

Potential benefits of genomic pre-selection of candidate bulls for genetic superiority and inbreeding rate of dairy cows in a progeny testing program: a simulation study

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Abstract

This study was performed to investigate the effect of pre-selection programme of young bull on genetic progress and inbreeding rate of dairy cows in a progeny test program. Dairy cattle population, consisted of 10,000 dairy cows across 5 parities, was simulated. Two scenarios including conventional progeny testing program (Con-PT) and genomic pre-selection of young bulls (Gen-PT) were compared. Genetic superiority and inbreeding were studied during 20 years of selection in four distinct paths of selection. Genetic superiorities of 62.5, 37.9, 27.3, and 89.5% were observed for active sires, young bulls, bull dams, and milking cows in Gen-PT relative to Con-PT scenario respectively. The result showed the large amounts of genetic gain are obtained via genomic pre-selection of young bulls in all paths of selection. Means of inbreeding were obtained 2.34 ± 0.44 and $3.36 \pm 0.63\%$ for Con-PT and Gen-PT scenarios respectively ($P < 0.001$). The average annual rate of inbreeding increased at a constant rate from 11th to 25th year at annual rate of 0.38 ± 0.01 and $0.54 \pm 0.004\%$ in Con-PT and Gen-PT scenarios respectively. According to different generation intervals in scenarios (5 years in Con-PT versus 3 years in Gen-PT), inbreeding rates per generation were 1.9 and 1.62% respectively, indicating less inbreeding rate per generation in Gen-PT in comparison to Con-PT. In general, use of genomic values for pre-selection of young bulls can be applied as an effective tool to enhance genetic merit of cows in dairy cattle breeding schemes.

Keywords: Genetic gain; pre-selection; progeny test; genomic; dairy cow

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Introduction

Thanks to genomic advancements, selection of animals based on their genomic values can lead to a tremendous improvement in dairy cattle populations. Genomic selection provides an opportunity to select animals at the time of birth with reliabilities varied from 0.27 to 0.67 (Hayes et al., 2009). In genomic selection, it is possible to select animals with no phenotypes based on their genomic values (Schaeffer, 2006; Hayes et al., 2009). Although, genomic selection may result in elimination of structured progeny testing program of bulls, however, it can be applied as an effective tool to increase efficiency of progeny testing

programs prior to widespread use of genomic bulls. Long waiting period around 5 years is needed to prove young bulls using their daughters' performance. Reliabilities of genomic values are higher than breeding values estimated via best linear unbiased prediction (BLUP) especially, for young animals (Schaeffer, 2006). Higher reliabilities tempt breeders to select young animals as parents resulting in shorter generation intervals. Therefore, the possibility of young bull pre-selection based on their genomic values can shorten generation intervals in this path of selection and lead to more rate of genetic gain in dairy cows. Furthermore, reduction in the rate of inbreeding as an extra benefit can be achieved by using genomic selection (Daetwyler et al., 2007).

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The present study aimed to assess the effect of young bull pre-selection based on genomic values on genetic gain and inbreeding rate of cows in a progeny testing program.

Materials and Methods

A simulation program described previously by Khalajzadeh et al. (2012) was followed in this study.

Population structure

A structure of dairy cattle population described by Kuhn et al. (1994) was used to create a virtual population of dairy cows. Population was consisted of 10,000 dairy cows across 5 parities with the respective constant proportion of 0.33, 0.26, 0.19, 0.14 and 0.08 for parity 1 to 5. Simulation was started with 1,000 males and 5,000 heifers varied by age from 1 to 12 months. All 5,000 heifers were mated with males randomly when they were 14 month old. Of the heifers mated annually, 3,300 heifers could make first lactation record according to constant proportion of 0.33 for first parity cows. Similar pattern was performed for subsequent parities to create whole population with the mentioned constant proportions. The population size was kept constant to avoid extra genetic gain due to population growth. The simulation was continued during first five years without any selection. Progeny testing program was begun at the end of fifth year by selecting the first list of bull dams and continued for the subsequent 20 years. Further information concerning population structure and mating programs could be found in Khalajzadeh et al. (2012).

Simulated trait

Model including average as a constant (μ), additive genetic effect (a), and residual effect (e) was used for simulating of milk production. Additive genetic and residual effects were supposed to distributed normally with mean 0 and corresponding genetic and residual variances. In this research, heritability, additive genetic variance, and residual variance were considered to be 0.25, 150,000 (kg^2), and 450,000 (kg^2) respectively. True breeding values of offspring were simulated by averaging additive genetic effects of parents plus with Mendelian sampling effect (Kennedy et al., 1988). Inbreeding coefficients for each animal were calculated using the algorithm of Meuwissen and Luo (1992).

