

Strategies for use of reproductive technologies in genomic dairy cattle breeding programs

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ABSTRACT: A simulation study was performed for testing the effect of using reproductive technologies in a genomic dairy cattle young bull breeding scheme. The breeding scheme parameters: 1) number of donors, 2) number of progeny per donor, 3) age of the donor, 4) number of sires, and 5) reliability of genomic breeding values. The breeding schemes were evaluated according to genetic gain and rate of inbreeding. The relative gain by use of reproductive technologies is 11 to 84 percent points depending on the choice of other breeding scheme parameters. A large donor program with high selection intensity of sires provides the highest genetic gain. A relatively higher genetic gain is obtained for higher reliability of GEBV. Extending the donor program and number of selected bulls has a major effect of reducing the rate of inbreeding without compromising genetic gain.

Keywords: Ovum pick up; Dairy cattle; Genomic selection

Introduction

Use of multiple ovulation and embryo transfer has for the last 40 years been used in many conventional progeny testing schemes aiming to recruit more progeny from the females with highest genetic merit (Hasler, (2014)). As genomic selection increases selection accuracy on young selection candidates by providing information of the Mendelian sampling term, within family selection and hence use of reproductive technologies (RT), which increase the number of full and or half sibs, will be even more important for future selection decisions (Daetwyler et al., (2007)). Studies have shown that positive interactions between genomic selection and use of MOET exist (Pedersen et al. (2012); Sørensen and Sørensen (2009)). In these studies the size of the donor program was not investigated.

The objectives of this study were to evaluate strategies for use of reproductive technologies in terms of genetic gain and inbreeding in dairy breeding schemes using genomic selection. The focus in this study was on investigating the effect of varying the parameters: 1) number of donors, 2) number of progeny per donor, 3) age of the donor, 4) number of sires, and 5) reliability of genomic breeding values.

Materials and Methods

Scenarios: A young bull scheme was simulated with equal use of each sire. Number of young bulls and

donors were 50, 100 or 200 (6 combinations in total). Each donor was simulated to produce either 10 or 20 calves with 5 different sires. The age of the donor at RT was either 2 or 14 month. The sex ratio of calves born was 0.5. All combinations of scenarios were investigated for a reliability of the direct genomic value (DGV) of either 0.36 (L) or 0.5 (H) of the total merit index. In total 48 different breeding schemes were investigated. In addition four reference scenarios without use of repro technologies were simulated with and without genotyping of females and for high and low reliability (Table 1).

Table 1. Genetic gain (ΔG) and rate of inbreeding (ΔF) for genomic young bull schemes without use of reproductive technologies high (H) and low (L) levels of reliability for GEBV

Rel. GEBV	#Bull dams genotyped	#Sires	ΔG (€)	ΔF (%)
L*	0	50	31.1	0.44
L	2000	50	32.2	0.40
H*	0	50	34.4	0.36
H	2000	50	35.1	0.34

*: Reference scenarios

Population. The simulated breeding population consisted of 20.000 cows from 200 different herds. The 2.000 highest ranking heifers according to the breeding goal were genotyped yearly. Out of these the best donors were selected by truncation. The young bulls chosen for semen production were selected among 2000 genotyped bull calves yearly.

Breeding goal and breeding values. The breeding goal consisted of two traits representing all traits in the breeding goal as in (Buch et al. (2012)); a milk production trait ($h^2=0.30$) and a functional trait ($h^2=0.04$) with an unfavorable genetic correlation ($r_g = -0.30$). The economic values were set to 83€ and 82€ per genetic standard deviation. The DGV was modeled as correlated pseudo-genomic information following the procedures in Buch et al. (2012). For all traits phenotypic values were simulated for the females completing first lactation and daughter yield deviations for progeny tested bulls. Selection of animals were based on genomically enhanced breeding values (GEBV) with blending of information from DGV and phenotypic information. The DMU package (Madsen and Jensen (2010)) was used for the prediction of breeding values.

Data analysis. The stochastic simulation program ADAM was used for simulations of the scenarios (Pedersen et al., 2009). Each scenario was investigated over 30 years and replicated 100 times. The genetic gain was presented as regression of true breeding value on year of birth for year 21 to 30 across replicates. The rate of inbreeding was presented per generation over the same years. Genetic gain and rate of inbreeding were presented as relative values compared to the values in the reference scenarios (Table 1). Differences in genetic gain and rate of inbreeding between scenarios were compared to the least significant difference (LSD) using a confidence level of 95%.

Results and Discussion

Reference scenarios. A genomic young bull scheme without use of reproductive technologies (Table 1) provides a genetic gain of 31.1 € yearly and a rate of inbreeding of 0.44 % per generation with a reliability on DGV of 0.36 without genotyping of bull dams. At a reliability of 0.50 the genetic gain increases by 4.0 € and the rate of inbreeding decreases by 0.08 percent points. The effect of genotyping the best females when there is no use of reproductive technologies is limited. The reason for this small effect is that the value of increased accuracy on females is limited, when the best females are not given a better change of contributing to future selection candidates (Sørensen and Sørensen (2009)).

