Genomic selection for any dairy breeding program via optimised investment in phenotyping and genotyping

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Abstract

Background: This paper evaluates the potential of maximizing genetic gain in dairy cattle breeding programmes by optimizing investment into phenotyping and genotyping. Conventional dairy breeding programmes focus on phenotyping selection candidates or their close relatives to increase selection accuracy, since this is the main driver of genetic gain and quality assurance for producers. Genomic selection decoupled phenotyping and selection and through this enabled increased genetic gain per year compared to the conventional selection. However, genomic selection requires a large initial investment, which limits the adoption of genomic selection for some breeding programmes. The aim of this study was to evaluate the potential of maximizing genetic gain by optimizing investment into phenotyping and genotyping in in a case-study and to provide suggestions for other dairy breeding programmes.

Methods: We simulated a case-study of a small dairy population with a number of scenarios under equal available resources. The conventional progeny testing scenario had 11 phenotype records per lactation. In genomic scenarios, we reduced phenotyping to collect between 10 and 1 record per lactation and invested the saved resources into genotyping. We tested these scenarios in settings with or without initial training population for genomic selection.

Results: Reallocating a part of phenotyping resources to genotyping increased genetic gain compared to the conventional scenario regardless of the amount and relative cost of phenotyping, and the availability of initial training population. We further increased the genetic gain by increasing investment in genotyping, despite reduced phenotyping, with high-genotyping scenarios not even using the total available resources. Compared to the conventional scenario, genomic scenarios also increased accuracy for young non-phenotyped male and female candidates, and cows.

Conclusions: This study shows that breeding programmes should optimise investment into phenotyping and genotyping to maximise return on investment. We argue that phenotyped animals

should be extensively genotyped to increase the impact of phenotyping investments. These conclusions suggest that any dairy breeding programme can implement genomic selection without increasing the level of investment.

Background

This paper evaluates the potential of maximizing genetic gain in dairy cattle breeding programmes by optimizing investment into phenotyping and genotyping. All breeding programmes strive to maximize genetic gain, which is a function of selection intensity, accuracy of selection, genetic variation, and generation interval. The conventional dairy breeding programme uses a long and expensive progeny testing, which limits selection intensity. This programme allocates the majority of resources into phenotyping to increase the accuracy of sire selection, since this is the main driver of genetic gain. Genomic selection [1, 2] (Meuwissen et al., 2001; Schaeffer, 2006), on the other hand, achieves genetic gain mainly through substantially reduced generation interval, increased selection intensity on the male side, and increased accuracy of selection for young animals [2, 3] (Schaeffer, 2006; Obšteter et al., 2019). Despite lower accuracy of sire selection compared to the conventional progeny testing, genomic selection doubles the rate of genetic gain per year in dairy cattle [4](Wiggans et al., 2017).

All breeding programmes operate with a certain amount of resources allocated between breeding activities with the aim to maximise return on investment. Genomic selection is now a de-facto standard in well-resourced breeding programmes, but is still challenging to implement for some breeding programmes. The major hurdle is the large initial investment in genotyping to establish a training population, though updating this population can also be challenging. These breeding programs need to evaluate priorities and could optimise phenotyping and genotyping to maximise return on investment.

The accuracy of conventional pedigree-based estimates of breeding values increases with increasing heritability and increasing number of phenotype records per animal or its closest relatives (e.g., [5]Mrode, 2005). To illustrate, assume a female-expressed trait with the heritability of 0.25 and progeny testing in a population with 100 sires each tested on 100 daughters (10,000 cows in total). Collecting 10 phenotype records per daughter gives the accuracy of 0.98 for progeny tested sires, 0.86 for cows, and 0.66 for non-phenotyped progeny. If we decrease the number of phenotype records per daughter to five, two, or one, the accuracy respectively decreases to 0.97, 0.96, or 0.93 for sires; to 0.81, 0. 70, or 0.62 for cows; and to 0.64, 0.59, or 0.56 for non-phenotyped progeny. This example shows diminishing returns with repeated phenotype records and a scope for optimizing return on investment. Namely, at the extreme we reduced phenotyping 10x, which reduced accuracy only for 0.04 in sires and 0.10 in non-phenotyped progeny.

We could invest the resources saved from reducing the number of phenotype records per daughter into phenotyping more daughters. Assuming resources for 100,000 phenotypes and decreasing the number of phenotype records per daughter to five, two, or one respectively enables phenotyping 200, 500, or 1,000 daughters per sire (100 sires). This change increases accuracy for sires to 0.99 in all cases, barely increases accuracy for cows, and respectively increases accuracy for non-phenotyped progeny to 0.64, 0.61, or 0.59.

The accuracy of genome-based estimates of breeding values also increases with increasing heritability and increasing number of phenotype records per genotyped animal, but also with increasing training population of phenotyped and genotyped animals, decreasing genetic distance between training and prediction individuals, and decreasing number of effective genome segments [6–10](Daetwyler et al. 2008; Goddard, 2009; Habier et al., 2010; Clark et al, 2011; Goddard et al., 2011). The latter dictates linkage-disequilibrium between markers and causal loci, which drives accuracy of genomic evaluation and prediction. Recombination, mutation, migration, drift, and selection change linkage-disequilibrium and decrease the accuracy of genomic prediction across generations, particularly when the training population is not continually updated [1, 8, 11, 12] (Meuwissen et al., 2001; Calus, 2010; Habier et al., 2010; Wolc et al., 2011).

Following the previous example, assume 10,000 effective genome segments, trait heritability of 0.25, and a training population of 10,000 cows. Recording 10 phenotype values per cow gives the heritability of phenotype for training population of 0.78 and genomic prediction accuracy of 0.68

for non-phenotyped progeny [6](Daetwyler et al, 2008). Reducing the number of phenotype records per cow to five, two, or one respectively reduces the heritability of phenotype for training population to 0.66, 0.50, or 0.40, and genomic prediction accuracy to 0.64, 0.58, or 0.53. This example again shows diminishing returns with replicated phenotyping and a scope for optimizing return on investment also with genomic breeding programmes. Namely, at the extreme we reduced phenotyping 10x, which reduced genomic prediction accuracy only for 0.11. Previous studies also explored the value of adding a record to the training population when a number of records is already available [13, 14] (Bijma, Recio). They concluded, that accuracy has a diminishing return relationship with increasing the number of records in the training population, hence additional phenotype is most valuable when the training population is small.

