



Genomic selection strategies in a small dairy cattle population evaluated for genetic gain and profit

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ABSTRACT

The objective of this study was to evaluate a genomic breeding scheme in a small dairy cattle population that was intermediate in terms of using both young bulls (YB) and progeny-tested bulls (PB). This scheme was compared with a conventional progeny testing program without use of genomic information and, as the extreme case, a juvenile scheme with genomic information, where all bulls were used before progeny information was available. The population structure, cost, and breeding plan parameters were chosen to reflect the Danish Jersey cattle population, being representative for a small dairy cattle population. The population consisted of 68,000 registered cows. Annually, 1,500 bull dams were screened to produce the 500 genotyped bull calves from which 60 YB were selected to be progeny tested. Two unfavorably correlated traits were included in the breeding goal, a production trait ($h^2 = 0.30$) and a functional trait ($h^2 = 0.04$). An increase in reliability of 5 percentage points for each trait was used in the default genomic scenario. A deterministic approach was used to model the different breeding programs, where the primary evaluation criterion was annual monetary genetic gain (AMGG). Discounted profit was used as an indicator of the economic outcome. We investigated the effect of varying the following parameters: (1) increase in reliability due to genomic information, (2) number of genotyped bull calves, (3) proportion of bull dam sires that are young bulls, and (4) proportion of cow sires that are young bulls. The genomic breeding scheme was both genetically and economically superior to the conventional breeding scheme, even in a small dairy cattle population where genomic information causes a relatively low increase in reliability of breeding values. Assuming low reliabilities of genomic predictions, the

optimal breeding scheme according to AMGG was characterized by mixed use of YB and PB as bull sires. Exclusive use of YB for production cows increased AMGG up to 3 percentage points. The results from this study supported our hypothesis that strong interaction effects exist. The strongest interaction effects were obtained between increased reliabilities of genomic estimated breeding values and more intensive use of YB. The juvenile scheme was genetically inferior when the increase in reliability was low (5 percentage points), but became genetically superior at higher reliabilities of genomic estimated breeding values. The juvenile scheme was always superior according to discounted profit because of the shorter generation interval and minimizing costs for housing and feeding waiting bulls.

Key words: genomic selection, genomic breeding scheme, dairy cattle, small population

INTRODUCTION

Combining information from pedigree and SNP markers leads to increased reliabilities of genomic EBV (**GEBV**) compared with parent average estimates (Hayes et al., 2009b). With increased reliability, young bulls (**YB**) become more competitive relative to progeny-tested bulls (**PB**) in populations with considerable genetic gain. Thus, several studies have shown that higher genetic gain can be achieved if young males without progeny performance are used as parents for the next generation (de Roos et al., 2011; Buch et al., 2012). In the pre-genomic era, conventional breeding schemes were characterized by long generation intervals. Now, cattle breeding organizations move toward breeding schemes with more intensive use of YB as bull sires and for inseminations of cows, partly because of higher reliability of genomic predictions and partly because of reduced cost when keeping fewer waiting bulls. Furthermore, the cost of genotyping has decreased, which has made it even more feasible to genotype more selection candidates followed by increased selection intensity for the YB selection pathway.

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The number of genotyped reference bulls with daughter proofs is the most important factor in determining reliabilities of genomic predictions for selection candidates (Goddard and Hayes, 2009). However, for small dairy cattle populations, the number of potential reference bulls is limited. Hence, the gain from using genomic information is low (Pryce et al., 2011). A gain in reliability of 4 percentage points was estimated in the Danish Jersey breed (Thomasen et al., 2012) based on a reference population of 1,000 bulls, whereas a gain of 20 percentage points was obtained in the Nordic Holstein breed (Lund et al., 2011) based on a larger European Holstein reference population consisting of nearly 20,000 bulls.

Most of the simulation studies on genomic selection published to date have focused on optimization of genomic breeding schemes in larger cattle populations (for a review, see Pryce and Daetwyler, 2012). Because genomic information adds less to reliabilities in smaller populations, we expect that conclusions from studies for larger populations might not apply to smaller populations. For example, annual genetic gain increases more with intensive use of YB because the reliability of genomic predictions increases (Buch et al., 2012). Hence, a key design parameter for such a small breeding scheme is what proportion of YB is optimal to maximize annual genetic gain, as we expect PB to remain competitive with YB.

The main objective of this paper was to evaluate different genomic selection schemes by changing the proportion of genomically selected YB among both bull sires and cow sires with different amounts of genomic information. We hypothesized that increased genomic information in the form of higher reliabilities of genomic predictions would interact positively with more widespread use of YB in the genomic breeding scheme. The second objective was to compare the default genomic breeding scheme to the conventional breeding scheme. The primary evaluation criterion for the comparison of the breeding schemes was annual monetary genetic gain (AMGG), and discounted profit (DP) was used as an indicator of the economic outcome of the breeding scheme. Furthermore, the balance of AMGG for a production trait and a functional trait is presented.

MATERIALS AND METHODS

Experimental Design

Three overall breeding designs were compared: (1) a progeny testing scheme without use of genomic information (conventional scheme), (2) a juvenile scheme with genomic information where bulls are used before progeny information is available (turbo scheme), and

(3) a scheme that is intermediate in terms of using both young and progeny tested bulls (hybrid scheme).

The main objective was investigated by varying parameters affecting annual genetic gain in the hybrid scheme: (1) increase in reliability due to genomic information, (2) number of genotyped bull calves, (3) proportion of bull dams mated with YB, and (4) proportion of cows mated with YB.

The population structure, parameters, and breeding schemes were chosen to mimic practically feasible options for the Danish Jersey cattle population, being representative of a small dairy cattle population.

Hybrid Scheme

The hybrid breeding scheme reflected the current breeding scheme with use of genomic information as carried out in the Danish Jersey breed. The general structure of the hybrid breeding scheme is illustrated in Figure 1. The population consisted of 68,000 cows with records. The 1,500 cows with the highest EBV according to the breeding goal were screened as bull dam candidates. It was assumed that these cows were inseminated with relevant bull sires to produce the 500 bull calves that would be genotyped. Sixty YB were selected for progeny testing according to their GEBV. These YB were randomly used for 50% of inseminations in the cow population. This corresponds to Danish Jersey farmers' current use of YB for insemination of cows. The 15 YB with the highest GEBV were selected as bull sires and mated to 25% of the bull dams. Finally, 4 PB were selected both for use as bull sires, contributing 75% of the inseminations, and for inseminations in the cow population, contributing 50% of the inseminations. These PB were available because a waiting bull system is run until their daughter proofs are available. For this breeding scheme, 4 key parameters were varied, as follows.

Increase in Reliability of GEBV. The value of genomic information was measured by the increase of reliability of genomic predictions compared with the reliability of the parent average. An increase in reliability of 5 percentage points was used in the reference scenario. This is approximately the current gain observed by including the genomic information in Danish Jersey (Thomasen et al., 2012). The reliability was increased in steps of 5 percentage points up to the level of the reliability of a progeny-tested bull, which was obtained by adding 40 percentage points to the reliability of the parent average. In this study, the EBV for the PB only included the information from daughter records and no genomic information.

Number of Genotyped YB. The number of genotyped bull calves was varied from 500 to 2,000 to evaluate the effect of increasing the selection intensity of bull

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