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Reproductive technologies combine well with genomic selection in dairy breeding programs

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ABSTRACT

The objective of the present study was to examine whether genomic selection of females interacts with the use of reproductive technologies (RT) to increase annual monetary genetic gain (AMGG). This was tested using a factorial design with 3 factors: genomic selection of females (0 or 2,000 genotyped heifers per year), RT (0 or 50 donors selected at 14 mo of age for producing 10 offspring), and 2 reliabilities of genomic prediction. In addition, different strategies for use of RT and how strategies interact with the reliability of genomic prediction were investigated using stochastic simulation by varying (1) number of donors (25, 50, 100, 200), (2) number of calves born per donor (10 or 20), (3) age of donor (2 or 14 mo), and (4) number of sires (25, 50, 100, 200). In total, 72 different breeding schemes were investigated. The profitability of the different breeding strategies was evaluated by deterministic simulation by varying the costs of a born calf with reproductive technologies at levels of €500, €1,000, and €1,500. The results confirm our hypothesis that combining genomic selection of females with use of RT increases AMGG more than in a reference scheme without genomic selection in females. When the reliability of genomic prediction is high, the effect on rate of inbreeding (ΔF) is small. The study also demonstrates favorable interaction effects between the components of the breeder's equation (selection intensity, selection accuracy, generation interval) for the bull dam donor path, leading to higher AMGG. Increasing the donor program and number of born calves to achieve higher AMGG is associated with the undesirable effect of increased ΔF. This can be alleviated, however, by increasing the numbers of sires without compromising AMGG remarkably. For the major part of the investigated donor schemes, the investment in RT is profitable in dairy cattle populations, even at high levels of costs for RT.
Key words: genomic breeding scheme, multiple ovulation and embryo transfer (MOET), ovum pick-up, genetic evaluation, economic evaluation

INTRODUCTION

Multiple ovulation and embryo transfer (**MOET**) has been used as a tool for recruiting more progeny from the females with highest genetic merit for the last 40 yr in many conventional progeny testing schemes (Hasler, 2014). Nicholas and Smith (1983) reported that genetic gain can be increased markedly (30%) by intensive use of MOET. The obtained gain was mainly due to a reduction of the generation interval and the more intensive use of the best females. Use of ovum pick-up (**OPU**) combined with in vitro fertilization of the oocytes can further reduce the generation interval, as OPU can be carried out on immature young females (Rick et al., 1996). Use of MOET in combination with OPU also increases the number of progeny per donor and hence increases selection among half or full sibs.

The benefits of using reproductive technologies (**RT**) in combination with genomic selection are 2-fold. First, the donors can be selected with higher accuracy as genomic selection provides information on the Mendelian sampling term (Brøndum et al., 2011; Lund et al., 2011; Thomasen et al., 2012). Second, as use of RT increases the number of full sibs and half sibs, selection intensity increases within family selection (Daetwyler et al., 2007). Studies have shown that more intensive use of MOET in a breeding scheme using genomic selection increases genetic gain (Sørensen and Sørensen, 2009; Pryce et al., 2010; Pedersen et al., 2012). With more intensive use of the best breeding candidates, we ex-

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pect in general higher inbreeding rates compared with a scheme without use of RT. However, with higher selection accuracy from genomic information, we also expect to select animals from more families and hence expect lower rates of inbreeding. Based on the above reasoning, we hypothesized that synergies exist between the use of genomic selection of females and the use of RT in respect to annual monetary genetic gain (**AMGG**) and rate of inbreeding (**ΔF**).

The main objective of the present study was to test the hypotheses using a factorial design with 3 factors: genomic selection of females (0 or 2,000 genotyped heifers per year), RT (0 or 50 donors selected at 14 mo of age for producing 10 offspring), and 2 different reliabilities of genomic prediction. In addition, we explored different strategies for use of RT and how strategies interact with the reliability of genomic prediction. We accordingly investigated a range of breeding schemes for 2 levels of predictions by varying (1) number of donors, (2) number of born calves per donor, (3) age of donor, and (4) number of sires, at 2 reliabilities of genomic prediction. The various breeding schemes were evaluated in terms of AMGG and ΔF using stochastic simulation. Finally, the profitability of the different breeding strategies was evaluated by sensitivity analysis of costs for use of RT using deterministic simulation.