We could invest the resources saved from reducing the number of phenotype records per daughter into genotyping. If we could increase the number of genotyped and phenotyped cows from 10,000 to 20,000, 50,000, or 100,000, each respectively phenotyped with five, two, or one record, we would respectively increase the genomic prediction accuracy to 0.77, 0.86, or 0.91. While these genomic prediction accuracies are lower than with progeny testing, shorter generation interval enables larger genetic gain per unit of time [2](Schaeffer, 2006).

However, the above calculations assume we have resources to genotype and phenotype large numbers of cows. In reality, breeding programmes consist of individuals with only phenotype, genotype, or both types of information. To handle this, we can use single-step genomic prediction that combines all phenotypic, pedigree, and genomic information and in turn increases prediction accuracy even further [15–17](Gao et al., 2012, Gray et al., 2012; Lourenco et al., 2015).

The above examples indicate that repeated phenotyping could be an internal financial reserve that enables any dairy breeding programme to implement genomic selection. In dairy breeding the most repeatedly and extensively recorded phenotypes are milk production traits. There are different milk recording methods that differ in the recording responsibility, sampling scheme, recording and sampling frequency, and the number of milkings per day [18](ICAR, 2017). The recording interval ranges from daily recording to recording every nine weeks, which translates to between 310 and 5 records per lactation. The different recording methods have different costs, which also vary considerably between recoding systems, countries, and even their regions. For example, some organizations require payment of a participation fee plus the cost per sample, while others include the fee in the sample cost, or cover the costs in other ways.

The aim of this study was to evaluate the potential of maximizing genetic gain by optimizing investment into phenotyping and genotyping in dairy breeding programmes. Since milk recording is an example of a repeated phenotype with diminishing returns, we aimed to optimize investment into milk recording and genotyping. To this end we have compared a dairy breeding programme with conventional progeny testing and genomic testing under equal available resources. To implement genomic selection we reduced the number of milk records per cow per lactation and invested the saved resources into genotyping. We compared these strategies in case-study with a small cattle breeding programme where implementing genomic selection is challenging. The results show that reallocating a part of phenotyping resources to genotyping increases genetic gain regardless of the cost and amount of genotyping, and the availability of initial training population. The genetic gain also increases with increasing investment into genotyping, despite reduced phenotyping.

Methods

The study aimed to evaluate the effect of different investment into phenotyping and genotyping with a simulation of a case-study of a small dairy breeding programme. The simulation mimicked a real dairy cattle population of ~30,000 animals analysed in our previous study [3]Obšteter et al. (2019). We evaluated 36 genomic scenarios against the conventional scenario, all with equal amount of available resources, but varying extent of phenotyping and genotyping. The conventional scenario implemented progeny testing and collected 11 phenotype records per lactation, while genomic scenarios reduced phenotyping and invested saved resources to genotyping. The genomic scenarios differed in i) the number of phenotype records per cow per lactation; ii) the relative cost of phenotyping and genotyping; and iii) the availability of an initial training population. All tested scenarios were compared based on their genetic gain and accuracy of selection.

Simulation of the base population, phenotype and historical breeding

The simulation mimicked a small dairy cattle breeding programme of ~30,000 animals with ~10,500 cows, where introduction of effective genomic selection is challenging. We use this population as a case-study to optimize investment into phenotyping and genotyping. The breeding programme aimed to improve dairy performance, which we simulated as a single polygenic trait. For this we used a coalescent process to simulate whole-genome comprised of 10 cattle-like chromosomes, each with 10^8 base pairs, 1,000 randomly chosen causal loci, and 2,000 randomly chosen marker loci. We sampled the effects of causal loci from a normal distribution and calculated animal's breeding value (a_i) for dairy performance (y_{ijkl}). We assigned permanent environment (p_i), herd (h_j), herd-year (hy_{jk}), herd-test-day (htd_{jkl}), and residual environment (e_{ijkl}) effects to the trait:

$$y_{ijkl} = a_i + p_i + h_j + hy_{jk} + htd_{jkl} + e_{ijkl}.$$

We sampled the permanent environment effects from a normal distribution with zero mean and variance equal to the additive genetic variance (σ^2_A). We sampled herd, herd-year, and herd-test-day effects each from a normal distribution with zero mean and variance of 1/3 σ^2_A. Finally, we sampled residual environment effects from a normal distribution with zero mean and variance of σ^2_A. This sampling scheme gave a trait with heritability 0.25 and repeatability of 0.50. With the simulated genome and phenotype architecture we have initiated the dairy cattle breeding programme and ran it for 20 years of conventional selection with progeny-testing based on 11 cow phenotype records per lactation. The detailed parameters of the simulation are described in [3]Obšteter et al. (2019). In summary, in the breeding programme we selected 3,849 out of 4,320 new-born females as cows and 139 as bull dams over their second, third, and fourth lactation. We generated 45 male calves from elite matings and out of these chose 8 for progeny testing of which 4 were eventually selected as elite sires. We made all selection decisions based on pedigree-based estimates of breeding values. The 20 years represented historical breeding and provided a starting point for evaluating future breeding scenarios, which we ran for additional 20 years.

Scenarios

We evaluated 36 genomic scenarios with varying the extent of phenotyping and genotyping against the conventional scenario. All scenarios had equal amount of available resources. The conventional scenario continued the breeding scheme from historical breeding. It used progeny testing and 11 phenotype records per lactation (named C11), corresponding to the standard ICAR recording interval of 4 weeks [18](ICAR, 2017). We assumed that this scenario represented the total amount of resources available for obtaining the data. We then created genomic scenarios that distributed the total resources between phenotyping and genotyping - we reduced phenotyping and invested the saved resources into genotyping. In the genomic scenarios we selected females as in the conventional scenario and males based on genomic prediction. We varied the number of genomically tested male candidates depending on the resources and always selected the best 5 as elite sires solely on genomic prediction. We evaluated the genomic scenarios under a range of factors: number of phenotype records per lactation, cost of genotyping, and the availability of an initial training population.

