

Inbreeding Rates in Breeding Programs with Different Strategies for Using Genomic Selection

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Abstract

This study used stochastic simulation to show that breeding plans for dairy cattle using genomic selection needs to be optimised for the number of genotypings, the proportion of genotypings in the two sexes, and possible unbalanced use of bulls. Annual gain increases with more genotypings, while the rate of inbreeding is decreasing. The marginal return of the last genotyping is smaller for gain than for inbreeding meaning that more genotypings should be made primarily to reduce the rate of inbreeding. Breeding plans with both males and females genotyped gave the highest annual gain and the lowest rate of inbreeding, since that gave the best possibilities for stacking favourable Mendelian sampling terms. Unbalanced use of selected bulls increased annual gain slightly while increasing the rate of inbreeding moderately to severely. Hence, unbalanced use of bulls is discouraged unless suggested by Optimum Contribution Selection.

Keywords: inbreeding, genetic gain, simulation, genomic selection, genotyping

Introduction

According to Daetwyler *et al.* (2007) the use of genomic selection can be expected to decrease the rate of inbreeding relative to conventional selection using BLUP breeding values. The reason for this is that genomic information especially increases accuracy of Mendelian sampling terms. The result is that selection is shifted towards selection within families. However, so far there is limited evidence as to what influences the relative decrease in the rate of inbreeding. The objective of this paper was therefore to evaluate what factors influence the rate of inbreeding in breeding schemes using genomic selection. The focus is on the number of genotypings, the proportion of genotypings in the two sexes, and possible unbalanced use of bulls. Both rate of genetic gain and rate of inbreeding are evaluated.

Materials and Methods

Stochastic simulations of the breeding part (20 000 cows) of a dairy cattle population were used. The breeding goal consisted of two traits resembling protein ($h^2 = 0.30$) and mastitis

resistance ($h^2 = 0.04$) with an unfavourable genetic correlation ($r_g = -0.30$). The two traits represented the production traits and the functional traits, and the weights in the breeding goal were 83€ and 82€ per genetic standard deviation, respectively.

So-called pseudo-genomic selection was used in this study. This means that no chromosomes, genes, or markers were simulated. In stead a direct genomic value (DGV) was sampled directly with a heritability of 0.99, which is the heritability of the marker information, and a genetic correlation to the observed trait that equals the assumed accuracy of the DGV. In this study a correlation of 0.71 was assumed for both traits, which equals a reliability of 50%. The DGV were then included in a traditional multivariate BLUP model as indicator traits without economic weight. The selection criteria are then comparable to genomically enhanced breeding values (GEBV).

Hence, four values were simulated per animal using **G** and **R** as the genetic and environmental covariance structures, respectively:

$$\mathbf{G} = \begin{bmatrix} 1 & -0.30 & 0.71 & -0.213 \\ -0.30 & 1 & -0.213 & 0.71 \\ 0.71 & -0.213 & 1 & -0.151 \\ -0.213 & 0.71 & -0.151 & 1 \end{bmatrix}, \quad \mathbf{R} = \begin{bmatrix} 2.33 & 0.262 & 0 & 0 \\ 0.262 & 24 & 0 & 0 \\ 0 & 0 & 0.01 & 0 \\ 0 & 0 & 0 & 0.01 \end{bmatrix}$$

The first two traits are protein and mastitis resistance and the last two traits are the DGV of protein and mastitis resistance, respectively. The first two traits are only realised for cows, while the DGV are only realised for genotyped animals whether males or females. For selected young bulls daughter yield deviations (DYD) were sampled directly based on 150 daughters for protein and 135 daughters for mastitis resistance, and the DYD were realised when the bull was 5 years old. 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.

A reference scenario was designed that is thought to reflect the breeding scheme in the near future using genomic selection for both males and females and disregarding the age of animals completely when selecting animals for breeding. Every year the best 400 females were flushed and each flush resulted in 5 calves. Bull calves born after MOET had priority when selecting bull calves to genotype, but potentially un-used genotyping capacity was spent on bull calves from natural births. Bull calves and heifer calves were selected for genotyping based on the parent average. Equally many male and female calves were genotyped. Only one year old animals were genotyped. Every year 200 one year old bulls were progeny tested, and the 30 best bulls across age groups were selected by truncation and used equally for mating at random among the 20 000 cows.