MATERIALS AND METHODS

Scenarios

To test our hypothesis of favorable interaction between genomic selection of females and RT, we examined 4 scenarios, with either 0 or 2,000 genotyped heifers per year, and either 0 or 50 donors selected at 14 mo of age for producing 10 offspring. These 4 scenarios were investigated assuming a reliability of the direct genomic value (**DGV**) of either 0.36 (low reliability, **L-REL**) or 0.50 (high reliability, **H-REL**) of the total merit index. Fifty young and genomically tested bulls were used equally for matings in the RT program.

For investigating RT strategies, a breeding scheme using only genomic-evaluated young bulls was simulated with equal use of each sire. The number of young bulls was varied at levels 25, 50, 100, and 200. The number of donors was 25, 50, 100, or 200. To reduce the number of scenarios, only 9 different combinations of donors and young bulls were evaluated. In the simulations, each donor produced either 10 or 20 born calves from 5 different sires. A sex ratio of 0.5 was used for all calves. The age of the donor for starting RT was either 2 or 14 mo of age; 2 mo represents the extreme scenario of reducing the generation interval to a minimum, and 14 mo represents a scenario where all progeny are born in the first calving. All combinations of scenarios were investigated for a reliability DGV of either L-REL or H-REL of the total merit index representing populations with low (Brøndum et al., 2011; Thomasen et al., 2012) and high (Lund et al., 2011) reliability of genomic prediction. In total, 72 different breeding schemes were investigated.

Population

The simulated breeding population consisted of 20,000 cows equally distributed in 200 different herds. The 2,000 highest-ranking heifers by parent average 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 2,000 genotyped bull calves yearly. The number of bull calves born in the donor program varied from 125 (25 donors producing 10 progeny each) to 2,000 (200 donors producing 20 progeny each). For the breeding schemes not producing a sufficient number of bull calves from the donor program, the remaining bull calves genotyped were selected among 1-yr-old bull calves in the rest of the breeding nucleus based on parent-average total merit. The proportion of genotyped bull calves originating from the donor program varied from 6.25 to 100% (Figure 1).

Breeding Goal and Breeding Values

The breeding goal consisted of 2 traits: a milk production trait ($h^2 = 0.30$) and a functional trait ($h^2 = 0.04$) with a negative genetic correlation ($r_g = -0.30$). The economic values were set to €83 and €82 per additive genetic standard deviation. For both traits, phenotypic values were simulated for the females completing first lactation and daughter yield deviations for bulls used for breeding. The DGV for all genotyped animals was modeled using pseudo-genomic selection, that is, without simulating chromosomes, genes, or markers (Dekkers, 2007). The genetic evaluation resembles single-step genomic BLUP with genotyped and nongenotyped animals evaluated together using all phenotypic records available. For a more detailed description, see Buch et al. (2012). The DMU package (Madsen and Jensen, 2010) was used for the prediction of breeding values.

Data Analysis

The stochastic simulation program ADAM (Pedersen et al., 2009) was used for simulations of the scenarios. Each scenario was investigated over 30 yr and