Genomic scenarios reduced phenotyping of the conventional scenario and varied the number of phenotype records per lactation between 10 and 1. The scenarios followed ICAR standards of 9, 8, and 5 records per lactation, corresponding to recording intervals of 5, 6, and 9 weeks. Additionally, we created three non-standard recording systems collecting 10, 2, and 1 records per lactation. We named the scenarios as "GX" with X being the number of records per lactation. The reduction in phenotyping and the relative cost of phenotyping to genotyping dictated the amount of saved resources and therefore the number of genotyped animals (Table 1). We invested the saved resources into genotyping females and males in ratio 7:1 based on our previous work [3] Obšteter et al. (2019). We genotyped first parity cows. This maximized the accuracy of genomic prediction, since it reduced the genetic distance between training and prediction population, prevented the loss of information due to culled heifers, and minimized the time to obtain a phenotype. If the available resources for genotyping females were larger than the cost of genotyping all first parity cows, we did not reallocate the excess of resources to male genotyping. To maximise the genetic gain, we genotyped male calves from elite matings and other high parent average matings.

Genomic scenarios next varied the relative cost of phenotyping ($P) to genotyping ($G). We compared the cost of one genotype to the cost of 11 phenotype records per lactation. Based on a survey of several breeding programmes, milk recording organizations, and genotyping providers we have considered three cost ratios of $P:$G: 2:1, 1:1, and 1:2. Following the survey, we also decreased the price of every additional milk recording, hence the first recording was the most expensive and the cost of each subsequent control was 95% of the preceding control.

Lastly, we created scenarios with and without an initial training population for genomic prediction. When we assumed an initial training population was available, we genotyped all active cows (10,653) and progeny tested sires (100) before the first genomic evaluation. When initial training population was not available, we yearly genotyped a designated number of first parity cows until the training population reached 2,000 cows. Once we reached this goal, we started to genotype both females and males as specified in Table 1. At that point we started genomic selection of males.

Estimation of breeding values

We selected the animals based on their estimated breeding values that we estimated with a pedigree or single-step genomic (Legarra et al., 2009) repeatability model with breeding value, permanent environment, and herd-year as random effects. We did not fit the herd-test-day effect as data structure of this small population did not enable its accurate estimation. We estimated breeding values once a year with blupf90 [19](Misztal et al, 2002) with default settings. In the estimation we included all available phenotype and pedigree records for all active, phenotyped, or genotyped animals and additional three generations of their ancestors. However, we used at most 25,000 genotyped animals due to a maximum number of animals allowed in the non-commercial software version. When we accumulated more than 25,000 genotyped animals, we removed the oldest animals in favour of the latest genotyped cows and male selection candidates.

Table 1. Number of genotyped animals per year by scenario and relative cost of phenotyping to genotyping.

	Scenario					
Relative cost	G10	G9	G8	G5	G2	G1
$P:$G = 1:2	160 F	350 F	590 F	1610 F	3230 F	3850 F
	22 M	50 M	85 M	235 M	465 M	565 M
$P:$G = 1:1	310 F	700 F	1180 F	3230 F	3850 F	3850 F
	45 M	100 M	165 M	465 M	925 M	1125 M
$P:$G = 2:1	620 F	1400 F	2360 F	3850 F	3850 F	3850 F
	90 M	295 M	335 M	925 M	1845 M	2245 M

Scenarios are named “G” for genomic, followed by the number of phenotype records per lactation. The number of phenotype records and the relative cost of phenotyping to genotyping ($P:$G) dictated the number of genotyped animals. We genotyped females (F) and males (M) in 7:1 ratio.

Analysis of scenarios

All scenarios had equal amount of available resources. We compared the scenarios based on their final genetic gain, which indicated return on investment, and accuracy of selection. We measured the genetic gain as an average true breeding value by year of birth and standardized it to have zero mean and unit standard genetic deviation in the first year of comparison. We measured the accuracy of breeding values as the mean correlation between true and estimated breeding values of the evaluation years. We measured the accuracy separately for four groups of animals: i) male candidates (genotyped and non-phenotyped); ii) sires (currently used in artificial insemination); iii) females candidates (non-genotyped non-phenotyped); and iv) cows (all active phenotyped cows and bull dams). We repeated simulation of the base population and each scenario 10 times and summarised them with mean and standard deviation across the replicates. We used Tukey's multiple comparison test to test the significance of the difference between means.

Results

Genomic scenarios increased the genetic gain compared to the conventional scenario regardless of the number of phenotype records per lactation, relative cost of phenotyping to genotyping, and the availability of an initial training population. Genomic scenarios with an existing initial training population increased the genetic gain of the conventional scenario by up to 143%, despite reduced phenotyping. The genetic gain further increased with increasing investment into genotyping, hence more animals genotyped. Compared to the conventional scenario, implementing genomic selection also increased the accuracy for non-phenotyped male and female candidates, and cows. Scenarios without an initial training population showed the same trends for genetic gain and accuracy. Although these scenarios had a slightly smaller genetic gain due to delayed implementation of genomic selection, they still increased the genetic gain of the conventional scenario by up to 134%.

Genetic gain with an initial training population

Table S1. Genetic gain by scenario, relative cost of phenotyping to genotyping, and availability of initial training population.

		Relative cost of phenotyping ($P) to genotyping ($G)		
	Scenario*	$P:$G = 1:2	$P:$G = 1:1	$P:$G = 2:1
	C11	$3.01_{0.22}^{a,A}$	$3.01_{0.22}^{a,A}$	$3.01_{0.22}^{a,A}$
With initial TP	G10	$5.43_{0.20}^{b,A}$	$5.41_{0.29}^{b,A}$	$6.50_{0.20}^{b,B}$
	G9	$5.58_{0.26}^{b,A}$	$6.30_{0.17}^{c,B}$	$7.02_{0.24}^{c,C}$
	G8	$6.35_{0.25}^{c,A}$	$6.62_{0.25}^{d,B}$	$7.02_{0.17}^{c,C}$
	G5	$6.78_{0.21}^{d,A}$	$7.07_{0.20}^{e,B}$	$\mathbf{7.26_{0.19}^{c,B}}$
	G2	$7.13_{0.29}^{e,A}$	$\mathbf{7.33_{0.26}^{e,A}}$	$\mathbf{7.28_{0.17}^{c,A}}$
	G1	$\mathbf{7.11_{0.16}^{e,A}}$	$\mathbf{7.27_{0.28}^{e,A}}$	$\mathbf{7.24_{0.22}^{c,A}}$
Without initial TP	G10	$3.93_{0.22}^{b,A}$	$4.54_{0.14}^{b,B}$	$5.61_{0.25}^{b,C}$
	G9	$4.64_{0.18}^{c,A}$	$5.75_{0.28}^{c,B}$	$6.52_{0.17}^{c,C}$
	G8	$5.61_{0.28}^{d,A}$	$6.24_{0.19}^{d\,B}$	$6.70_{0.25}^{cd,C}$
	G5	$6.43_{0.21}^{e,A}$	$6.90_{0.22}^{e,B}$	$\mathbf{7.05_{0.27}^{de,B}}$

