Effects of Alternative Genomic Selection Breeding Schemes on Genetic Gain in Dairy Cattle

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Introduction

Using genomic selection, breeding values are estimated based on thousands of SNP-markers in stead of pedigree information (Meuwissen et al (2001)). Replacing conventional breeding values by breeding values based on genomic information can increase genetic gain without increasing the rate of inbreeding, due to an increased accuracy of breeding values (Daetwyler et al. (2007)). Using conventional BLUP breeding values, a high accuracy is dependent on own or progeny records, but genomic breeding values can be accurately estimated at any stage of the animal's life. For dairy cattle, this provides an opportunity to shorten the generation interval by omitting the progeny test and select elite sires at a younger age (Schaeffer (2006)). Another possibility is to use genomic selection to pre-select young bulls for progeny testing, which will leave the generation interval unaffected but may increase the genetic gain through an increased genetic level of young bulls entering the progeny test (Dekkers and Hospital, 2002).

When genomic selection is to be implemented, SNP-effects are estimated based on a reference population, typically consisting of thousands of animals with reliable phenotypic information that are genotyped. Every generation of selection will change linkage disequilibrium between the SNP-markers and surrounding QTL, causing SNP-effects to change over time (Muir (2007)). Re-estimation of SNP-effects is therefore important to keep the accuracy of the genomic breeding values from declining over time (Sonesson and Meuwissen (2009)). In a breeding program, this re-estimation can be performed by adding newly genotyped animals to the reference population, after they have got own or progeny records. For dairy cattle, if genomic selection is used for pre-selection of young bulls, all the progeny tested sires can be added to the reference population, while if the genomic breeding values are used to select elite sires directly, only the elite sires will have progeny and be added to the reference population. This difference in numbers of genotyped bulls with progeny will affect the accuracy of the genomic EBV, and thus genetic gain. In this study, stochastic simulations were used to compare the genetic gain over time when using genomic selection for pre-selection of young bulls and using genomic selection to select elite sires to a conventional breeding scheme, based on the breeding structure of the Norwegian Red population.

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Material and methods

Simulation of a base population. A population with effective population size of 200 was simulated for 2000 generations as described in Sonesson and Meuwissen (2009). The genome was simulated to consist of 30 pairs of chromosomes, each with a size of 1M. Polymorphisms and recombinations were simulated as in Sonesson and Meuwissen (2009), and 100 SNP per chromosome were randomly selected as QTL. QTL-effects were sampled from a gamma-distribution with a shape parameter of 0.4 and a scale parameter of 1.66 (Hayes and Goddard (2001)). 100 males and 100 females from the last generation of this simulation was randomly mated to create generation 0, consisting of 3000 animals. The following generations were simulated according to the breeding schemes described below.

Breeding schemes. In all the tested breeding schemes, 1500 females were selected, based on conventional BLUP breeding values, as elite dams and mated to elite sires. This gave a selection fraction of cows of 8%, similar to the Norwegian Red population. The elite matings resulted in 750 male calves and 750 female calves born. The bull calves were regarded selection candidates and genotyped in the schemes involving genomic selection. Random cows were selected among the best 90% of the cow population to be mated to elite sires and produce commercial replacement heifers in addition to the females born from elite matings. Females were selection candidates at 2 years of age, and remained candidates until they passed 6 years of age. From the age of 3, a random third of the cows was culled each year.

In the conventional breeding scheme, 125 young bulls were pre-selected for progeny testing based on BLUP breeding values, and 12 elite sires were selected after the sires got their progeny test results. Two genomic breeding schemes for selection of bulls were compared to the conventional breeding scheme. Genomic selection was used for pre-selection of young bulls for progeny testing (PS) or for selection of elite bulls directly at 3 years of age (GS). Using PS, the bulls were pre-selected at 2 years of age, based on genomic breeding values. The pre-selected bulls were progeny tested and were selection candidates for elite sires at 6 years of age. Using PS, pre-selection was based on genomic breeding values, but selection fractions remained unchanged from the conventional scheme, where young bulls were preselected on their pedigree index before entering the progeny test. Using GS, 20 elite sires were selected, to achieve approximately the same rate of inbreeding as with the other schemes. Each selection scheme was run for 19 years and replicated 100 times.