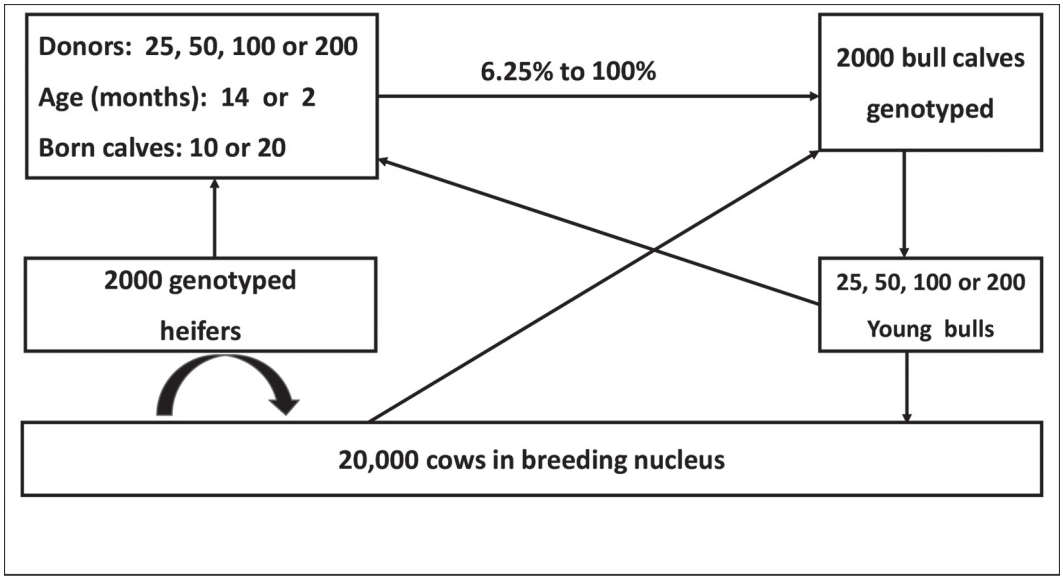

Figure 1. Illustration of selection groups in the donor schemes.

replicated 100 times. Annual monetary genetic gain is presented as the regression of true breeding value for the breeding goal on year of birth for year 21 to 30; ΔF was calculated as the regression of ln(1 – Ft) on GEt, where Ft is the average degree of inbreeding and GEt is the average generation equivalent for animals born in year t (t = 21 to 30). The implied generation interval in this calculation is the average age of parents of newborn eventually to be selected. When AMGG is large, this generation interval is somewhat smaller than the generation interval based on the usual definition as the average age of parents of all newborn animals (Bijma and Woolliams, 2000). Both AMGG and ΔF were averaged across replicates and presented as relative values compared with the values in the reference scenario (Table 1). Differences in AMGG and ΔF between scenarios were compared with the least significant difference (**LSD**) using a significance level of 5%. The scenario without use of RT, no genotyping of females, and low reliability of DGV was used as reference (Table 1). The AMGG and ΔF were set to 100 for this scenario. All results for AMGG and ΔF in Tables 2 and 3 are presented as relative values compared with this reference scenario.

To test the direct and interaction effects of the various factors in the breeding schemes scenarios, the appropriate ANOVA analyses were performed using R (http://www.R-project.org).

Economic Evaluation

The deterministic simulation program ZPLAN (Willam et al., 2008) was used to evaluate the economic efficiency of using RT. A reference scenario without use of RT was set up to calculate the discounted return (**DR**) defined as the monetary revenue per cow expressing the genetic superiority in the population over the investment period of 15 yr discounted by an interest rate of 6% (Thomasen et al., 2014a). The discounted costs (**DC**) were defined as the variable breeding costs per

Table 1. Annual monetary genetic gain (AMGG) and rate of inbreeding per generation (ΔF) for genomic young bull schemes with or without use of reproductive technologies (RT) for low (0.36) and high (0.50) reliability of direct genomic value (DGV)

Item	No. of bull dams genotyped	No. of sires	AMGG (€)		ΔF (%)	
			No RT	RT[1]	No RT	RT[1]
Reliability 0.36	0	50	31.1[2]	33.0	0.44[2]	0.64
	2,000	50	31.2	35.6	0.40	0.55
Reliability 0.50	0	50	34.4	36.5	0.36	0.51
	2,000	50	35.1	39.9	0.34	0.46

[1]Two hundred donors, 14 mo of age, each producing 10 progeny.
[2]Reference scenario.

Table 2. Relative annual monetary genetic gain (AMGG) for different sizes of donor programs for low (0.36) and high (0.50) reliability for direct genomic value (DGV)[1,2]

Age of donor (mo)	No. of donors	No. of sires	Reliability = 0.36		Reliability = 0.50	
			10 Calves	20 Calves	10 Calves	20 Calves
2	50	25	137	160	159	186
14	50	25	119	131	136	150
2	100	25	148	170	174	201
14	100	25	125	138	142	158
2	200	25	161	180	186	210
14	200	25	131	144	149	164
2	50	50	130	152	150	176
14	50	50	114	125	128	142
2	100	50	142	164	164	192
14	100	50	119	133	135	151
2	200	50	154	176	179	204
14	200	50	125	140	142	160
2	100	100	132	155	151	180
14	100	100	111	126	126	142
2	200	100	143	166	166	193
14	200	100	118	133	133	152
2	200	200	132	155	152	179
14	200	200	109	125	122	141

[1]An AMGG of €31.1 relates to a relative value of 100.
[2]Least significance difference at 5% level is 1.5.

cow during the investment period of 15 yr discounted by an interest rate of 4%.