Scenarios

Two scenarios including a conventional progeny testing program (Con-PT) and genomic pre-selection progeny testing program (Gen-PT) were compared. In Con-PT scenario, the first list of bull dams was selected at the end of fifth year. Bull dams should be mated with 50% of best active sires to produce young bulls. Annually, 10 and 20 bulls were selected as active sires

and young bulls respectively. Semen of young bulls was available at 1 year of age and young bulls after producing 60 daughters entered waiting period until the records of daughters were completed. We supposed five years are needed for daughter's record completion indicating, five years are required for promoting young bulls to active sires. It means the first list of active sires was prepared at the end of tenth year. In Gene-PT scenario, young bulls did not enter progeny testing program and were selected based on genomic values at the time of birth. It means top ten of young bulls could be introduced as active sires when they became mature. In the current study, true breeding value was considered as selection criteria. The accuracies of selection were supposed to be 0.6 and 1 in female and male pathways (reliability of 0.36 and 1) respectively. Although selection of males with reliability of 1 is far from reality especially in genomic selection, we ideally supposed genomic values with perfect reliabilities are available to estimate maximum potential of genetic gain in genomic strategies.

Parameters

Genetic superiority as well as inbreeding was compared between scenarios from 11th to 25th year of selection. Each scenario was replicated 25 times and the presented results are averages over the 25 replicates. Genetic superiority was studied in four distinct path of selection including active sires, young bulls, bull dams, and milking cows. Genetic superiority was computed using formula 1.

$$\sum_{i=1}^{25} ((\text{GenPT} - \text{ConPT}) / \text{ConPT}) \times 100 \quad (1)$$

Statistical analysis

Scenarios were compared statistically using a paired samples t-test by SPSS 19 software. Mean differences were considered to be significant at $P < 0.05$.

Results and Discussion

Genetic superiority

Genetic superiorities of 62.5, 37.9, 27.3, and 89.5% were observed for active sires, young bulls, bull dams, and milking cows in Gen-PT relative to Con-PT scenario respectively (Table 1). The result showed that large amount of genetic gain can be achieved via genomic pre-selection of young bulls in all paths of selection. Numerically, huge genetic superiorities were observed during first three years in milking cow pathway. These large numbers were produced due to division operation. For instance, true breeding values of milking cows in Con-PT and Gen-PT were 69 and 304 kg for 11th year of selection respectively (Fig. 1). Consequently, replacing the numbers in formula 1 will result in a large superiority. Differences in genetic merit of milking cows between

Table 1: Genetic superiority (%) of Gen-PT relative to Con-PT scenario in four distinct paths of selection from 11th to 25th year of selection

Year	Active sires	Young bulls	Bull dams	Milking cows
11	34.1	44.7	16.6	340.6
12	75.7	27.5	19.7	210.1
13	90.4	26.5	17.9	112.5
14	99.6	33.1	20.7	82.5
15	67.9	38.1	24.5	69.9
16	54.2	39.5	27.2	62.9
17	53.6	38.4	28.5	59.7
18	55.6	37.6	28.3	55.9
19	58.4	38.2	29.7	53.2
20	60.6	37.9	30.3	51.2
21	60.9	39.7	31.1	49.7
22	60.1	41	32.4	48.9
23	56.6	42.3	33.5	48.6
24	55.7	42.5	33.9	48.6
25	54.1	41.9	35.1	48.9
Overall ¹	62.5±4.1	37.9±1.3	27.3±1.5	89.5±20.9

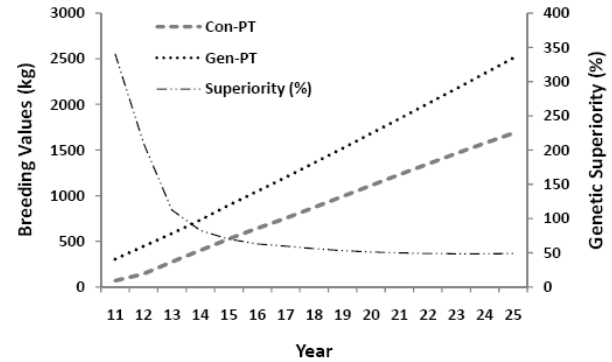
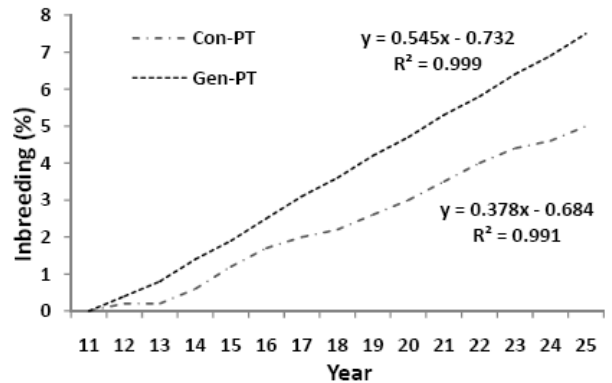
¹-Genetic superiority in all pathways differ significantly with Con-PT ($P < 0.001$); Con-PT = conventional progeny testing program; Gen-PT = genomic pre-selection progeny testing program

corresponding years increased gradually over time however, genetic superiority remained nearly constant (Fig. 1). Similar patterns were also observed in other paths of selection.

