Response using genome-wide selection in dairy cattle breeding schemes

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Introduction

Schaeffer (2006) predicted that genetic change obtained from a genome-wide selection scheme would be two times greater than that achieved through a traditional progeny test scheme. The results were based on a trait with a heritability of 0.40 and the predictions were made by altering the accuracy of selection and the generation interval in three of the four pathways of selection. An accuracy of of genomic evaluation of 75% (i.e. reliability of 56%) was assumed. All sires of bulls (SB) and sires of cows (SC) were one year of age at selection and dams of bulls (DB) were 15 months at selection.

The assumptions used by Schaeffer (2006) don't accurately reflect what can be achieved in most national breeding programmes. Semen production of bulls increases with age (Foote et al. (1977)) and one-year-old bulls would not likely be able to produce enough semen to service a national population of dairy cows. The work was done using an across-the-board value of 75% for the accuracy of evaluation. This value was based on the simulation work of Meuwissen et al. (2001) where evaluations included only genomic information. In New Zealand, blended breeding values are calculated using genomic and ancestral information. The reliability of the blended breeding values of young sires reached 60% (accuracy of 77%) only when the bulls were the progeny of proven sires (Harris and Johnson (2010)). Progeny of one-year-old sires would be less accurately evaluated than progeny of proven sires. Finally, no account was taken of the greater variability in response that would occur when using SB and SC that are evaluated at 75% accuracy versus that obtained when using more accurately evaluated proven sires. This study uses stochastic simulation to examine the impact of genomic selection on genetic gain in a population that reflects the dairy cattle population in New Zealand. Responses obtained in schemes using genome-wide selection are compared to those obtained using traditional progeny testing.

Methods

The traditional progeny testing (PT) scheme modeled in this study was based on the system practiced at LIC prior to the possibility of enhancing estimated breeding values (EBV) using genomic information. In this system, one-year-old bulls are first used as SC in dedicated sire proving (SP) herds . The number of SP herds is the same as the number of young sires sampled. Proven sires (aged five to seven) are used as SC in the remaining herds. Schemes in which genome-wide selection was modeled (i.e. genomic selection (GS) schemes) used genomic

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information to increase the accuracy of the EBV of selected one-year-old bulls, thereby more accurately identifying bulls to enter the SP herds.

With the traditional PT breeding scheme, there were two types of herds. SP, in which SC were one-year-old bulls and the remaining herds in which SC were proven bulls. The latter herds will be referred to as other (OT) herds. The GS schemes had SP and OT herds as well as dedicated genomically enhanced (GE) herds, in which the SC, aged two and three years, selected on their genomically enhanced EBV, were used.

The study was undertaken using a trait with a heritability of 35% and a repeatability of 60%. The initial (base generation) genetic standard deviation (gSD) was set to 10. Stochastic simulation was used to generate true breeding values (TBV) and a series of EBV for all animals. An EBV was generated by adding a random deviate to an animal's TBV that reflected the accuracy of evaluation. For bulls without progeny or genomic information, the EBV was calculated as the parent average (EBV_{PA}). Progeny test EBV (EBV_{PT}) were calculated for sires with progeny. In the PT scheme, young bulls were selected on EBV_{PA} and the older bulls were selected on EBV_{PT}. In the GS schemes, young bulls for the SP herds were chosen using a multi-stage selection approach. The reliabilities of the EBV increased with each successive stage of selection. Two-stage and three-stage schemes were modeled. In all cases, the first stage involved selecting bulls based on their EBV_{PA}. In subsequent stages, selection was on EBV that incorporated genomic information. Two levels of genomic information were considered; one from a primary screen and the other from a secondary screen, with the secondary screen having a higher reliability (i.e. providing more information) than the primary screen. EBV that incorporate genomic information will be referred to as genomic BV (GBV); GBV_1 and GBV_2 denote GBV that incorporate information from the primary and secondary screen, respectively. In the three-stage selection scheme, the second stage involved selecting on GBV_1 and the third stage involved selecting on GBV_2. No primary screening was used in the two-stage selection scheme; the second stage of selection was done on GBV_2. Bulls selected at the final stage were used in the SP herds. The reliability of the primary and secondary screens was 0.20 and 0.36, respectively. The reliabilties of the genomic screens were combined with the reliabilities of the EBV_{PA} in the manner outlined by Harris and Johnson (1998) to obtain the reliabilities of the the GBV. The reliabilities of the EBV_{PA}, GBV_1, GBV_2 and EBV_{PT} were 0.35, 0.44, 0.52 and 0.85, respectively.

The lactating cow population consisted of 400,000 cows, aged two to six years. Cows were equally distributed over 1000 herds and age class within herd. Thus, each herd contained 400 lactating cows, with 80 cows in each age class. This herd size is representative of the herd size in New Zealand. Seasonal mating/calving was assumed (as is the case in N.Z.) so entire age classes joined the herd (and left the herd) at the same time. Twenty cows in each age class were randomly selected to produce the next generation of heifers each year. Cows had no genomic information. Three levels of lactation information were modeled; no information (i.e. one year old), one lactation and two or more lactations. Reliabilities of EBV of one-year-old cows in SP herds were 0.225 and 0.269 without and with genomic information on their sires, respectively. Reliabilities of EBV of one-year-old cows in GE and OT herds were 0.269 and 0.35, respectively. Reliabilities of two-year-old cows ranged from 0.453 (SP herds with no genomic information on sires) to 0.519 (OT herds). The reliability of evaluation was 0.568

for all cows older than two years.