The same breeding scheme parameters and selection index parameters as in ADAM were used (Table 1). For modeling the young bull breeding schemes, the variable cost parameters, biological parameters, and interest rates from Thomasen et al. (2014a) were used for a dairy cattle population of 500,000 cows.

The ratio of the change in DR relative to the reference scenario (Δ**DR**) and the increased DC relative to the reference scenario (Δ**DC**) by use of genomic selection and RT in females was used as the criterion for evaluating the investment (Thomasen et al., 2014b). Generally, the investment was profitable for a ratio greater than or equal to unity ($\Delta DR/\Delta DC \geq 1$), when it was assumed that all value of improvement was returned to

Table 3. Relative rate of inbreeding per generation (ΔF) for different sizes of donor programs for low (0.36) and high (0.50) reliability for direct genomic value (DGV)[1,2]

Age of donor (mo)	No. of donors	No. of sires	Low reliability		High reliability	
			10 Calves	20 Calves	10 Calves	20 Calves
2	50	25	247	287	211	227
14	50	25	214	295	188	230
2	100	25	234	249	188	200
14	100	25	245	314	179	221
2	200	25	218	230	171	173
14	200	25	227	267	180	218
2	50	50	156	189	129	151
14	50	50	124	178	104	137
2	100	50	144	151	113	123
14	100	50	127	170	101	118
2	200	50	128	134	102	104
14	200	50	127	155	99	118
2	100	100	83	98	69	80
14	100	100	70	99	56	73
2	200	100	73	81	58	64
14	200	100	69	92	54	69
2	200	200	44	52	36	40
14	200	200	39	52	30	39

[1]A rate of inbreeding per generation of 0.44% relates to a relative value of 100.
[2]Least significance difference at 5% level is 9.9.

the breeding program. Assuming that only 20% was returned to the breeding program, a value of 5 or larger could be interpreted as a profitable breeding program.

The L-REL and H-REL levels of DGV were modeled in ZPLAN by adding either 10 or 25 percentage points to the reliability of parent average of each trait in the selection index. The same procedure was used by Thomasen et al. (2014a) to model different levels of reliability for genomic breeding values. The same selection intensities for each selection group were used in ADAM and ZPLAN for modeling the different scenarios. For donors 14 mo of age, the calculated genetic gain from ADAM and ZPLAN corresponds well. For the scenarios using young donors, ZPLAN underestimates the genetic gain and hence provides conservative estimates of profit.

Cost Assumptions

Three levels of cost per born calf using RT ranging from a labor extensive system on farms (primarily MOET) to a labor-intensive system on centralized stations (primarily OPU) were assumed, namely €500, €1,000, or €1,500. The range of cost levels also accounts for different success rates of RT by breeds (Boselmann, 2007).

For both MOET and OPU, fixed costs per donor (e.g., hormone treatment of donor, time on station, costs of RT) and variable costs per born calf (e.g., synchronization of estrus of recipients, purchase of recipients) were modeled as a single variable cost component per born calf. The reason is that the large number of progeny assumed in this study will require several hormone treatments, several flushes, and more days on station, causing the total cost to be dependent on the number of born calves. This range of costs overlaps with the costs calculated by Faasch (2009).

RESULTS

Combining RT with Genotyping of Females

The breeding scheme using genomic evaluated bulls without RT (Table 1) provided an AMGG of €31.1 and a ΔF of 0.44% per generation based on a reliability of 0.36 for DGV with no genotyping of bull dams. Using RT (50 donors, 14 mo of age, producing 10 progeny), AMGG increased by €1.9 and ΔF increased by 0.2 percentage points when bull dams were not genotyped. For the scenario with bull dams genotyped, the gain in AMGG of using RT was €4.4. The ΔF increased by only 0.15 percentage points. At a reliability of 0.50 and with use of RT, AMGG increased by €2.1 (from €34.4 to €36.5), and ΔF increased by 0.15 percentage points per generation, from 0.36 to 0.51%, when bull dams were not genotyped. When bull dams were genotyped, the increase in ΔF by using RT was 0.12 percentage points. The increase in AMGG was €4.8.

An ANOVA including the factors genotyping, reliability, and effect of RT showed, for AMGG, significant direct effects of all factors and significant interaction effects between genotyping of females and reliability, and between genotyping of females and RT. For ΔF, interaction effects between reliability and RT and between genotyping of females and RT were significant in addition to the direct effects.

