The Impact Of Genomic Selection And Short Generation Interval On Dairy Cattle Breeding Programs

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Introduction

Genomic selection may result in higher rates of genetic gain over traditional selection because genomic EBVs have higher reliabilities than BLUP EBVs, especially for young animals, and secondly because young animals with high genomic EBVs become attractive to be selected as parents, which reduces the generation interval (Meuwissen et al. (2001)). The advantages of genomic selection may be highest for dairy cattle breeding programs because the generation interval in traditional progeny testing schemes is large and selection of young bulls for progeny testing is inaccurate (Schaeffer (2006)) Furthermore, thousands of bulls that have been progeny tested in the last decades are available as a reference population with very reliable phenotypes, leading to genomic EBVs with high reliabilities (VanRaden et al. (2009)). For these reasons, the uptake of genomic selection in dairy cattle in recent years has been very high.

Genomic selection may decrease the rate of inbreeding because Mendelian sampling effects can be estimated more accurately, which reduces the co-selection of relatives (Daetwyler et al. (2007)). If young bulls as opposed to proven bulls are used as sires, however, the Mendelian sampling effects are in fact less accurately estimated. As a result, truncation selection of young sires on genomic EBVs may increase the rate inbreeding. Hence, the effects of genomic selection and using young animals as parents on the rate of inbreeding needs further study.

A second question that dairy cattle breeding organizations face is how many bulls should still be progeny tested. This will depend on the future market share of proven bulls compared to young bulls, which indirectly depends on the rate of genetic gain and the number of bulls progeny tested.

The objective of this study was to assess the effects of reliability of genomic EBVs, the use of young animals as parents and the number of progeny test bulls on the rate of genetic gain, the rate of inbreeding, and relative merit of proven bulls compared to young bulls.

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Material and methods

Breeding scheme design. A closed nucleus breeding scheme was simulated in which 1000 males and 1000 females were born annually. All females and 200 progeny tested males per year obtained a phenotype when they were 3 and 5 yr old, respectively. Each year, 200 females and 20 males were selected as parents for the next generation based on their EBV. In scenario Age35 only dams ≥3 yr and sires ≥5 yr were selected, whereas in scenario Age11 dams and sires were ≥1 yr. The breeding program was run for 50 yr, where the first 25 yr were based on scenario Age35 without genomic information.

Simulation of breeding values. True breeding values for one total merit index for animal *i* were simulated as $u_i = u_{i,M} + u_{i,P}$, where $u_{i,M}$ is the marker component than can be explained without error by genetic markers, and $u_{i,P}$ is the polygenic component that cannot be explained by genetic markers but needs to estimated from phenotypes and pedigree. The marker component $u_{i,M}$ is simulated as $u_{i,M} = \frac{1}{2}u_{i,M,sire} + \frac{1}{2}u_{i,M,dam} + u_{i,M,MS}$, where $u_{i,M,sire}$ and $u_{i,M,dam}$ are the marker breeding values of the sire and dam of animal *i*, respectively, and $u_{i,M,MS}$ is the marker Mendelian sampling effect, which was drawn from a univariate normal distribution: $u_{i,M,MS} \sim \mathrm{N}\left(0, \frac{1}{2}\left(1 - \frac{1}{2}\left(F_{i,sire} + F_{i,dam}\right)\right)\sigma_M^2\right)$, where $F_{i,sire}$ and $F_{i,dam}$ are the pedigree inbreeding coefficients of the sire and dam of animal *i* (Meuwissen and Luo, 1992), respectively, and σ_M^2 was the variance of the marker components in the base population which was equal to *M* = 0, 20, 40, 60, 80, and 100% of the total genetic variance which was equal to $\sigma_A^2 = 1$. The polygenic components ($u_{i,P}$) were simulated similarly, where the variance of the polygenic components was $1 - \sigma_M^2$.

Breeding value estimation. Phenotypes of cows and progeny tested bulls were simulated with a heritability of 0.3 and 0.9, respectively. EBV were computed as the sum of the marker component $u_{i,M}$, which was known, and the BLUP estimate of the polygenic component ($\hat{u}_{i,P}$) which was obtained by solving the model $\mathbf{y} - \mathbf{u}_M = \mathbf{u}_P + \mathbf{e}$, using iteration on data. Note that for *M* = 40%, the reliability for a young animal whose parents have a phenotype and no other information is 0.40 + (1-0.40) x (0.30+0.90)/4 = 0.58, which approximates the reliabilities of genomic EBVs that have been observed in cross-validation studies in dairy cattle (VanRaden et al. (2009)).

Alternative breeding schemes. Alternative scenarios differed by the minimum age of parents (Age35 vs. Age11) and the variance that can be explained by genetic markers (*M*). Furthermore, the number of progeny test bulls was reduced from the default value of 200 per year to 100, 50 or 25 per year. Breeding schemes were compared by the rate of genetic gain, rate of inbreeding, and the difference in genetic merit between young bulls and proven bulls.