Scenarios testing the effect of number of genotypes were set up varying the number of genotypes. Everything else was kept constant including the equal split of genotypings among male and female calves.

Scenarios testing the proportion of genotypings in the two sexes were set up from no genotypings on females to all genotypings being performed on females. Everything else

was kept constant including the genotyping effort of 4000 genotypings per year.

Scenarios testing the effect of unbalanced use of bulls were set by dividing the 30 bulls into the best and the second best. The best were allocated more matings, while the second best were allocated fewer matings.

Each scenario was replicated 100 times and the results presented are averages of the replicates.

Results and Discussion

Increasing number of genotypings increases rate of gain and decreases the rate of inbreeding, but at decreasing marginal rates (Figure 1). The marginal effect is most rapidly decreasing for rate of gain. Hence, the last genotyping made is more important in decreasing the rate of inbreeding than increasing the genetic gain.

The maximum rate of gain is achieved when both males and females are genotyped (Figure 2). And the smallest rate of inbreeding was also found when both males and females were genotyped. This is because genotyping of both sexes allows accumulation of superior Mendelian sampling terms. It has not been investigated here, but the optimal proportion of females among genotyped animals is probably dependent whether genomically selected females are flushed in order to generate groups of full sibs to select superior males from. With no MOET performed the optimal proportion of females is expected to be lower than what is found in this study.

The unbalanced use of bulls led to 2-4% higher annual gain (Table 1), while the rate of inbreeding was increased by more than 20% in the best case and more than doubled in the most unbalanced case. There is therefore no

reason to experiment with unbalanced use of the selected bulls in order to gain a little in terms of progress, while losing a lot in terms of higher rate of inbreeding. If Optimum Contribution Selection (OCS) was used instead of truncation selection, the OCS solutions would be unbalanced, but then the relatedness of the bulls and their future mates will already have been taken into account to ensure the best combination of genetic gain and rate of inbreeding.

Conclusion

This study has shown that when optimising the breeding plan, while including genomic information, the number of genotypings, the distribution of genotypings among males and

females, and the use of selected bulls are crucial parameters. Increasing the number of genotypings will aid in terms of generating more gain, but especially in reducing the rate of inbreeding. It seems that it is favourable to genotype both males and females in order to stack the positive Mendelian sampling terms. And it is crucial to use the selected bulls equally in order not to waste the possibilities that genomic selection offers in terms of reducing the rate of inbreeding.

References

Daetwyler, H.D., Villanueva, B., Bijma, P. & Woolliams, J.A. 2007. Inbreeding in genome-wide selection. *J. Anim. Breed. Genet.* 124, 369-376.

Table 1. Annual gain and rate of inbreeding per generation relative to a scenario with equal use of the 30 selected bulls per year (set to 100). The scenarios shown here are all unbalanced and to a larger degree the further down the table.

Best bulls		Second best bulls		Annual Gain	Rate of inbreeding
Number	Contribution	Number	Contribution		
20	4.5%	10	1.0%	102	121
15	5.0%	15	1.7%	102	122
10	6.0%	20	2.0%	103	134
5	10.0%	25	2.0%	104	188
5	15.0%	25	1.0%	104	254