In the PT scheme, DBs were obtained through contract mating (CM) where 100 cows were randomly selected from the best 500 (aged one to five years) in the population (based on EBV). In the GS schemes, young bulls were generated from CM cows as well as selected from the wider population of bulls born each year. The latter will be referred to as farmer sourced (FS) bulls. They came from the top 25% of herds (based on mean EBV). A random sample of the cows (aged one to five years) from the top half of the cows in these herds were used to generate FS bulls. This process resulted in 25,000 young sires being available as FS. The young sires from CM and FS were ranked on their EBV_{PA}. GBV were then used to rank the selected animals.

For the traditional scheme, 100 young sires were generated each year. In the GS schemes, between 40 and 80 young sires were generated each year for use in the SP herds. For all GS schemes, there were 200 GE herds. Hence, there were between 720 and 780 OT herds.

The GS schemes differed in the number of bulls selected at each stage of selection. The three-stage selection schemes used primary genomic screening on 1000 bulls (that had been selected on EBV_{PA}) and secondary genomic screening on 200 bulls (that had been selected on GBV_1). The third stage of selection was based on GBV_2. Because the reliability of the young bulls in GS schemes is higher than that in the PT scheme, fewer young bulls need to be tested in the SP herds. Schemes where 40, 60 and 80 young sires were selected to enter the SP herds were modeled. Two two-stage selection scenarios were modeled. One used secondary genomic screening on 500 young bulls and the other used secondary genomic screening on 1000 young bulls. In both cases, 60 young bulls were selected to enter the SP herds. Table 1 shows the five GS schemes investigated.

Table 1: GS schemes - numbers of bulls that received primary (1°) and secondary (2°) genomic screens and numbers of bulls selected for use in the SP herds.

Scheme	1°	2°	SP
GS40	1000	200	40
GS60a	1000	200	60
GS80	1000	200	80
GS60b	0	500	60
GS60c	0	1000	60

The numbers of SB and SC used varied across breeding scheme and herd type. In the PT scheme there were 5 SB and 10 SC selected each year. In the GS schemes, 10 SB were chosen. A greater number of SB were chosen for the GS schemes than for the PT schemes because the greater risk associated with selecting bulls with lower reliability. Fifteen sires were selected as SC for GE herds. In the PT scheme, only proven bulls were selected as SB. In the GS schemes, SB were selected from animals aged two to seven.

Simulations were run for 100 years (base population was year 1) and replicated 30 times.

Results and discussion

The results for numbers of sires selected in each age group are averaged over years 25 to 100. As expected in a population undergoing selection, SB and SC were selected more frequently from the younger age groups than the older age groups. In the PT scheme, sires aged 5, 6 and 7 produced, on average 3.0, 1.4 and 0.6, respectively, of the out of 5 of the SB. In the GS schemes, sires aged two and three years produced 8.3 and 1.4 of the 10 SB, respectively. A similar trend was found for SC. In PT schemes, 5.8, 2.8 and 1.4 SC were selected from age groups five, six and seven respectively. For the GS schemes, 7.0 and 2.3 of the 10 SC used in OT herds were selected from ages five and six, respectively. Of the 15 SC used in the GE herds, 12.7 and 2.3 came from ages two and three, respectively.

In the GS schemes, CM contributed, on average, 2.5 (1.5 in GS40) bulls to the team that entered the SP herds. In the GS60 and GS80 schemes, approximately 75%, 24% and 1% of the bulls came from GE, SP and COM herds, respectively. The corresponding figures for the GS40 scheme were 79%, 18% and 3%.

Genetic gain is calculated using the TBV of the young bulls that were selected for use in the SP herds. The results were almost identical to those obtained using the cows born in each year. The rate of genetic gain, expressed in gSD units, averaged over the bulls born in years 10 to 100, was 0.249 in the PT scheme. The rate of gain in the GS40 scheme was 0.319. For all other GS schemes, the rate of genetic gain was 0.322. Hence, the rate is 29% higher in the GS schemes than the PT scheme. There was no benefit is using a primary and secondary screen.

Conclusions

The results show that the rate of genetic gain in GS schemes is higher than that obtained using the PT scheme. However, the results are considerably lower than that predicted by Schaeffer (2006). The upper limit of the annual rate of gain was 0.322 gSD, regardless of the GS scheme used. This study has some limitations. Only five schemes were investigated. When using primary and secondary screening, a set number of animals were selected at the first two stages of selection. Just the number selected at the third stage differed. Only two scenarios were investigated in which secondary screening alone was used. Alternative scenarios, where different numbers of young bulls are evaluated and selected at each stage of selection, and where higher reliabilities of secondary genomic screening are modeled, should be examined.

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