Results and discussion

Rate of genetic gain. The rate of genetic gain in the default scenario (Age35 with *M* = 0%) was 0.238 σ_A per year (Figure 1). The use of genomic information increased the rate of genetic gain with 30% to 0.309 σ_A per year (Age35 with *M* = 100%). When also animals ≥1 yr old were eligible to be selected as parents the rate of genetic gain was 0.292 σ_A per year without the use of genomic information (Age11 with *M* = 0%), but this increased to 0.704 σ_A per year when genomic information explained all genetic variance (Age 11 with *M* = 100%). The effects of using marker information and reducing the generation interval on the rate of genetic gain were consistent with Spelman et al. (1999) and Schrooten et al. (2005).

Rate of inbreeding. In the base scenario (Age35 with *M* = 0%), the rate of inbreeding was 0.18% per year (Figure 2). With a generation interval of 5.50 yr this corresponds to a rate of inbreeding of 1.00% per generation (Figure 2). Using genetic markers to pre-select young bulls before progeny testing decreased the rate of inbreeding to 0.42% per generation (Age35 with *M* = 100%). When animals ≥1 yr old were eligible for selection as parents (Age11), the rate of inbreeding was 3.15% per generation for *M* = 0% (generation interval 3.43 yr), whereas it decreased to 0.63% per generation for *M* = 100% (generation interval 2.12 yr).

The number of sires was varied between 5 and 200 and the rate of genetic gain was obtained from the scenario that gave a rate of inbreeding of 1% per generation (data not shown). Compared to using 20 sires (Figure 1), the rate of genetic gain with a fixed rate of inbreeding was 0.05 σ_A per year lower for Age11 with *M* = 0% and 0.03 0.05 σ_A per year higher for both Age 11 and Age35 with *M* = 100%.

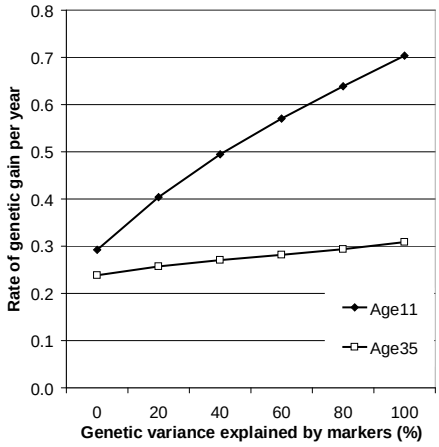

Figure 1: Rate of genetic gain per year (in σ_A) when minimum age was 3 and 5 yr for dams and bulls (Age35) or 1 and 1 yr (Age11)

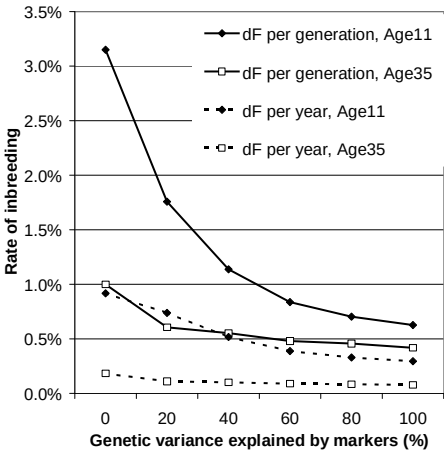

Figure 2: Rate of inbreeding per year and per generation when minimum age was 3 and 5 yr for dams and bulls (Age35) or 1 and 1 yr (Age11)

Relative merit of proven bulls vs. young bulls. The number of proven bulls in the top 25 EBV list was 67% for Age35 with M = 0%, but this decreased to 0% for Age35 with M = 100% and also for Age11 with $M \geq 40\%$. In scenario Age11, the top 25 EBV young bulls were superior to the top 25 EBV proven bulls for all M, and the difference in average EBV increased from 0.16 σ_A for M = 0% to 2.74 σ_A for M = 100% (Table 1).

Number of progeny tested bulls. Reducing the number of progeny tested bulls from 200 to 25 decreased the rate of genetic gain by 14% and 5% for Age35 with M = 0% and Age11 with M = 0%, respectively. For larger M, the effects on rate of genetic gain were smaller or absent. When 25 instead of 200 bulls were progeny tested, some superior bulls were not tested anymore, which increased the difference with the top 25 young bulls from 0.16 to 0.66 σ_A for M = 0% (Table 1). For larger M, however, the probability of not testing superior bulls decreased so progeny testing less bulls had only small effects on the average EBV of the top 25 proven bulls. Therefore, in genomic selection schemes with short generation intervals and medium to high reliabilities of genomic EBVs, the number of progeny test bulls can be greatly reduced.

Table 1: Difference in average EBV of top 25 proven bulls and top 25 young bulls (in σ_A) for scenario Age11 (animals ≥1 yr were used as parents) when the number of progeny tested bulls was decreased from 200 to 25.

% variance expl.	Number of progeny tested bulls			
by markers (M)	200	100	50	25
0	-0.16	-0.29	-0.42	-0.66
20	-0.75	-0.85	-1.00	-1.18
40	-1.30	-1.36	-1.47	-1.62
60	-1.83	-1.84	-1.91	-2.01
80	-2.31	-2.32	-2.32	-2.39
100	-2.74	-2.74	-2.73	-2.73

Conclusions

Genomic selection in combination with a reduced generation interval may double the rate of genetic gain while keeping the rate of inbreeding per generation constant. Young bulls will be superior to proven bulls, and the number of progeny test bulls can be greatly reduced.

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