) and calculates genetic gain within and over selection paths, discounted return and costs. Additional new developments were implemented as multiple stage selection (Börner und Reinsch, 2010) and the definition of genomic measured traits (Dekkers, 2007; Daetwyler *et al.*, 2008).

Breeding goal

The desired breeding goal in the German Holstein population is the total merit index

RZG. It is a composite of following partial indexes: RZM (milk-kg, fat-kg and protein-kg), RZS (somatic cell count), feet & legs index, udder index, RZN (combined herd life), RZR (fertility index) and calving traits.

The composites derive from a total of 26 traits. The calculation of RZG is based on selection index theory. This provides the optimum overall selection response in all traits. The calculation of a total merit index with ZPLAN+ is also based on a selection index, but there are differences in the basic definition. In a breeding program the relative emphasis of each trait is defined by using economic weights and phenotypic/genetic parameters between traits. The software needs a clear definition of single traits, not indexes. To define the total merit index RZG in our computer program, we normally should define all 26 single traits, which will technically be no problem for ZPLAN+. But genetic and phenotypic parameters and economic weights are not available for all 26 traits, and the presentation of results would be very complicated. For this reason we decided to calculate a total merit index based on 6 representative single traits, which define the largest part of the partial index:

- RZM: protein-kg
- RZS / SCS
- Conformation: Feet & legs score, udder score
- RZN / direct longevity in days
- RZR: Days open
- Calving traits: (not considered)

For the definition of the breeding goal in German Holsteins there are 6 main traits remaining in this study. These traits are defined phenotypically and genetically, all needed heritabilities and correlations are used in the routine evaluation by **vit**. The relative economic values were defined in ZPLAN+ and it was possible to represent the total merit index RZG with that reduced model using the 6 mentioned representative traits.

To define genomic measured traits in the software, it is possible to define these traits as measured traits, not as target traits. ZPLAN+ adopts the method described by Dekkers (2007) and Daetwyler *et al.* (2008) to calculate genetic and phenotypic correlations between

genomic and polygenic traits. It is also possible to adjust reliabilities for genomic traits as cross-validated in the genomic evaluation systems.

Breeding programs

Three different scenarios were modeled in ZPLAN+:

1. A conventional breeding program using test bulls, waiting bulls and selection of proven bulls at the age of 5 to 6 years (**CS**).
2. A genomic breeding program without waiting bulls, but immediate use of genomic proven bulls as service sire at an age of 15 months (**GS**).
3. A mixed breeding program, where a part of genomic proven bull will be directly used as service sires and the rest will be used as test bulls similar to program 1 (**MS**).

All three scenarios have on common a size of 250,000 dairy cows under milk recording, from which the best 1% will be selected as bull dams based on their breeding value (own performance). From these dams 1,250 male selection candidates are born. Daughter performances will be recorded during or after the first lactation.

Breeding program CS describes a conventional breeding program without use of genomic information. Due to a limited test capacity, only 100 of these bulls will be tested with 100 daughters that have performance in all traits. 10 proven bulls will be selected as service sire based on breeding values estimated on daughter records with the age of 6 years. One year later only 7 proven bulls remain in the breeding program, two further years later only two proven bulls. One bull has the chance to remain in service with 99% reliability (1000 daughters) up to an age of 10 years. The relative proportion of all inseminations splits up to 20% use of test bulls and 80% use of proven bulls. Test bulls will only become cow sires, not sire of sons.

In the genomic breeding program GS, 500 bull calves will be genotyped from the 1,250 candidates based on non-genetic parameters (e.g. pedigree diversification). 20 of these 500 bull calves will be selected on genomics and

used as service sire as soon as they produce semen (15 months). After gathering daughter information the reliability of the genomic enhanced breeding value increases and more selection steps will follow until only one of the 20 selected bulls will remain in second crop service. The genomic tested bulls have an average age of 2.5 years, when their first daughters are born. After one year only 10 bulls remain, half of them will drop out of service based on random reasons (e.g. semen quality). Only 5 bulls remain after one more year. The last remaining proven bull is 6 years old and further used as now daughter proven bull. Bulls at all ages have the same possibility to become sire of sons and cow sires. To realise as much genetic gain as possible, 97% of sire of sons are young genomic tested bulls, only 3% of all sire of sons are also daughter proven. Cow sires are 66% genomic proven and 33% daughter proven bulls. Similar to the conventional breeding program the average bull sire is much younger than the average cow sire, because dairy farmers still rely on high reliabilities of breeding values.

The mixed program (MS) corresponds to one half the conventional (CS) and the other half genomic breeding program (GS). The only difference is the early selection of young CS-bulls, which is based on genomic information instead of parent average. Similar to breeding program GS, there are 500 bull calves genotyped, but this time 50 will be selected based on the genomic EBV instead of 20. From these 50, the best 10 will be chosen for direct use as genomic proven service sires, the next best 40 bulls will be used to be tested in a conventional testing scheme. Out of this group 5 proven bulls will be selected at an age of 6 years as additional service sires. It should be mentioned to keep in mind, that the genomic proven bulls in service receive first daughter information when conventional proven bulls receive test daughter information. The ratio of cow sires with daughter information and cow sires without daughter information is 1/3 to 2/3. Sire of sons are 80% young genomic proven and 20% daughter proven bulls.