AMGG

Table 2 shows the relative AMGG for all simulated variants of breeding schemes using RT. Overall, the relative AMGG varied from 109 to 210 compared with the reference scenario (€31.1). Differences greater than 1.5 units in AMGG between schemes were significantly different at 5% level. In general, increasing the number of sires reduced AMGG for the same size of donor program. The reduction was independent on the reliability for DGV, number of calves born, and age of donor.

The results of the ANOVA for AMGG showed that significant interactions existed between most of the breeding scheme parameters. Using the scenario with 50 sires, 50 donors at 14 mo of age, producing 10 calves, H-REL as point of departure, the relative AMGG was 128 (€39.8). An increase in the number of progeny to 20 born calves increased relative AMGG by 14 percentage points up to 142. Using 200 donors instead of 50 donors increased AMGG from 128 to 142 as well. A reduction in the age of donors to 2 mo increased AMGG by 22 relative units to 150. The sum of these direct effects was 52 (14 + 14 + 22) relative units. The relative AMGG for the scheme with 50 sires, 200 donors at 2 mo of age, producing 20 born calves at H-REL was 204 relative units and so resulted in a gain of 76 units compared with the scenario with 50 sires, 50 donors at an age of 14 mo of age, producing 10 born calves. The difference to the gain of the direct effects (52) expresses the outcome of the interaction effects of 24 units (76 − 52). The combination of number of progeny, age of donor, and number of donors was also highly significant ($P < 0.001$) by ANOVA.

For donors 14 mo of age, the relative gain by increasing the donor program from 100 to 200 donors was in the range of 9 to 13 units, independent on the number of sires, number of calves, and reliability of DGV. For donors at 2 mo of age, the gain was in the range of 6 to 9 relative units.

The schemes varied in generation interval from 1.55 to 1.76 yr for the breeding schemes with donors at 2

mo of age. For schemes with donors 14 mo of age, the generation interval was in the range of 2.05 to 2.25 yr (individual results not shown).

Inbreeding

Overall, the relative ΔF varied from 30 to 314 compared with the reference scheme, with an increase in ΔF of 0.44% per generation (= 100; Table 3). The schemes with 200 sires resulted in the lowest ΔF (30 to 52). The scheme with 25 sires, 100 donors at an age of 14 mo, and producing 20 calves at L-REL resulted in the highest ΔF. In general, schemes with 20 calves per donor for L-REL resulted in the highest ΔF. Increasing the genomic information source from L-REL to H-REL decreased ΔF on average from 157 to 124.

The results of the ANOVA for ΔF showed that significant interaction effects existed between most of the breeding scheme parameters. The combination of number of progeny, age of donor, and number of sires was also highly significant ($P < 0.001$) by ANOVA.

The breeding schemes using 50 sires with H-REL and a large donor program with 200 donors, producing 10 calves provided relative ΔF at the same level (99 to 102) as the reference scenario without use of RT. When the donor program was small (50 donors), using younger donors gave higher ΔF (129 compared with 104). For the large donor program with young donors, ΔF was maintained at the same level (102 to 104) when numbers of progeny were increased from 10 to 20. However, for the small donor program with 50 donors, ΔF was increased from 129 to 151 by increasing the number of progeny from 10 to 20. In the large donor program with 20 progeny per donor, the young donors gave lower ΔF (104) compared with donors at 14 mo of age (118). This is in contrast to the small donor program, where younger donors resulted in the largest ΔF (151 compared with 137). Similar associations were seen for 25 and 100 sires.

Economic Evaluation

The profitability of investment in the various donor programs are shown in Tables 4, 5, and 6 for the 3 cost levels of €500, €1,000, and €1,500 per born calf. All donor schemes showed ΔDR/ΔDC ≥1 at H-REL of genomic prediction except the scheme with 200 sires and 200 donors at an age of 14 mo producing 10 calves each. At a cost of €500, the investment was returned up to 76 times (Table 4). At the L-REL level of genomic predictions, all donor schemes with 25 or 50 sires were profitable. In contrast, a major part (8 out of 12) of the donor schemes showed values of ΔDR/ΔDC <1 when 100 or 200 sires were used in the breeding program.

Assuming a cow population of 50,000 instead of the 500,000 assumed in the current calculations would reduce all calculated ΔDR/ΔDC by a factor of 10, meaning that all schemes with ΔDR/ΔDC ≤10 would not return the investment. At a cost of €1,500, only 5 out of 24 schemes with 25 sires and 50 donors were profitable for the L-REL case in a small population.