G2	$6.81_{0.28}^{f, A}$	**$6.96_{0.17}^{e, A}$**	**$7.00_{0.30}^{de, A}$**
G1	**$6.78_{0.29}^{f,A}$**	**$6.92_{0.26}^{e, A}$**	**$7.01_{0.23}^{e,A}$**

*The table presents the means and standard deviations (subscript) across 10 replicates for the conventional (C) and genomic (G) scenarios, with numbers indicating the number of phenotype records per lactation. The scenarios in bold cells did not spend all the available resources. The table presents the results within three relative costs of phenotyping to genotyping ($P:$G). The genomic scenarios differ in the availability of the initial training population. Lower-case letters denote statistically significant differences between scenarios within the same $P:$G and upper-case letters between different $P:$G within the same scenario.

Table S2. Intensity of sire selection by scenario and relative cost of phenotyping to genotyping.

Scenario	Relative cost of phenotyping ($P) to genotyping ($G)		
	$P:$G = 1:2	$P:$G = 1:1	$P:$G = 2:1
C11	0.80	0.80	0.80
G10	1.32	1.71	2.02
G9	1.76	2.06	2.48
G8	1.99	2.27	2.52
G5	2.40	2.63	2.85
G2	2.63	2.86	3.11
G1	2.70	2.93	3.14

The scenarios are named C/G for conventional/genomic with numbers indicating the number of phenotype records per lactation.

With the same amount of available resources, genomic scenarios with an initial training population increased the genetic gain of the conventional scenario between 79% and 143%. The genetic gain increased with the increasing investment in genotyping, despite reduced phenotyping. We show this in Figure 1 and Table S1 with genetic gain by scenario and by relative cost of phenotyping to genotyping with an initial training population. We show the intensities of sire selection in Table S2. When the cost of phenotyping was the same as the cost of genotyping ($P:$G = 1:1), the genomic scenarios increased the genetic gain of the conventional scenario between 79% and 143%. By reducing the number of phenotype records from 11 (C11) to 10 per lactation (G10), we saved resources for genotyping 355 animals per year (310 cows and 45 male candidates). This small change increased the male selection intensity from 0.80 to 1.71 and increased the genetic gain by 79% (from 3.01 to 5.41). By reducing the phenotype records to nine or eight per lactation (G9 or G8), we respectively saved resources to genotype 800 or 1,345 animals per year, of which 100 or 165 were male candidates. This respectively increased the males selection intensity to 2.06 or 2.27, and genetic gain by 109% or 120% (from 3.01 to 6.30 or 6.62). We achieved the highest genetic gain, between 135% and 143% of the conventional scenario (between 7.07 and 7.33), when we collected five, two, or one phenotype records per lactation. In these three scenarios we saved resources for genotyping between 3,230 and 3,850 (all) cows and between 465 and 1,125 male candidates per year, and achieved the males selection intensity between 2.63 and 2.93.

We observed a similar trend for genetic gain when the cost of phenotyping was half or twice the cost of genotyping. Changing the relative cost of phenotyping to genotyping had the largest effect in the scenario with the smallest amount of genotyping (G10). In this scenario, when phenotyping was twice or half the cost of genotyping, we respectively saved resources for genotyping 182 or 710 animals, of which 22 or 90 were males, and increased the genetic gain for 80% (from 3.01 to 5.43) or 116% (from 3.01 to 6.50). When we maximized the investment into genotyping (G1), we genotyped all females at all three price ratios and between 565 and 2,245 male candidates. Correspondingly, we achieved a comparable genetic gain, between 136% and 143% of the conventional scenario, regardless of the relative cost of phenotyping to genotyping and different male selection intensities.

The high-genotyping scenarios achieved the observed genetic gain without using all the available resources (marked bold in Table S1). In these scenarios the resources designated to genotyping females exceeded the cost of genotyping all females. This made additional savings of between 85 (42) and 11,900 (23,800) genotypes (phenotypes).

In Figure 1 we also show the growth of the training population for genomic prediction. The training population started with a ~10,000 individuals and grew until reaching 25,000 individuals. However, the increase was not linear throughout generations, since the procedure for choosing the training animal changed when the size was to exceed 25,000 (only latest females and male candidates included).

