Selection of Young Sires in Genomic Breeding Programs

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Abstract

Stochastic simulations were performed to evaluate a variety of scenarios to select young sires in genomic breeding programs. Scenarios included variation of accuracies of genomic breeding values and h^2 in combination with selection intensities and different types of pre-selection. For conventional methods as done in the past, i.e. contracting bull dams and using their male offspring for AI, true breeding values of selected sires were substantially lower and their inbreeding coefficients were higher compared to direct selection of genotyped male calves. For all types of pre-selection, it is imperative to genotype male calves, even if genomic breeding values of parents are available. Selection intensity of young sires remains a crucial point also in the genomic era for generating genetic gain.

Introduction

In conventional progeny testing programs, selection of bull dams was characterized by a multitude of pre-defined selection criteria. In addition to EBVs, these criteria included phenotypic requirements for conformation traits, test-day and lactation yields of bull dams and their female ancestors, as well as requirements for pedigree indices (**PI**) for a variety of traits or trait complexes. Selection can be interpreted as a variant of truncation selection, where all requirements have to be fulfilled. However, this broad variety of more or less important phenotypic selection criteria hampered overall genetic gain (König *et al.,* 2007). In general, selection of bull dams was the 'weak point' in 4-paths selection schemes. So called 'pedigree slippage' occurred due to preferential treatment (Kuhn *et al.,* 1994), or due to heterogeneous intra-herd variances (Garrick and Van Vleck, 1987).

Availability of genomic breeding values (**GBV**) enable completely different selection strategies by discarding the bull dam pathway of selection. In a deterministic approach, König and Swalve (2009) suggested a 2-pathway scheme, which focuses on genotyping a huge amount of male calves. The question remains, if any type of pre-selection of bull dams and / or bull sires when selecting calves for genotyping should still exist.

This paper discusses the addressed question from the perspective of a breeding organization mainly based on specific results from stochastic simulations as introduced by Wensch-Dorendorf *et al.* (2011). Extensions included evaluations of selection intensities, inbreeding coefficients, and the value of genotyped natural servic sires.

Material and Methods

Stochastic simulations were performed by using the QMSIM program (Sargolzaei and Schenkel, 2009). Extensions to relevant practical breeding scenarios were developed by own programming in SAS and C. In detail, QMSIM was used to built up a population of 100,000 cows and 500 sires over a period of 20 yrs corresponding to the average population size of German breeding organizations. From the practical point of view and according to a progeny testing program, most important parameters of the simulation from generations 1 to 20 were 1.) Simulation of TBV, EBV, and phenotypes (**PHEN**) 2.) annual replacement rate of cows = 25%, 3.) replacement rate of sires = 50% with bulls of the following generation, 4.) Selection of bulls and cows based on EBV, 5.) random mating within selected fractions of bulls and cows. QMSIM allows mimicking population genomics like frequency of mutation rates for QTL and

markers or the no. of QTL along with their effects, and modelling dense marker maps for the estimation of SNP effects. At this step, we continued and simplified the simulation using own programming. Based on simulated TBV and pre-defined accuracies of GEBV(r_{mg}), GEBV for an animal i in generation t were derived applying the following formula (1):

$$GBV_i \left[\sqrt{1-r_{mg}^2} RND_i + r_{mg} \cdot \frac{TBV_i}{SD(TBV_t)} \right] SD(TBV_t)$$

A second extension to QMSIM focussed on the distribution of cows to herds, and the estimation of herd effects. This was done to depict the idea of contract herds, i.e. generating a nucleus of large-scale herds with herd sizes of 500 cows per herd. for genomic selection activities. Contract herds were selected based on herd effects (**HERD**), i.e. assuming a correlation of 0.3 between herd effects and average EBV within herd, and applying the framework of formula (1). Implementation of GS will likely benefit genotyped natural service sires (**NSS**). For evaluation of NSS breeding scenarios, a sub-population of 1,200 cows located in 60 small herds, and only using NSS being progeny from cows of these herds, was created.