Estimation of breeding values. It was assumed that the 3000 animals in generation 0 had progeny test results available, which reflects the situation in dairy cattle where a historical population of progeny tested bulls is used as an initial training population to estimate SNP-effects. SNP-effects were estimated using the BLUP-method (Meuwissen et al. (2001)). Thereafter, the SNP-effects were re-estimated annually, including newly genotyped sires with progeny in the training population. Genomic breeding values of genotyped bulls that had not got any progeny yet were estimated as the sum of the estimated SNP-effects. True breeding values were calculated as sum of QTL-effects and phenotypes were simulated by adding a random error term, sampled from the normal distribution (Sonesson and Meuwissen (2009)). The genetic variance was set to 30, and the error variance to 170, to obtain a heritability of 0.15, which is approximately the heritability of the total merit index for dairy cattle. The accuracy of the genomic breeding values was estimated as the correlation

between estimated genomic breeding values and true breeding values. All cows were given a phenotypic record at 3 years of age, while each bull that had offspring got a progeny test record at 6 years of age.

Results and discussion

PS and GS resulted in an increased rate of inbreeding of 13% and 18%, respectively, compared to the conventional scheme. Figure 1 shows the accumulated genetic gain from year 10 to 19 after the start of the simulation.

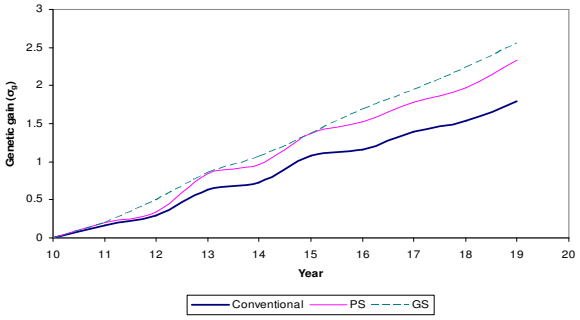

Figure 1: Accumulated genetic gain from year 10 to 19 after the start of the simulation, measured in genetic standard deviations. The conventional scheme uses only BLUP breeding values. PS uses genomic selection for pre-selection of young bulls and GS uses genomic selection for selection of elite sires at a younger age.

GS gave the highest genetic gain, mainly due to the reduced generation interval. This effect was however partly compensated by a lower selection intensity, due to more selected elite sires and partly by a lower accuracy of the breeding values. Figure 2 shows that GS gave a reduction in accuracy of the genomic breeding values over time and lower accuracy than PS. This can be explained by the shortened generation interval of GS, combined with fewer sires with progeny every year, compared to PS.

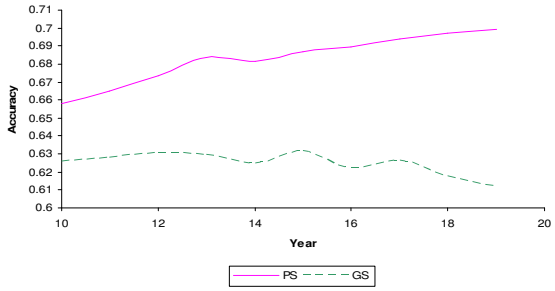

Figure 2: Accuracy of the genomic breeding values from year 10 to 19 after the start of the simulation. PS uses genomic selection for pre-selection of young bulls and GS uses genomic selection for selection of elite sires at a younger age. The re-estimation of SNP-effects is based on the availability of newly genotyped bulls with progeny test records.

The benefit of omitting the progeny test became lower than what has been reported in deterministic studies (Schaeffer (2006); König et al. (2009)). In deterministic studies, accuracies of genomic breeding values are assumed fixed, while in this study the accuracy was dependent on the breeding scheme. The schemes were therefore not compared at the same accuracy, but at the accuracies achieved when other assumptions were equal. When omitting the progeny test, the accuracy of the genomic breeding values becomes more important than when genomic selection is used for pre-selection, as they represent the accuracy of the breeding values used to market the bulls. A low accuracy of the elite sires' breeding values can cause a higher variation in performance between the elite sires and a higher risk of single sires to perform poorly.

Conclusion

The highest genetic gain was achieved by omitting the progeny test (GS), due to the reduced generation interval, i.e. genetic gain was 46% higher than that of a conventional scheme. However, the difference between GS and PS was smaller than the difference between PS and the conventional breeding program. About 2/3 of the additional gain that can be achieved by GS was also achieved by PS. Using genomic selection to pre-select young bulls for progeny testing could be a way to implement genomic selection without completely restructure the breeding scheme.

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