Cost factors

The cost factors for the breeding programs are shown on table 1 for one tested bull each. A conventional tested bull with 100 daughters caused costs of 20,000 € for raising, keeping, progeny test etc. Purchase costs for the calf will add to this. A bull calf selected on parent average in CS costs 5,000 € so altogether 25,000 € In MS the bull calf is already genotyped and has a genomic breeding value. The highest genotyped bulls that can directly be used as service sires have a price of 11,000 € The next best bulls (2nd choice) to be used for progeny test costs 6,000 € Full costs for genotyping will be 125€incl. logistics and pre-investments for the genomic system.

In total in CS the testing costs sum up to 2,050,000 € (100 tested bulls x 20,000 € test costs and 10 selected bulls x 5,000 €), in the GS to 282,500 € (500 genotypes x 125 € and 20 selected bulls x 11,000 €) and in the MS to 1,212,500 € (500 genotypes x 125 € 10 selected 1st choice bulls for 11,000 € 40 2nd choice selected bulls for 6,000 € and 40 progeny tests for 20,000 €).

Table 1. Cost factors.

Source	per bull
Testing costs (from calf to 5 years)	20,000.00 €
purchase bull calf (CS)	5,000.00 €
genotyping per animal	125.00 €
purchase best genomic bull calves	11,000.00 €
purchase 2nd best genomic bull calves	6,000.00 €

Results

Generation intervals

A generation interval is defined as age of parents when their replacing offspring is born. ZPLAN+ calculates the generation interval directly from the gene flow-matrix.

Mean generation intervals are shown in table 2.

Table 2. Generation intervals in the three breeding programs.

Breeding program	(CS)	(GS)	(MS)
Generation interval	5.03	3.44	4.65

Accuracies

In all three breeding programs information sources for bulls add up cumulative as a bull gets older. It is important to know, what kind of information source is available to estimate breeding values and how old the bull is at this time. Table 3 gives an overview of accuracies derived from a selection index in the three examples. Accuracies are derived from a multiple trait selection index for all traits including correlated information.

Table 3. Accuracies derived from a multiple trait selection index using different sources of information.

Source of information		Accuracy in selection index
CS	Test bull	0.54
	Proven bull	0.89
	99%-pr. bull	0.99
GS	G-proven bull	0.73
	G-99%-pr. bull	0.99
MS	G-proven bull	0.73
	G-99%-pr. bull	0.99
	G-Test bull	0.73
	G-Dau-bull	0.91
	G-99%-pr. bull	0.99

Monetary genetic gain

The main target in each breeding program is to maximise the genetic gain per generation and per year. The genetic gain in natural units of all traits is of interest, but even more the monetary genetic gain is the important factor. Monetary genetic gain is shown as a composite of single

traits based on the relative economic weights in the total merit index. Monetary genetic gain is genetic gain weighted by economic values and expressed in currency units.

Results in table 4 are based on one time unit (one year). Results are undiscounted and future investments are not corrected using the discount factor for the investment period.

Results in table 5 show a structured comparison of discounted monetary genetic gain per generation between the three

examples. These values are the return of investment, where realisations over several years are added but they are less weighted the further in the future they are realised. It can be seen that GS shows highest genetic gain of all three scenarios. In terms of return the superiority increases because the higher genetic gain will be realised in a shorter time (lower generation interval). This is on the one side remarkable, because selection of bulls will be made with a lower accuracy, but higher selection intensities in this breeding program compensates the disadvantage. MS loses especially in the discounted genetic gain, because a lot of time is needed to realise the genetic gain from service sires in the conventional progeny test. Although a lower number of bulls are progeny tested, the higher accuracy based on genomic preselection should end in higher genetic gain than the conventional breeding program. The lower generation interval of the combined system in comparison to the conventional shows the superiority of the MS in particular when discounted results are compared.

Breeding costs

Breeding costs are extremely different between the three examples. In CS the costs for a (progeny) test is 20,000 € for each single test bull, where as in GS only 125 € have to be paid. Although the price to buy a genomic selected young bull calf is twice as high as the price of a bull calf selected on parent average, the sum of costs is much lower, because the number of bulls needed is much lower, too.

As the return of a breeding program, also the costs have to be discounted, because they arise at different times during a breeding program. All different costs added up to total costs per breeding program and divided by the number of cows in the population. The costs have to be paid per bull, but genetic progress is inherited to all cows in the population and the costs have to be spread over all animals receiving genetic gain.

The breeding costs per realisation unit (1 cow) are 8.42 € 1.13 € und 4.29 € in the conventional, genomic and combined breeding program.