Genetic gain. In general breeding schemes with use of reproductive techniques (Table 2) are genetically superior compared to breeding schemes without use of reproductive technologies (Table 1). A large donor program (200 donors) and use of few sires (50) provides the highest genetic gain. The relative gain is 11 to 84 percent points depending on the choice of other parameters. Increasing the donor program from 50 to 200 donors with use of 50 sires increases the relative genetic gain by 11 to 17 units for a donor age of 14 month. For a donor age of 2 month the genetics gains are from 23 to 26 relative units.

Table 2. Relative genetic gain for different sizes of donor program for high (H) and low (L) levels of reliability for GEBV

Age Donor	#Donors	#Sires	L		H	
			10 calves	20 calves	10 calves	20 calves
2	50	50	131	153	136	160
14	50	50	114	125	116	129
2	100	50	142	167	149	174
14	100	50	120	134	122	137
2	200	50	154	177	162	184
14	200	50	125	141	129	144
2	100	100	132	155	136	166
14	100	100	112	126	114	129
2	200	100	143	166	150	175
14	200	100	118	133	120	138
2	200	200	132	155	137	163

14	200	200	109	125	111	128
LSD _{0.05} =1.05						

In all donor programs 2000 females were genotyped in order to increase selection accuracy of heifers selected as donors. Genotyping heifers combined with more intensive use of the 50 to 200 best heifers increases genetic gain with at least 11 relative units when 10 calves are produced increasing to 25 units when 20 calves are produced.

Increasing the donor program and number of offspring per donor increases the selection intensity when choosing future breeding bulls and thereby increasing genetic gain.

Inbreeding. Any donor program (50 to 200 donors) with the same number of selected sires as in the reference scheme (50 sires) results in a higher rate of inbreeding in relation to the reference schemes (Table 3). This is expected as the best females are used more intensively compared to the reference scheme. The H-reliability schemes provides in general lower rates of inbreeding compared to the L-reliability schemes. The higher reliability of GEBV provides more information of the Mendelian sampling term, which cause selection of candidates from a wider range of families. Reducing the age of the donors from 14 to 2 month has the general effect that female selection candidates are further removed from phenotypic information. This reduces the reliability of GEBV a little and thereby increases the rate of inbreeding. A large variation in relative rate of inbreeding is observed between the different breeding schemes, varying from 39 and up 186 compared to the level observed in the reference schemes. Increasing the number of sires has the largest influence in the reduction of inbreeding.

Table 3. Relative rate of inbreeding for different sizes of donor program for high (H) and low (L) levels of reliability for GEBV

Age Donor	#Donors	#Sires	L		H	
			10 calves	20 calves	10 calves	20 calves
2	50	50	155	189	158	186
14	50	50	125	175	128	164
2	100	50	141	152	139	150
14	100	50	130	168	122	144
2	200	50	127	132	122	128
14	200	50	125	157	119	142
2	100	100	82	100	83	97
14	100	100	75	100	69	89
2	200	100	75	82	72	78
14	200	100	70	91	67	83
2	200	200	43	52	44	50
14	200	200	39	52	39	47

LSD_{0.05}=4.95

Interaction effects. In general, interaction effects are present, because of multiplicative effects of increased selection accuracy, higher selection intensity, and reduced generation interval in the breeder's equation formula.

The scheme resulting in highest genetic gain with a high reliability (Index 184) benefits from the large (200 donors instead of 50) and intensive (20 progeny per donor instead of 10) donor program, which contributes to high selection intensity and a short generation interval (donor 2 month old instead of 14) as well as a multiplicative effect of these, which cause a positive interaction. The individual main effects explain 46 of the index points, leaving 22 index points to be explained by the interactions relative to the alternative (Index 116). For the L-reliability scenario the interaction effect is of the same magnitude (24 index points). These results show that positive interaction effects contribute to higher genetic gain in genomic breeding schemes, and these favorable interactions are obtained even in breeding schemes with low reliabilities of genomic predictions.

A high reliability of GEBV provides a relatively higher increase in genetic gain due to RT compared to the low reliability scenario, as the young breeding candidates without own phenotypic information is selected more accurately. Small interaction effects are observed between number of calves produced and reliability of GEBV. A reduction in the generation interval in the donors provides the same.

Optimal breeding schemes. Choosing the optimal breeding scheme based on long-term decisions is often a balance between short-term genetic gain and short-term value of inbreeding. This study shows that by choosing the right breeding program the genetic gain can be maintained and rate of inbreeding reduced at the same time. Or one can achieve a large increase in genetic gain without increased rates of inbreeding.

The schemes with equal numbers of donors and sires provide nearly the same genetic gain, but show approximately 3 fold difference in rate of inbreeding. However, the cost by running such a breeding scheme is expected to be high, which is not evaluated in this study.

In the present study the reliability of GEBV is assumed to be fixed over time, without accounting for the fact that genotyped females are included in the reference population and hence has the potential to increase reliability of GEBV over time. Including the genotyped cows in the reference is expected to increase genetic gain and reduce the rate of inbreeding (Thomassen et al (2014)).

Conclusion

The results from this study showed that use of reproductive technologies in genomic selection schemes increases genetic gain. A large donor program with high selection intensity of sires and a large number of progenies

provides the highest genetic gain. A relatively larger increase in genetic gain due to RT is obtained for higher reliability of GEBV. Interaction effects between varied breeding schemes parameters exist for both high and low reliabilities for genomic breeding values. Extending the donor program and number of selected bulls has a major effect of reducing the rate of inbreeding without compromising genetic gain.

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