Four main factors that affect selection response in animal breeding schemes are selection intensity, reliability, additive genetic standard deviation, and generation interval (Falconer and MacKay, 1996). Of the mentioned factors, the primary ones affecting selection response in this research are generation interval and additive genetic standard deviation. Selection intensity and reliability are similar between strategies whereas a reduction in generation interval (due to young bull pre-selection) and standard deviation (Bulmer, 1971) are expected. Pre-selection of young bulls can cause a noticeable reduction in generation interval almost from 5 to 3 years, resulting in nearly 1.5 fold increase in selection response (equivalent to 50% superiority). Negatively, reduction in standard deviation can decrease selection response but its effect is much less than generation interval. Additionally, increase in the genetic merit of males can extend to female animals because of better parent selection.

Mc Hugh et al. (2011) simulated a population of approximately 3500 female and 500 male representation of the Irish national herd to assess benefits of genomic selection.

Results from this simulation showed that the inclusion of female phenotypic and genomic information can lead to an almost three fold increase in the rate of genetic gain. Previous simulation studies have shown an annual rate of genetic gain in genomic selection schemes

**Fig. 1: Genetic progress (kg) and genetic superiority (%) of milking cows in Con-PT and Gen-PT relative to Con-PT from 11th to 25th year of selection; Con-PT = conventional progeny testing program; Gen-PT = genomic pre-selection progeny testing program****Fig. 2: Inbreeding trend (%) of milking cows in Con-PT and Gen-PT scenarios from 11th to 25th year of selection; Con-PT = conventional progeny testing program; Gen-PT = genomic pre-selection progeny testing program**

of between 49 and 231% (Buch et al., 2010; Lillehammer et al., 2010; Pryce et al., 2010) relative to traditional BLUP breeding programs. De Roos et al. (2011) stated using genetic markers to preselect young bulls before progeny testing increased the rate of genetic gain by 30%. Moreover, co-selection of cows and bulls of 1 year old based on genetic markers increased genetic progress by 195%. Pre-selection of young bulls based on their genomic values without their progeny's performance information can cause noticeable genetic progress in compared with conventional progeny testing program (Schrooten et al., 2005).

To sum up, genomic pre-selection of young bulls can be used as a powerful tool for genetic improvement of cows without the need for genotyping of large numbers of animals.

Inbreeding

Means of inbreeding obtained were 2.34 ± 0.44 and $3.36 \pm 0.63\%$ for Con-PT and Gen-PT scenarios

respectively ($P < 0.001$). The average annual rate of inbreeding increased at a constant rate from 11th to 25th year at annual rate of 0.38 ± 0.01 and $0.54 \pm 0.004\%$ in Con-PT and Gen-PT scenarios respectively (Fig. 2).

The result showed genomic pre-selection of young bull increases annual inbreeding rate in population regardless of generation length. According to less generation length for Gen-PT, it is necessary to implement more precise criteria to compare inbreeding between scenarios, that is, inbreeding rates per generation. With a generation interval of 5 years, annual inbreeding rate in Con-PT (0.38% per annum) corresponds to a rate of 1.9% per generation. Corresponding value for Gen-PT (0.54% per annum) with a generation interval of 3 years is computed 1.62% per generation indicating less inbreeding per generation in Gen-PT scenario. De Roos et al. (2011) showed using genetic markers to pre-select young bulls before progeny testing increased annual rate of inbreeding from 0.18 to 0.52% whereas inbreeding rate reduced from 1 to 0.42% per generation. In sum, although pre-selection of young bulls increases inbreeding rate per annum less inbreeding can be expected per generation.

Conclusions

This simulation study showed pre-selection of young bull increases significantly genetic merit of cows in all paths of selection ranging from 27 to 89%. The rate of inbreeding per annum increases significantly from 0.38 to 0.54% but decreases from 1.9 to 1.62% per generation. It seems that use of genomic values for pre-selection of young bulls can be applied as an effective tool to enhance genetic merit of cows in dairy cattle breeding schemes.

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