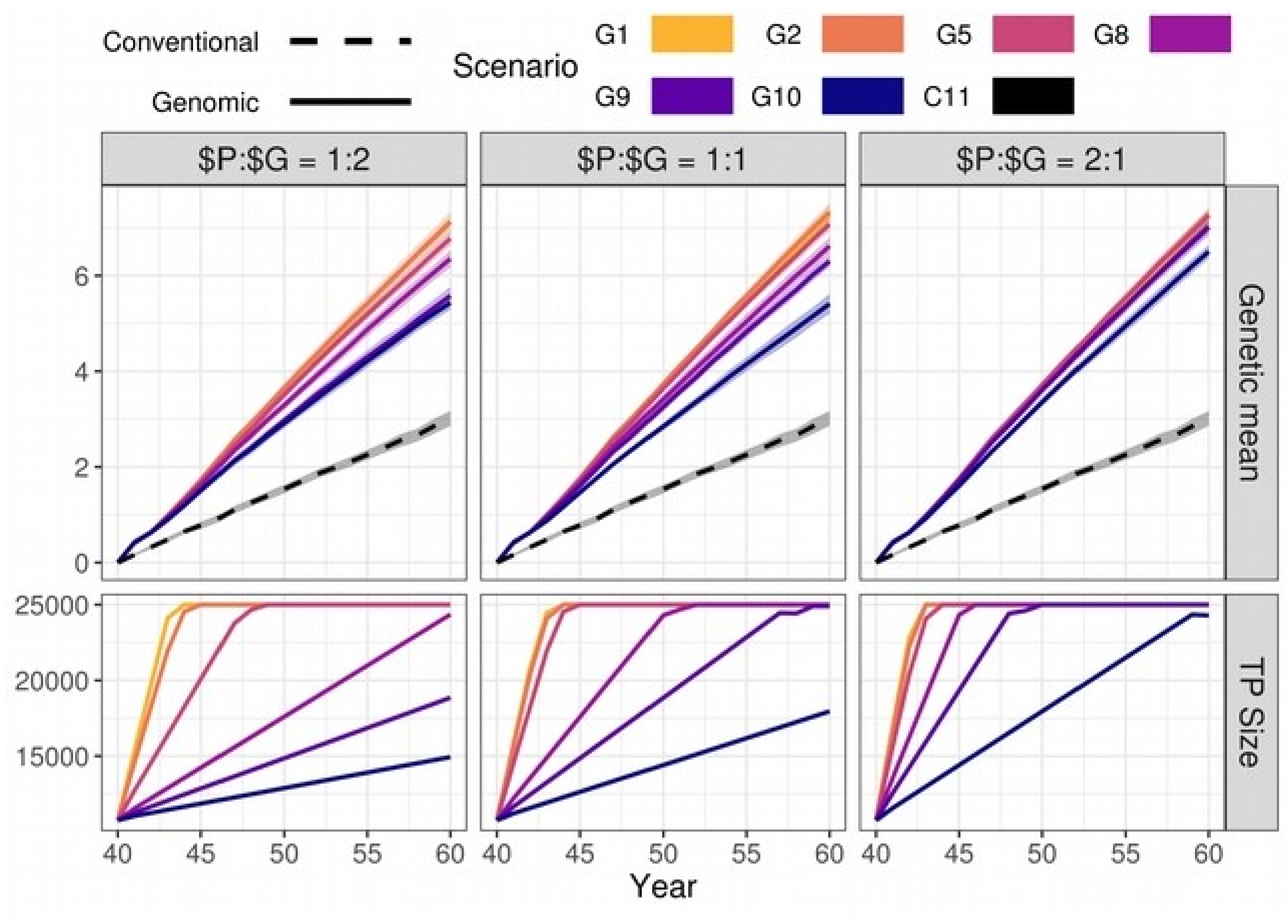

Figure 1 Genetic gain and training population size by scenario and relative cost of genotyping with initial training population (TP). The figure presents the means (lines) and 95% confidence intervals (polygons) across 10 replicates for the conventional (C) and genomic (G) scenarios, with numbers indicating the number of phenotype records per lactation. The figure presents the results within three relative costs of phenotyping to genotyping ($P:$G).

Accuracy with an initial training population

Table S3 Selection accuracy by scenario, relative cost of genotyping, and the availability of initial training population (TP).