Evaluated breeding scenarios were: 1.) **S1** = selection of young sires based on PI = [(EBV-sire) + (EBV-dam)] / 2. This was the 'simplest way' to select male calves in the conventional PT program. 2.) **S2** = pre-selection of bull dams based on PHEN or on EBV, and final selection of bull dams based on GBV. This would be an extension of conventional selection strategies, i.e. including the GBV as an additional selection criteria for bull dams 3.) **S3** = genotyping of male calves, and direct selection of male calves according to GBV. Pre-selection included variants of PI, PHEN-dam, and herd effects. 4.) **S4** = comparison of NSS selection strategies with AI-programs. All scenarios were run for a low (0.05) and a moderate (0.30) heritability trait. In scenarios S1, S2, and S3 the ultimate evaluation criterion was the average TBV of selected sires. In scenario S4, TBV of selected NSS in generation 20 and of their female progeny in generation 21 were compared to respective values obtained from an AI program.

Results and Discussion

From the multitude of possible 'grid combinations' including selection scenarios, r_{mg}, and h^2, results presented in Table 1 (evaluation criterion = TBV), and Table 2 (evaluation criterion = inbreeding coefficient) are from $h^2 = 0.30$ and $r_{mg} = 0.9$.

Table 1. Aver. TBV of 5, 10, and 20 selected sires for different types of pre-selection and no. of genotyped bull dams (S2) or genotyped male calves (S3); (h^2=0.30; r_{mg}=0.90).

	Pre-selection		No. of selected sires		
	Type	No.	5	10	20
S1	-	-	6.61	6.54	6.51
S2	-	-	6.71	6.68	6.62
S2	PHEN	50	6.39	6.32	6.24
S2	PHEN	100	6.44	6.39	6.31
S2	EBV	50	6.56	6.48	6.40
S2	EBV	100	6.61	6.52	6.46
S3	-	-	7.33	7.27	7.19
S3	RND	1000	6.80	6.69	6.59
S3	RND	5000	7.02	6.93	6.83
S3	PHEN	1000	7.06	6.98	6.88
S3	PHEN	5000	7.19	7.12	7.03
S3	PI	1000	7.18	7.10	7.01
S3	PI	5000	7.28	7.19	7.11
S3	HERD	1000	6.79	6.70	6.59
S3	HERD	5000	7.01	6.92	6.83
S3	P-GBV	1000	7.31	7.22	7.13
S3	P-GBV	5000	7.34	7.26	7.18

Heritability for the respective trait or accuracy of EBV of animals used in the calibration group, strongly determine accuracy of GEBV. Following formulas by Daetwyler *et al.* (2010), $h^2 = 0.30$ approximately corresponds to $r_{mg} = 0.90$, while $h^2 = 0.05$ relates to $r_{mg} = 0.70$.

The relatively small no. of pre-selected bull dams (50 or 100) for scenarios S2 is in agreement with traditional selection schemes. At that time, EBV and PHEN were used as pre-selection criteria, but final selection based on visual inspections. Nowadays in the genomic era, the major cost component of visual inspections is replaced by genotyping of bull dams. However, scenarios that keep the old designs and only include the GEBV of bull dams as the final selection criterion, are not competitive with scenarios S3 (genotyping of male calves). Applying the best S3-scenario

(pre-selection of bull dams and bull sires according to GEBV, final selection of male calves according to GEBV) allows an increase in TBV by almost 2 SD (SD = 0.55) compared to scenario S2 (pre-selection of 50 bull dams according to PHEN). Generally, an increase of pre-selected bull dams is associated with higher TBV of selected sires, and basing selection decisions on bull dams EBV is better than focusing on bull dams PHEN. However, even using an unlimited pool of bull dams for genotyping (S2, type ='-', No. = '-'), this strategy cannot be recommend, provided that breeding organizations have the possibility to directly genotype the bull dams' male progeny. This finding was expected as the step from dam to son includes an additional meiosis, always resulting in genetic individuality, i.e. specific SNP- patterns in offspring.

