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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 expect in general higher inbreeding rates compared with a scheme without use of RT. However, with higher selec-

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tion 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 replicated 100 times. Annual monetary genetic gain is presented as the regression of true breeding value for