Scenario	With initial training population			Without initial training population		
	Relative cost of phenotyping ($P) to genotyping ($G)					
	$P:$G = 1:2	$P:$G = 1:1	$P:$G = 2:1	$P:$G = 1:2	$P:$G = 1:1	$P:$G = 2:1
Male candidates						
C11, S1	$0.37_{0.04}^{a,A}$	$0.37_{0.04}^{a,A}$	$0.37_{0.04}^{a,A}$	$0.37_{0.04}^{a,A}$	$0.37_{0.04}^{a,A}$	$0.37_{0.04}^{a,A}$
C11, S2	$0.94_{0.01}^{b,A}$	$0.94_{0.01}^{b,A}$	$0.94_{0.01}^{b,A}$	$0.94_{0.01}^{b,A}$	$0.94_{0.01}^{b,A}$	$0.94_{0.01}^{b,A}$
G10	$0.89_{0.03}^{c,A}$	$0.90_{0.02}^{bc,AB}$	$0.91_{0.01}^{bc,B}$	$0.81_{0.03}^{b,A\,*}$	$0.84_{0.01}^{b,B\,*}$	$0.87_{0.01}^{b,C\,*}$
G9	$0.90_{0.03}^{bc,A}$	$0.91_{0.02}^{bc,A}$	$0.91_{0.01}^{bc,A}$	$0.85_{0.02}^{c,A\,*}$	$0.87_{0.01}^{bc,B\,*}$	$0.90_{0.01}^{bc,C\,*}$
G8	$0.91_{0.01}^{bc,A}$	$0.91_{0.01}^{bc,A}$	$0.91_{0.01}^{bc,A}$	$0.86_{0.01}^{cd,A\,*}$	$0.89_{0.01}^{c,B\,*}$	$0.90_{0.01}^{bc,B}$
G5	$0.91_{0.01}^{bc,A}$	$0.91_{0.00}^{bc,A}$	$0.91_{0.01}^{bc,A}$	$0.90_{0.01}^{d,A}$	$0.91_{0.01}^{c,A}$	$0.91_{0.01}^{c,A}$
G2	$0.91_{0.01}^{bc,A}$	$0.91_{0.00}^{bc,A}$	$0.90_{0.01}^{bc,A}$	$0.90_{0.01}^{d,A}$	$0.90_{0.01}^{c,A}$	$0.90_{0.01}^{bc,A}$
G1	$0.89_{0.01}^{c,A}$	$0.90_{0.01}^{c,A}$	$0.89_{0.01}^{c,A}$	$0.89_{0.01}^{cd,A}$	$0.89_{0.01}^{c,A}$	$0.89_{0.01}^{bc,A}$
Sires						
C11	$0.86_{0.05}^{a,A}$	$0.86_{0.05}^{a,A}$	$0.86_{0.05}^{a,A}$	$0.86_{0.05}^{a,A}$	$0.86_{0.05}^{a,A}$	$0.86_{0.05}^{a,A}$
G10	$0.75_{0.04}^{b,A}$	$0.75_{0.03}^{b,A}$	$0.73_{0.05}^{b,A}$	$0.67_{0.08}^{bc,A\,*}$	$0.68_{0.05}^{cde,A\,*}$	$0.67_{0.06}^{b,A\,*}$
G9	$0.76_{0.04}^{b,A}$	$0.72_{0.06}^{bc,AB}$	$0.69_{0.05}^{c,A}$	$0.70_{0.05}^{b,A\,*}$	$0.72_{0.05}^{bc,A}$	$0.71_{0.05}^{b,A}$
G8	$0.76_{0.03}^{b,A}$	$0.69_{0.05}^{cd,B}$	$0.68_{0.06}^{c,B}$	$0.71_{0.05}^{b,A\,*}$	$0.74_{0.05}^{b,A\,*}$	$0.70_{0.07}^{b,A}$
G5	$0.68_{0.07}^{c,A}$	$0.67_{0.08}^{de,A}$	$0.69_{0.04}^{c,A}$	$0.68_{0.05}^{bc,A}$	$0.69_{0.05}^{cd,A}$	$0.69_{0.03}^{b,A}$
G2	$0.67_{0.05}^{c,A}$	$0.67_{0.05}^{de,A}$	$0.67_{0.04}^{c,A}$	$0.65_{0.06}^{c,A}$	$0.64_{0.07}^{e,A}$	$0.69_{0.05}^{b,A}$
G1	$0.66_{0.06}^{c,A}$	$0.63_{0.05}^{e,A}$	$0.67_{0.04}^{c,A}$	$0.67_{0.04}^{bc,A}$	$0.67_{0.03}^{de,A}$	$0.69_{0.05}^{b,A}$
Female candidates						
C11	$0.45_{0.02}^{a,A}$	$0.45_{0.02}^{a,A}$	$0.45_{0.02}^{a,A}$	$0.45_{0.02}^{a,A}$	$0.45_{0.02}^{a,A}$	$0.45_{0.02}^{a,A}$
G10	$0.48_{0.01}^{ab,A}$	$0.48_{0.01}^{ab,A}$	$0.51_{0.01}^{b,B}$	$0.46_{0.02}^{ab,A\,*}$	$0.47_{0.02}^{ab,AB}$	$0.49_{0.01}^{b,B\,*}$
G9	$0.49_{0.02}^{b,A}$	$0.50_{0.01}^{b,B}$	$0.52_{0.01}^{b,C}$	$0.47_{0.02}^{ab,A\,*}$	$0.49_{0.02}^{bc,B}$	$0.52_{0.01}^{bc,C}$
G8	$0.51_{0.01}^{b,A}$	$0.51_{0.01}^{b,A}$	$0.54_{0.01}^{bc,B}$	$0.49_{0.02}^{bc,A\,*}$	$0.52_{0.01}^{cd,B}$	$0.53_{0.01}^{cd,C}$
G5	$0.51_{0.01}^{bc,A}$	$0.55_{0.01}^{c,B}$	$0.57_{0.01}^{c,C}$	$0.52_{0.01}^{cd,A}$	$0.55_{0.01}^{de,B}$	$0.57_{0.01}^{d,C}$
G2	$0.55_{0.01}^{cd,A}$	$0.57_{0.01}^{c,B}$	$0.57_{0.01}^{c,B}$	$0.55_{0.01}^{d,A}$	$0.56_{0.02}^{e,AB}$	$0.57_{0.01}^{d,B}$
G1	$0.56_{0.01}^{d,A}$	$0.56_{0.01}^{c,A}$	$0.56_{0.01}^{c,A}$	$0.55_{0.01}^{d,A}$	$0.56_{0.01}^{e,A}$	$0.56_{0.01}^{d,A}$
Cows						
C11	$0.48_{0.03}^{a,A}$	$0.48_{0.03}^{a,A}$	$0.48_{0.03}^{a,A}$	$0.48_{0.03}^{a,A}$	$0.48_{0.03}^{a,A}$	$0.48_{0.03}^{a,A}$
G10	$0.56_{0.02}^{b,A}$	$0.59_{0.02}^{b,B}$	$0.63_{0.01}^{b,C}$	$0.53_{0.01}^{b,A\,*}$	$0.56_{0.01}^{b,B\,*}$	$0.61_{0.01}^{b,C\,*}$
G9	$0.59_{0.03}^{bc,A}$	$0.63_{0.02}^{c,B}$	$0.70_{0.01}^{c,C}$	$0.57_{0.02}^{bc,A\,*}$	$0.62_{0.02}^{c,B}$	$0.68_{0.02}^{c,C\,*}$
G8	$0.62_{0.02}^{c,A}$	$0.67_{0.02}^{c,B}$	$0.74_{0.02}^{d,C}$	$0.60_{0.02}^{c,A\,*}$	$0.66_{0.01}^{d,B}$	$0.73_{0.02}^{d,C}$
G5	$0.70_{0.02}^{d,A}$	$0.77_{0.01}^{d,B}$	$0.79_{0.02}^{e,C}$	$0.69_{0.02}^{d,A}$	$0.76_{0.01}^{e,B}$	$0.78_{0.02}^{e,B}$
G2	$0.76_{0.02}^{e,A}$	$0.79_{0.02}^{d,B}$	$0.78_{0.01}^{e,AB}$	$0.76_{0.01}^{e,A}$	$0.77_{0.02}^{e,A\,*}$	$0.77_{0.01}^{de,A}$
G1	$0.77_{0.02}^{e,A}$	$0.77_{0.02}^{d,A}$	$0.77_{0.01}^{de,A}$	$0.76_{0.01}^{e,A}$	$0.76_{0.02}^{e,A}$	$0.76_{0.02}^{de,A}$

[*]The table presents the means and standard deviations (subscript) across 10 replicates for the conventional (C) and genomic (G) scenarios, with numbers indicating the number of phenotype records per lactation. The tables presents the results within three relative costs of phenotyping to genotyping ($P:$G). Conventional selection implemented two-stage selection for males, hence we present the accuracy of pre-selection of male candidates for progeny testing (S1) and the accuracy of selection of proven sires (S2). In genomic scenarios the male candidates were genotyped and non-phenotyped males. We also present the accuracy for sires currently used in artificial insemination (sires), for non-genotyped non-phenotyped females (female candidates), and for all active phenotyped cows and bull dams (cows). Lower-case letters denote statistically significant differences between scenarios within the same $P:$G and upper-case letters between different $P:$G within the same scenario. Stars denote statistically significant difference between corresponding scenarios with and without an initial training population.