Optimal Donor Schemes in Practice

The 8 most realistic donor schemes that could feasibly be implemented in the near future for a large dairy

Table 4. Ratio of change in return to change in costs (i.e., profitability of investment) for different sizes of donor programs for low (0.36) and high (0.50) reliability for direct genomic value at cost for calf born of €500

Age of donor (mo)	No. of donors	No. of sires	Low reliability		High reliability	
			10 Calves	20 Calves	10 Calves	20 Calves
2	50	25	32.9	28.7	76.0	58.9
14	50	25	29.2	23.7	71.6	53.0
2	100	25	26.9	23.4	56.7	43.1
14	100	25	22.0	17.4	51.1	36.1
2	200	25	20.8	18.9	40.0	31.5
14	200	25	15.2	12.0	33.4	23.5
2	50	50	10.1	13.6	49.2	41.0
14	50	50	6.5	8.7	45.2	35.6
2	100	50	11.6	14.2	38.9	32.2
14	100	50	7.0	8.5	33.6	25.6
2	200	50	11.6	13.5	29.2	25.2
14	200	50	6.2	7.0	23.0	17.6
2	100	100	−5.4	3.8	18.9	20.0
14	100	100	−9.7	−1.5	13.9	13.9
2	200	100	1.2	7.4	17.0	18.1
14	200	100	−3.8	1.4	11.2	11.0
2	200	200	−10.4	0.7	3.4	10.2
14	200	200	−15.0	−5.0	−1.9	3.6

Table 5. Ratio of change in return to change in costs (i.e., profitability of investment) for different sizes of donor programs for low (0.36) and high (0.50) reliability for direct genomic value (DGV) at cost for calf born of €1,000

Age of donor (mo)	No. of donors	No. of sires	Low reliability		High reliability	
			10 Calves	20 Calves	10 Calves	20 Calves
2	50	25	21.7	17.0	50.1	34.9
14	50	25	19.3	14.0	47.2	31.4
2	100	25	15.9	12.9	33.6	23.7
14	100	25	13.0	9.6	30.3	19.9
2	200	25	11.5	10.0	22.1	16.6
14	200	25	8.4	6.3	18.4	12.4
2	50	50	6.7	8.0	32.4	24.3
14	50	50	4.3	5.2	29.8	21.1
2	100	50	6.9	7.8	23.0	17.7
14	100	50	4.2	4.7	19.9	14.1
2	200	50	6.4	7.1	16.1	13.3
14	200	50	3.4	3.7	12.7	9.3
2	100	100	−3.2	2.1	11.2	11.0
14	100	100	−5.7	−0.8	8.2	7.6
2	200	100	0.7	3.9	9.4	9.6
14	200	100	−2.1	0.7	6.2	5.8
2	200	200	−5.7	0.7	1.9	5.4
14	200	200	−8.3	−2.7	−1.1	1.9

population of 500,000 cows are summarized in Table 7. This implies donors of 14 mo of age producing 10 calves (Boselmann, 2007). The number of sires in the schemes varied from 25 to 100. Overall, AMGG varied from 126 (€39.2) to 149 (€46.3) compared with the reference scenario. A large variation between the schemes was seen for ΔF, from 54 to 188 (0.24 to 0.83%). All schemes provided values of $\Delta DR/\Delta DC \geq 1$ for all cost levels. For the low cost level of €500 per calf born, the investment was returned from 11.2 to 71.6 times. For the high cost level of €1,500 per calf born, the investment was returned 4.3 to 35 times depending on the scheme.

DISCUSSION

This study confirms our hypothesis that combining genomic selection of females with use of RT increases AMGG, because of favorable interactions. The interaction effect on ΔF between RT and genomic selection was also favorable, despite the marginal effect of RT being unfavorable. The study also demonstrated several interaction effects between the components defining the donor scheme, leading to higher AMGG. Increasing the donor program and number of born calves per donor to achieve higher AMGG was associated with the negative

Table 6. Ratio of change in return to change in costs (i.e., profitability of investment) for different sizes of donor programs for low (0.36) and high (0.50) reliability for direct genomic value at cost for calf born of €1,500