Breeding profit

Profit is calculated by subtracting discounted breeding costs from discounted breeding return, based on one realisation unit (1 cow). That gives a profit of 238.63 € 532.55 € and 407.32 € per realisation unit (1 cow).

Table 6 shows an overview of breeding return, costs and profit.

Discussion

Goal of this study was a comparison of three example breeding programs using a new software ZPLAN+. The examples should describe the breeding programs as designed before genomic selection was developed and two scenarios with different use of genomic information. The conventional and pure genomic breeding program give the frame of possible use of genomic information, the MS is between the other two.

Population parameters estimated by *vit* (as used in routine evaluation) provide all necessary information to weight traits in the correct way in order to represent the German total merit index RZG. Modeling the total merit index has not been done in former publications where mostly only one or two representative traits were analysed. (König *et al.*, 2009; Hinrichs *et al.*, 2008; Schaeffer, 2006).

A further task is the implementation of genomic measured traits in a breeding program and a selection index. The program ZPLAN+ allows to define genomic measured traits based on polygenic information and to include them as information sources in a selection index. Most complicated calculations will be done almost automatically and makes handling of the new information very easy.

The genomic breeding value estimation allows to genotype a lot of very young animals and to select young service sires or candidates for a testing scheme. This is a two-step selection approach, which is not covered correctly by old-fashioned selection theory. The calculation of selection intensities requires normal distributed data, but in this case the second step selection is based on already pre-selected data. ZPLAN+ uses a procedure to calculate multiple step selection, which corrects selection steps and includes index information based on pre-selected data. (Börner and Reinsch, 2010).

The implementation of these new methods allows a more detailed description of the breeding programs.

Shorter generation intervals are an advantage of the genomic breeding programs. Bulls are not progeny tested anymore but used directly as service sires at an age of 15 months. The MS has a lower generation interval than the CS, but the use of 40 sires in a waiting period causes delayed gene flow to the cow population.

Regarding undiscounted monetary genetic gain the genomic system has a huge advantage of +130% and the combined system of +95% compared to the conventional system. This confirms the results of former studies that estimate twice as much genetic gain of a strict genomic system. (Schaeffer 2006; Hinrichs *et al.*, 2008). The of returns must be discounted for later realisation of genetic gain. Then we estimate an advantage of the genomic system of +215% per year compared to the conventional system. The already calculated higher genetic gain will be weighted even higher because it will be realised much earlier

than in conventional systems and needs less investments. The disappointing low advantage of the MS is caused by the ½ conventional part with time consuming progeny test.

The discounted monetary profit of the genomic system is three times higher than the profit of a conventional system, after we take all the premises into account. The combined system is more profitable than the conventional, but not as much as the pure genomic breeding program. The advantage of such a genomic breeding program has been described in other studies, too. But it is always recommended, to add a conventional progeny test to the genomic information in order to raise the accuracy of selection. (König *et al.*, 2009; Hayes *et al.*, 2009). Even if the economic superiority of genomic breeding program is confirmed in the future less than here predicted, conventional and combined systems are not competitive in the long term.

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Table 4. Undiscounted monetary genetic gain for the total merit index RZG in € and genetic gain for single traits per year in the three breeding programs.

Breeding program	CS	GS	MS
Monetary genetic gain per year (€)	18.25	41.91	35.75
protein-kg	3.02	6.53	5.61
Longevity (days)	11.51	29.88	35.45
Feet&legs (score)	0.043	0.11	0.13
Udder (score)	0.06	0.15	0.17
SCS	0.03	0.06	0.07
Days Open	-0.14	0.08	0.37

CS = conventional system, GS = genomic system, MS = mixed system

Table 5. Monetary discounted genetic gain in € for the breeding goal and single traits per generation and year in the three breeding programs.

Breeding program	CS		GS		MS	
	Per gen.	Per year	Per gen	Per year	Per gen	Per year
Mkg/year	247.05	49.13	533.68	155.25	411.60	88.52
Protein-kg	194.33	38.64	394.23	114.68	264.30	56.85
Longevity (d)	31.06	6.18	78.77	22.91	79.30	17.06
Feet&legs	7.01	1.39	17.53	5.10	19.30	4.15
Udder	6.68	1.32	16.22	4.72	16.47	3.54
SCS	12.29	2.44	25.84	7.52	24.56	5.28
Days Open	-4.32	-0.86	1.09	0.32	7.63	1.64

CS = conventional system, GS = genomic system, MS = mixed system

Table 6. Return, costs and profit of the breeding programs in € expressed per realisation unit (1 cow).

Breeding program	CS	GS	MS
Return per generation	247.05	533.68	411.60
Return per year	49.13	155.25	88.52
Costs	8.42	1.13	4.32
Profit per generation	247.46	532.55	407.28
Profit per year	47.46	155.26	87.59

CS = conventional system, GS = genomic system, MS = mixed system