Compared to the conventional scenario, genomic scenarios increased accuracy for young non-phenotyped male and female candidates, and cows, but decreased accuracy for sires. We show this in Figure 2 with the accuracy for male candidates, female candidates, sires, and cows with an initial training population and equal cost of phenotyping and genotyping. In Table S3 we compare accuracies at all three relative costs of phenotyping to genotyping. When the cost of phenotyping was equal to the cost of genotyping, the accuracy for young genomically tested male candidates ranged between 0.90 and 0.91 and did not depend on the amount of phenotyping and genotyping. This was 0.53-0.54 higher compared to the first stage of male selection in the conventional scenario (young un-phenotyped male candidates for progeny testing - same age point). However, this was 0.03 - 0.04 lower compared to the second stage of male selection in the conventional scenario (proven sires - same selection point). In contrast, the accuracy for sires decreased with reallocating phenotyping resources into genotyping. We observed the lowest accuracy for sires, 0.63, when we invested the most into genotyping (G1), and the highest, 0.75, when we invested the most into phenotyping (G10). Compared to the conventional scenario, the accuracy for proven sires in the genomic scenarios was between 0.11 and 0.23 lower. The accuracy for female candidates increased with increasing genotyping, despite reduced phenotyping. We observed the highest accuracy for female candidates, between 0.55 and 0.57, when we recorded five, two, or one phenotype record per lactation and invested the rest into genotyping. Compared to the conventional scenario, the genomic scenarios increased the accuracy for female candidates between 0.03 and 0.11. The accuracy for cows followed the same trends, but with higher values. We observed the highest accuracy for cows, between 0.77 and 0.79, by collecting five, two, or one phenotype record per lactation and investing the rest in genotyping. Compared to the conventional scenario, genomic scenarios increased the accuracy for cows between 0.11 and 0.29.

Changing the relative cost of phenotyping to genotyping affected primarily the accuracy for female candidates and cows. We observed that in the majority of scenarios the accuracy increased with decreasing the relative cost of genotyping, which enabled genotyping more animals. We observed the largest difference of 0.06 for female candidates and 0.12 for cows when we changed the relative cost of phenotyping from half to twice the cost of genotyping. Changing the relative costs, however, did not change the trends.

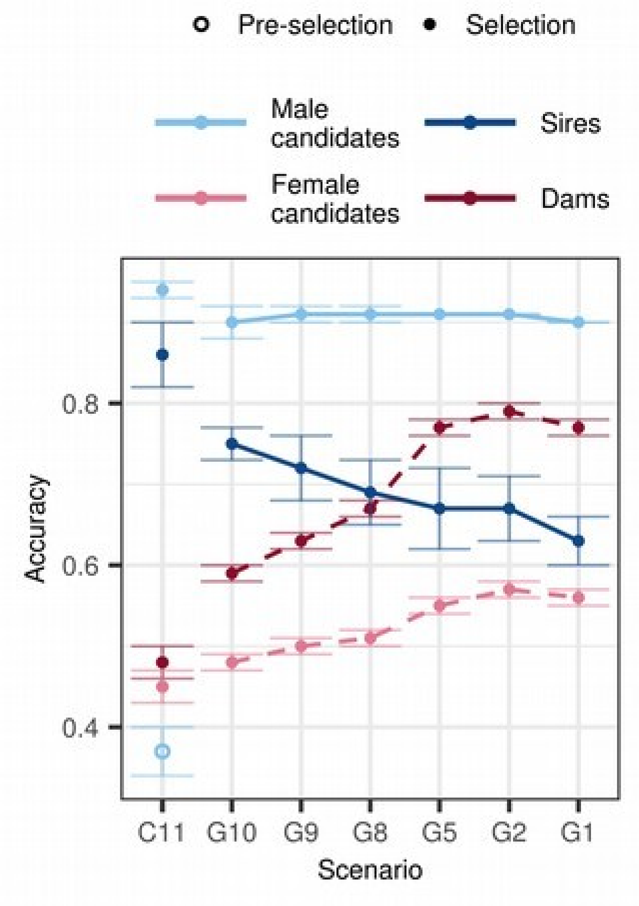

Figure 2 Accuracy by scenario with initial training population and equal cost of phenotyping and genotyping. The figure presents the means (lines) and 95% confidence intervals (error bars) across 10 replicates for the conventional (C) and genomic (G) scenarios with numbers indicating the number of phenotype records per lactation. Conventional selection implemented two-stage selection for males, hence we present the accuracy of pre-selection of males for progeny testing (empty point) and the accuracy of selection of proven sires (solid point).

Genetic gain and accuracy without an initial training population

Genetic gain

When an initial training population was not available, we increased the genetic gain of the conventional scenario between 31% and 134% by optimizing investment in phenotyping and genotyping. We show this in Figure 3 with the genetic gain, training population size, and accuracy by scenario without an initial training population and equal cost of phenotyping and genotyping.

The observed trends were in line with what we observed with an initial training population, that is, increasing genotyping increased genetic gain despite reduced phenotyping. However, all corresponding scenarios achieved between 2% and 28% smaller genetic gain than when an initial training population was available. We show this in Tables S1 that compare the genetic gain of all scenarios.

When the cost of phenotyping was equal to the cost of genotyping, genomic scenarios increased the genetic gain of the conventional scenario between 51% and 131%. Compared to when we had an initial training population, the corresponding scenarios achieved between 2% and 16% lower genetic gain. We observed the largest difference in the scenario that invested the least into genotyping (G10). In this scenario we needed six years to build an adequate training population and implement genomic selection, since we only genotyped 355 cows per year. Increasing the investment into genotyping decreased this difference. We observed the smallest difference in the scenario that collected two phenotype records per lactations (G2) and implemented genomic selection in the first evaluation year.

Changing the relative cost of phenotyping to genotyping did not change the overall trend, only the level of genetic gain in the low-genotyping scenarios. When the cost of phenotyping was half the cost of genotyping, the genomic scenarios increased genetic gain of the conventional scenario between 31% and 126%. The corresponding scenarios achieved between 4% and 28% lower genetic gain than when we had an initial training population. When the cost of phenotyping was twice the cost of genotyping, the genomic scenarios increased the genetic gain of the conventional scenario between 86% and 133%. The corresponding scenarios achieved between 3% and 14% lower genetic gain than when we had an initial training population.