Age of donor (mo)	No. of donors	No. of sires	Reliability = 0.36		Reliability = 0.50	
			10 Calves	20 Calves	10 Calves	20 Calves
2	50	25	16.1	12.1	37.1	24.8
14	50	25	14.3	10.0	35.0	22.3
2	100	25	11.3	8.9	23.8	16.4
14	100	25	9.3	6.6	21.5	13.7
2	200	25	7.9	6.8	15.2	11.3
14	200	25	5.8	4.3	12.7	8.4
2	50	50	4.9	5.7	24.1	17.3
14	50	50	3.2	3.7	22.1	15.0
2	100	50	4.9	5.4	16.4	12.2
14	100	50	3.0	3.2	14.1	9.7
2	200	50	4.4	4.8	11.1	9.0
14	200	50	2.4	2.5	8.7	6.3
2	100	100	−2.3	1.5	7.9	7.6
14	100	100	−4.1	−0.6	5.9	5.3
2	200	100	0.4	2.7	6.5	6.5
14	200	100	−1.5	0.5	4.3	4.0
2	200	200	−4.0	0.2	1.3	3.6
14	200	200	−5.7	−1.8	−0.7	1.3

effect of increased ΔF. This can be alleviated, however, by increasing the number of sires with a large effect on reducing ΔF and a small effect on AMGG, while AMGG is still larger than without RT. For most of the investigated donor schemes, the investment in RT was profitable in larger dairy cattle populations, even at high costs for RT. Therefore, RT and genomic selection will arguably be a key factor for the competitiveness of future dairy cattle breeding schemes.

Interaction Effects

This study clearly showed favorable interaction effects between the breeding scheme parameters for AMGG. Genomic selection facilitates reliable selection of donors early in life. This is in contrast to the use of RT in conventional schemes without genomic selection, where selection accuracy is limited by the unavailability of performance information until later in life. However, RT facilitates a higher selection intensity of bull dams by using fewer cows to produce the required bull calves. The best candidates among the produced full-sib families from the donor program can be selected more accurately with use of genomic information at the same time. So, genomic selection combines well with RT, because these effects act multiplicatively, as indicated in the breeder's equation.

The interaction effects between the breeding scheme parameters are even more complex for ΔF than for AMGG, as demonstrated in the ANOVA. The example described in the Results section shows the interaction between age of donor, number of donors, and number of progeny. When the donor program is large, the donors can be selected at a young age and used intensively without compromising ΔF, which is not the case for the small donor program.

The multitude of interaction effects for both AMGG and ΔF found in this study indicates the importance of joint decision-making on several factors of male and female selection strategies in a breeding program.

Bull Selection

Increasing the number of sires decreased AMGG by up to 25%, while ΔF could be reduced by a factor of 6. Therefore, the direct effects of increasing the number of sires are relatively larger for ΔF than for AMGG. In breeding schemes with short generation intervals, the young breeding candidates are only selected based on genomic information without own performance, so the accuracy of males and females are similar. In this case, the maximum AMGG for constant ΔF is achieved by equalizing the selection intensities in the 2 sexes (Gjerde et al., 1996). This is exactly what RT enables. Thus, RT in combination with modified sire selection can be a way to make dairy cattle breeding schemes more sustainable in terms of genetic diversity.

In the present study, 2,000 bull calves were genotyped in all scenarios, which correspond to the maximum number of bull calves produced in the donor schemes in this study. Additional simulations showed no effect of increasing number of genotyped bull calves in the investigated donor schemes. This can be explained by the fact that progeny produced by donors are superior on average to progeny of nondonors and additional bull calves from the rest of the population have a negligible chance of being selected. This implies that an extension of the donor program in combination with genotyping more bull calves could provide higher AMGG.

It is costly to select and collect semen from more bulls due to the cost of purchasing bull calves and entering more bulls in semen production. But in young bull schemes, the cost of selecting more bulls is much lower compared with proven bull schemes, as the bulls do not need to be kept in the period waiting for daughter records but can be slaughtered after finishing semen

Table 7. Relative annual monetary genetic gain (AMGG), relative rate of inbreeding per generation (ΔF), and ratio of change in return to change in costs (ΔReturn/ΔCosts; i.e., profitability of investment) for different sizes of donor programs for reliability of 0.50, age of donor of 14 mo, 10 calves, and costs of €500, €1,000, or €1,500 per calf born in a population of 500,000 cows[1]

No. of donors	No. of sires	AMGG	ΔF	ΔReturn/ΔCosts		
				Cost: €500	Cost: €1,000	Cost: €1,500
50	25	136	188	71.6	47.2	35.0
100	25	142	179	51.1	30.3	21.5
200	25	149	180	33.4	18.4	12.7
50	50	128	104	45.2	29.8	22.1
100	50	135	101	33.6	19.9	14.1
200	50	142	99	23.0	12.7	8.7
100	100	126	56	13.9	8.2	5.9
200	100	133	54	11.2	6.2	4.3

[1]An AMGG of €31.1 relates to a relative value of 100. A rate of inbreeding per generation of 0.44% relates to a relative value of 100.

production. Consequently, the use of more sires and RT is a sustainable combination in terms of both genetic diversity and economy.