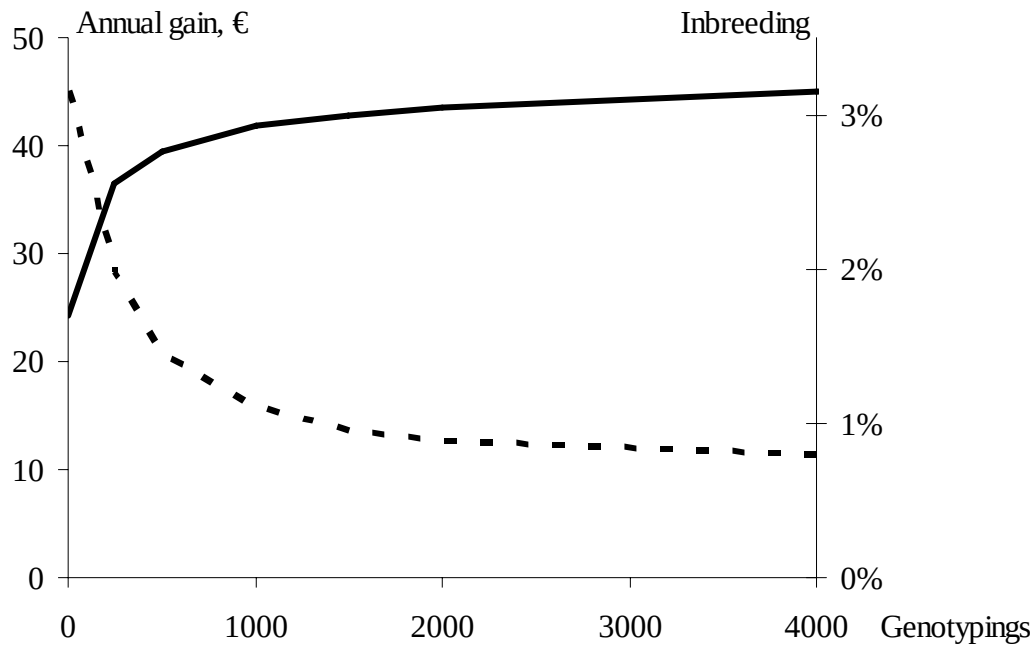


Figure 1. Annual gain (bold line) and rate of inbreeding per generation (dotted line) as a function of how many animals are genotyped per year. Equal proportions of males and females among genotyped animals are assumed.

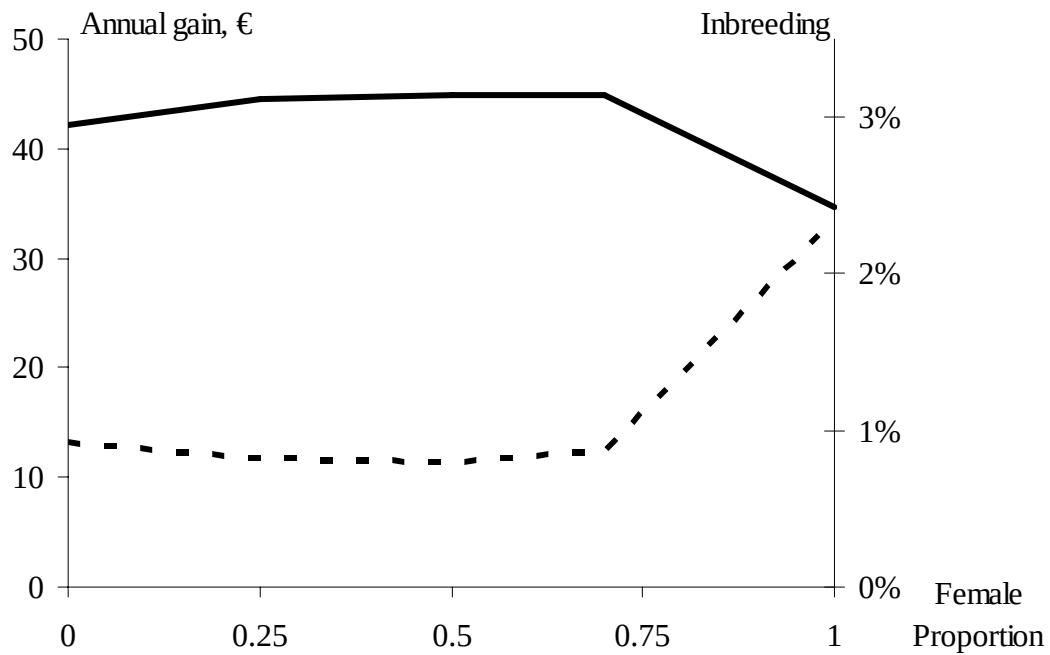


Figure 2. Annual gain (bold line) and rate of inbreeding per generation (dotted line) as a function of the proportion of females among genotyped animals. 4000 genotypings are performed per year.