Dairy Cattle Breeding Schemes with or without Genomic Selection and Progeny Testing

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Introduction

In dairy cattle, nearly all traits of economic importance are expressed only in females and most functional traits have low heritabilities. On this basis, progeny testing has been the only way to achieve accurate estimated breeding values based on phenotypic information (EBV) but then selection decisions are postponed. Due to the introduction of new reproduction technologies Nicholas and Smith (1983) suggested a breeding scheme that included multiple ovulation and embryo transfer (MOET) and no progeny testing. The reasons behind this scheme were to increase genetic gain per unit of time by reducing the generation interval and tolerating less accuracy at the time of selection. While this suggestion only has been used sparingly in practice it illustrates that it is difficult to maximize response to selection because there are trade-offs between the parameters contributing to selection response per year.

Genomic selection creates opportunities to modify the breeding schemes because direct genomic values (DGV) and genomically enhanced breeding values (GEBV) are characterized by moderate to high accuracies and can be predicted shortly after the selection candidates are born. DGV or GEBV can be used as a pre-selection criterion in a progeny testing scheme or as a selection criterion per se. Thus, the trade-off between accuracy of selection and generation interval is expected to be weaker in breeding schemes using DGV or GEBV.

The accuracy of selection and the generation interval are included multiplicative in the expression for selection response per year. For that reason, a positive interaction between the use of GEBV and a short generation interval is expected on annual genetic gain. The objectives of this study were to test the expectation and to quantify the effect of four breeding schemes with or without progeny testing and with or without GEBV on annual genetic gain and rate of inbreeding in a stochastic simulation study.

Material and methods

To test the expectation four scenarios were designed.

The conventional scheme. This scenario was thought to reflect a conventional progeny testing scheme without genotyping and was taken as a reference scenario. In schemes with

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progeny testing two hundred one-year-old bulls were progeny tested each year and active sires were at least five years old.

The juvenile scheme. To study the effect of a short generation interval a scenario without progeny testing and genotyping was designed. In schemes without progeny testing active sires were at most four years old.

The pre-selection scheme. The effect of using GEBV was studied in a scenario with genotyping and progeny testing. Two thousand one-year-old males and 2000 one-year-old females were genotyped each year. These animals were selected for genotyping based on parent average. When bull calves were selected for genotyping, bull calves born after MOET had priority.

The turbo scheme. Finally, we wanted to study if an interaction between the use of GEBV and a short generation interval occurs. Therefore, a scenario with genotyping and without progeny testing was designed.

General assumptions. The breeding nucleus of a dairy cattle population was simulated using the stochastic simulation program ADAM (Pedersen et al. (2009)). The nucleus consisted of 20,000 cows that were simulated individually and allocated to 200 equally sized herds.

The breeding goal consisted of two traits that were similar to protein yield ($h^2 = 0.30$) and mastitis resistance ($h^2 = 0.04$). The genetic and residual correlations between the traits were -0.30 and 0.10, respectively. The two traits represented all milk production traits and all functional traits in the breeding goal, and the economic values were €83 and €82 per genetic standard deviation, respectively. The traits were only realized for cows.

A DGV was sampled for each of the traits, that is, no chromosomes, genes, or markers were simulated. Each DGV had a heritability of 0.99 and a genetic correlation to the true breeding value of the observed trait of 0.71. The heritability of the DGV is the heritability of the marker information, and the genetic correlation implies a reliability of 50 %. The DGV were included in a conventional multivariate BLUP model as information traits without economic values and as a result the selection indices were comparable to GEBV. The DGV were only realized for genotyped animals.

For selected young bulls daughter yield deviations (DYD) were sampled directly. The DYD corresponded to registration on 150 daughters for protein yield and 135 daughters for mastitis resistance. Two times the DYD were included in the BLUP model using a weight according to the information in the DYD relative to a single phenotype. The DYD were realized when the bulls were five years old.

Each year the best 400 females based on EBV, or GEBV if available, were flushed, and each flush resulted in five calves. In addition, the best 30 bulls across age groups were selected by truncation as active sires and used equally for random mating among all cows in the nucleus.

To keep inbreeding at a reasonable level we included the restrictions that a bull could have a maximum of 20 sons per year and 40 sons in total in the selection step from bull calf to young bull. Furthermore, a bull could at the maximum have 6 sons per year and 9 sons in total in the selection step from young bull to active sire.