Among evaluated S3-scenarios, outsourcing selection into specific nucleus or contract herds, resulted in lowest values of TBV of selected sires. Consequently, results may be improved when selecting herds according to genetic values and genetic differentiation as suggested by Schierenbeck *et al.* (2011a).

Also in the genomic era, old principles of selection are still valid. Decreasing the no. of sires for AI increases genetic gain. This is especially valid when evaluating economic criteria (discounted profit or discounted return) in genomic breeding programs as done by König *et al.* (2009). Beyond suboptimal selection of bull dams, offering of too many cow sires for AI was identified as a major component when explaining the gap between theoretical and realized genetic gain in conventional progeny test programs (König *et al.,* 2007).

Using inbreeding coefficients of selected sires as an evaluation criteria (Table 2) only depicts the genetic structure in the current generation on the male pathway of selection. For the management of inbreeding in a long-term perspective, mating designs should consider genetic relationships among selection candidates, and, if available, on the genomic level (Schierenbeck *et al.,* 2011b).

Table 2. Aver. inbreeding coefficient (in %) of 5, 10, and 20 selected sires for different types of pre-selection and no. of genotyped bull dams (S2) or genotyped male calves (S3); (h^2=0.30; r_{mg}=0.90).

	Pre-selection		No. of selected sires		
	Type	No.	5	10	20
S1	-	-	6.24	6.15	6.06
S2	-	-	5.63	5.41	5.36
S2	PHEN	50	5.30	5.40	5.30
S2	PHEN	100	5.37	5.40	5.31
S2	EBV	50	5.95	6.05	6.05
S2	EBV	100	5.97	6.09	6.13
S3	-	-	5.21	5.24	5.18
S3	RND	1000	5.06	5.11	5.06
S3	RND	5000	5.04	5.05	5.12
S3	PHEN	1000	5.29	5.34	5.22
S3	PHEN	5000	5.28	5.22	5.22
S3	PI	1000	5.90	5.86	5.74
S3	PI	5000	5.47	5.49	5.54
S3	HERD	1000	5.19	5.14	5.04
S3	HERD	5000	5.17	5.20	5.17
S3	PI-GBV	1000	5.40	5.38	5.36
S3	PI-GBV	5000	5.31	5.26	5.33

The 'old style' of selection, i.e. focusing on PI (scenario S1) resulted in highest inbreeding coefficients of selected sires. This was also a substantial drawback in conventional breeding programs when selecting heifers without own performance as potential bull dams. Top-lists of heifers were characterized by large groups of half-sibs. Also for the management of inbreeding, SNP patterns of selection candidates depict an animals' individuality.

Two NSS per herd to avoid mating between close relatives (NSS - dam, NNS - grand dam, NSS - fullsib, NSS - halfsib) were selected either based on PI or on GEBV. Sub-scenario **S4-ALL** allows for the use of selected NSS across herds within the small sub-population of 1,200 cows, whereas for Scenario **S4-HERD**, the use of selected sires is restricted to only one specific herd. **S4-ALL** can be seen from the point of a consortium of breeders focusing on specific breeding goals (e.g. organic farmers), and exchanging genotyped young bulls, maybe also via AI. Comparison of TBV of selected sires for a low heritability trait clearly shows (Fig. 1) for the evaluated range

of r_{mg}: Genotyping sires and using them across herds promises highest genetic gain, followed by genotyped NSS within herds, and NSS selected based on PI.
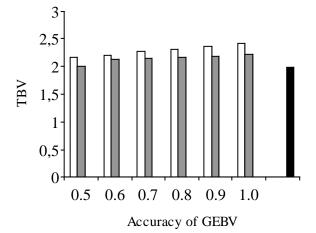

Figure 1. True breeding value (TBV) of selected sires for different breeding scenarios (white bars = S4-ALL, grey bars = S4-HERD, black bar = S4-PI; $h^2 = 0.05$)

Conclusions

The present study shows the potential of GS for improving dairy cattle breeding programs. The focus must be on genotyping of male selection candidates, and a large no. of genotypings should be realized. Also in the genomic era, selection intensity remains a crucial parameter when increasing genetic gain.

Acknowledgement

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