Age of Donors

To achieve higher AMGG, it is worth aiming for younger donors. Choosing younger donors results in no substantial reduction in selection accuracy as genomic information is potentially available at birth. For this reason, the scenarios with 2-mo-old donors illustrate the potential of increasing AMGG by reducing generation interval to a minimum. Although this is not currently possible in practice, it might be worthwhile to explore possibilities in the future. In general, the generation intervals in this study were short compared with conventional schemes. The reason is that the young progeny created from the donor nucleus are superior on average compared with progeny from the conventional part of the scheme (Figure 1). Furthermore, with larger nuclei, the selection of the best candidates become less dependent on the remaining population with the consequence that the breeding scheme moves toward a velo-genetic scheme, as described by Haley and Visscher (1998). However, in such schemes, it is a challenge to maintain high reliability of genomic prediction when the generational gap between selection candidates and reference animals increases (Habier et al., 2007). Therefore, strategies for maintaining high reliability through an informative reference population should follow any strategies to reduce generation intervals significantly.

Reliability of Genomic Prediction

All the simulated breeding schemes were young bull schemes relying on accurate genomic information. This had a great effect on the obtained AMGG and ΔF in the simulated schemes. The higher selection accuracy favored selection from more families due to more accurate information on the Mendelian sampling term and, hence, resulted in 22% lower ΔF across all schemes for the H-REL level compared with the L-REL level.

In smaller dairy cattle populations, the profitability of implementing RT as a part of the breeding scheme relies on the possibilities of obtaining a high reliability of genomic prediction and of producing progeny from RT at a lower level of cost. For a program with 25 sires, 200 donors at 14 mo of age with 10 calves born per donor, the rate of profitability increases from 6.3 to 12.4 (Table 5) by increasing the reliability from low to high level. In the present study, no costs of increasing the reliability of genomic prediction were considered. However, a study by Thomasen et al. (2014b) showed that it is profitable to genotype cows for the reference population in a small dairy cattle population of 68,000 production cows. Therefore, investments in RT will be more profitable when combined with investments in improving the reference population.

Implications for Practical Dairy Cattle Breeding

We consistently found favorable effects on AMGG due to recruiting a larger part of male and female breeding candidates from a donor program (Figure 1). This implies that use of RT might become an integrated part of future dairy breeding schemes. In larger dairy cattle populations, the use of RT is profitable, even at high costs (Table 7), assuming high reliability of genomic prediction. To obtain a high AMGG in practice, it is important that many progeny be produced in a short period. This may require combinations of several MOET and OPU flushings of the donor. If the number of progeny cannot be increased, more donors can be selected. At the H-REL level, AMGG was reduced relatively from 151 to 142 by producing 10 born calves from each of 200 donors instead of 20 born calves from each of 100 donors using 50 sires. Because of the use of more donors, ΔF was reduced from 118 to 99. A simulation study by Pedersen et al. (2012), assuming 5 born calves per donor, showed 18 to 23% extra AMGG depending on the number of donors compared with a scheme without use of MOET. These lower outcomes of using MOET are in line with the smaller number of progeny per donor. Hence, it is not only the number of born calves from a donor that affects AMGG, it also depends on the selection intensity of the donors and the accuracy of the within family selection.

CONCLUSIONS

Use of RT in combination with genomic selection has the potential to improve AMGG in dairy breeding programs. Using more sires can reduce the otherwise higher ΔF. The net result of using RT is to increase AMGG without compromising genetic diversity. The favorable interaction effects might stimulate the dairy breeding sector to improve RT by producing more calves per donor within a short period and by using younger donors. If selection accuracy increases in the future (e.g., due to more genotyped females in the reference population), RT is expected to be more commonly used and, therefore, to be more important.

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