Each scenario covered a thirty-year period and was replicated 100 times.

Results and discussion

The annual genetic gain was 22.38 euros under the conventional scheme (Table 1). Selecting active sires on the basis of parent average instead of progeny tests increased genetic gain by 9 % when no animals were genotyped. This was due to the generation interval decreasing from 4.7 to 2.7 years but at the same time the realized accuracy of the selection index for active sires decreased from 0.83 to 0.45. Genetic gain increased by 29 % when the pre-selection scheme was compared to the conventional scheme. This is because genotyping increases the accuracy of the selection index, especially for young bulls and bull dams. Using the turbo scheme instead of the conventional scheme increased genetic gain by 102 %. Thus, a positive interaction exists between a short generation interval and the use of GEBV.

Table 1: Annual genetic gain in euros (ΔG) and rate of inbreeding in percentage per generation (ΔF) with standard errors in brackets for four scenarios with or without progeny testing and with or without genomically enhanced breeding values (GEBV)

Scheme	Progeny testing	GEBV	ΔG	ΔF
Conventional	+	-	22.38 (0.09)	1.15 (0.03)
Juvenile	-	-	24.44 (0.2)	2.55 (0.07)
Pre-selection	+	+	28.89 (0.06)	0.48 (0.008)
Turbo	-	+	45.11 (0.1)	0.74 (0.02)

Nicholas and Smith (1983) compared two scenarios that resemble the juvenile scheme and the conventional scheme in this study and found that annual genetic gain increased by 22 % when a breeding scheme without progeny testing and with 16 donors per male and 4 progeny per donor was used. The reduction in generation interval was larger in the study by Nicholas and Smith (1983) than in this study which may be the reason why the increase in annual genetic gain was larger in their study than in this study. Schrooten et al. (2005) quantified the effect of single-stage and multi-stage breeding schemes where information on quantitative trait loci (QTL) was available in the first stage of selection. That is, the scenarios resemble the pre-selection scheme, the turbo scheme and the conventional scheme in this study. Due to the simulation methods the results can be interpreted as response to genomic selection. Annual genetic gain increased by 21 and 68 % when a pre-selection scheme and a turbo scheme (the QTL explained 50 % of the genetic variance in both cases) were compared to a conventional scheme. A larger part of the male selection candidates was selected to enter the progeny test in the study by Schrooten et al. (2005). This may be the reason why the increases in annual genetic gain were smaller in their study than the increases in this study. Schaeffer (2006) compared a turbo scheme based on DGV and a conventional scheme and found that annual genetic gain increased by 117 % when the former breeding scheme was used. In the study by Schaeffer (2006) the generation interval of the conventional scheme was assumed longer than the corresponding generation interval in this study whereas the generation intervals of the turbo schemes were almost equally long. This may explain why the increase in annual genetic gain was slightly larger in the study by Schaeffer (2006) than the increase in this study.

The rate of inbreeding was 1.15 % per generation under the conventional scheme (Table 1). The absence of information on progeny increases the correlation between EBV of relatives and the probability of co-selection of relatives. This is the reason why the rate of inbreeding increased by 122 % when the juvenile scheme was compared to the conventional scheme. The rate of inbreeding decreased by 58 and 36 % when the pre-selection scheme and the turbo scheme were compared to the conventional scheme. This is because selection is more within-family in the schemes with genotyping than in the conventional scheme.

Other studies of rate of inbreeding show the same tendencies as this study. Nicholas and Smith (1983) found for instance that rate of inbreeding increased when the juvenile scheme and the conventional scheme were compared. Dekkers (2007) compared different scenarios for a pig breeding scheme and found that rate of inbreeding was reduced when the selection criterion was DGV or GEBV instead of EBV.

Based on earlier studies Bijma (2000) suggested that the acceptable level of rate of inbreeding is between 0.5 and 1 % per generation. This was the case for both the breeding schemes where genotype information was used.

Conclusion

These results indicate that a positive interaction exists between the use of GEBV and a short generation interval on annual genetic gain. The turbo scheme with genotyping and without progeny testing was superior as regards annual genetic gain. Additionally, the rate of inbreeding was less than 1 % per generation. Thus, a turbo scheme seems to be the method of choice as genomic selection weakens the relationship between accuracy of selection and generation interval.

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