Accuracy

As when we had an initial training population, genomic scenarios without an initial training population increased the accuracy for non-phenotyped male and female candidates, and cows. We show this in Figure 3 with the accuracy without an initial training population and equal cost of phenotyping and genotyping. In Table S3 we compare the accuracies of all scenarios. When the cost of phenotyping was the same as the cost of genotyping, the accuracy for male candidates ranged between 0.84 and 0.91. In contrast to scenarios with initial training population, the accuracy increased with increasing the investment into genotyping, hence was significantly lower in the scenario that invested the least into genotyping. The accuracy for sires ranged between 0.64 and 0.74. Contrary to when we had an initial training population, we observed no clear trend of either increasing or decreasing accuracy. For female candidates the accuracy ranged between 0.47 and 0.56, and for cows between 0.56 and 0.76. For female candidates and cows the accuracies followed the trends of when we had an initial training population, where increasing genotyping increased the accuracy.

As in the scenarios with an initial training population, changing the relative cost of phenotyping to genotyping affected the accuracy for female candidates and cows, but also male candidates. Here, decreasing the relative cost of genotyping, and genotyping more animals, increased the accuracy in the majority of the scenarios, particularly the low-genotyping ones.

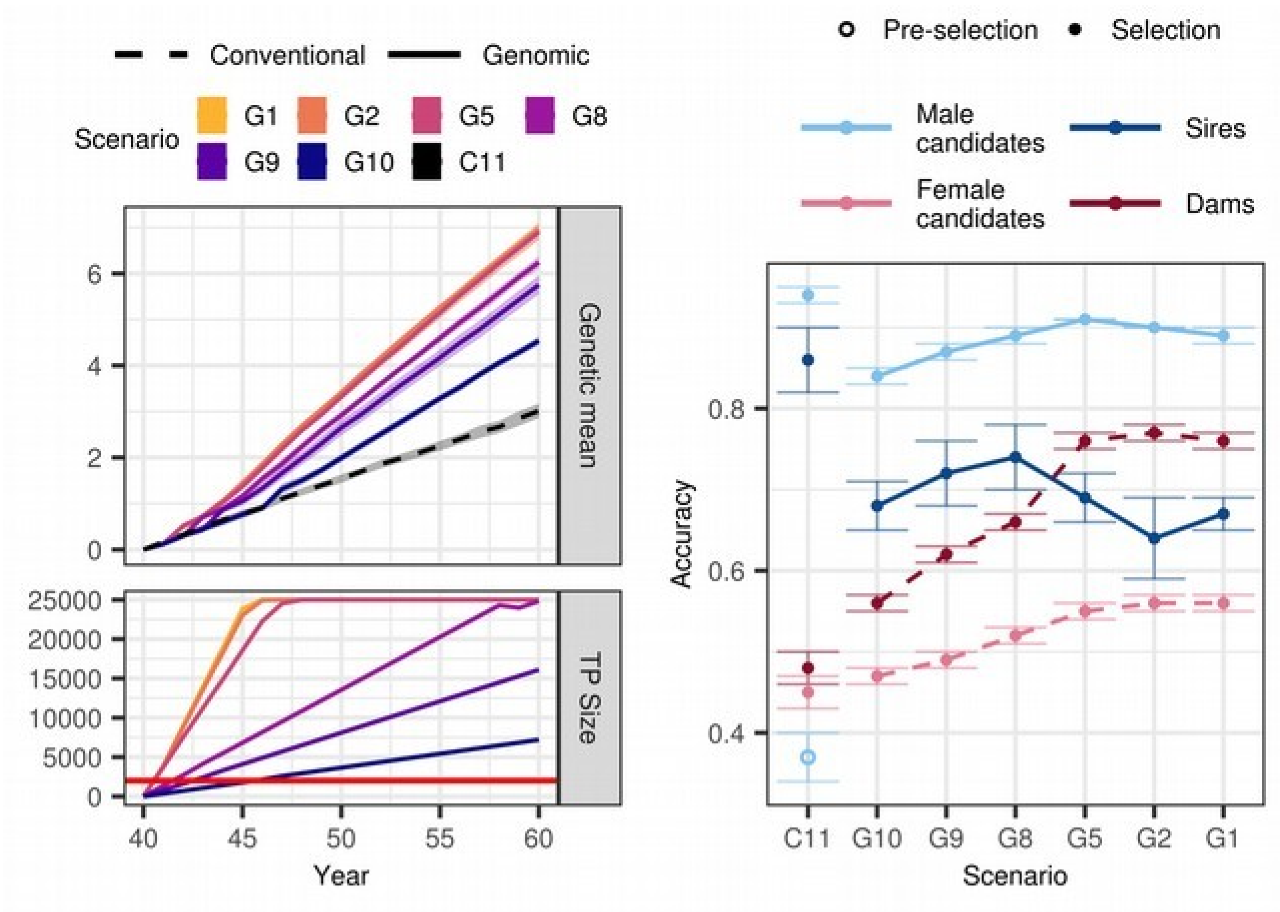

Figure 3 Genetic gain, training population size, and accuracy by scenario without initial training population (TP) and equal cost of phenotyping and genotyping. The figure presents the means (lines or points) and 95% confidence intervals (polygons or errorbars) across 10 replicates for the conventional (C) and genomic (G) scenarios with numbers indicating the number of phenotype records per lactation. The red line marks the condition of 2,000 animal in the training population to implement genomic selection. Conventional selection implemented two-stage selection for males, hence we present the accuracy of the pre-selection stage for progeny testing (empty point) and the accuracy of selection for proven sires (solid point).

Discussion

Conclusions

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Availability of data and materials

Competing interests

Not applicable

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Authors' contributions

JO designed the testing scenarios, ran the simulation, analyzed the data, wrote the papers and interpreted the results. JJ particited in designing the scenarios, troubleshooting the simulation problems, interpreting the results, and has substantially revised the manuscript. JMH participated in the design of the work, interpretation of the results, and has substantially revised the manuscript. GG has participated in designing the work, troubleshooting the problems, analysis of the data, interpretations of the results, and has substantially revised the manuscript.

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Author's information (optional)

Not applicable.

References

[1] Meuwissen TH, Hayes BJ, Goddard ME. Prediction of total genetic value using genome-wide dense marker maps. Genetics. 2001;157: 1819–1829.

[2] Schaeffer LR. Strategy for applying genome-wide selection in dairy cattle. J Anim Breed Genet. 2006; 123: 218–223.

[3] Obšteter J, Jenko J, Hickey JM, Gorjanc G. Efficient use of genomic information for sustainable genetic improvement in small cattle populations. Journal of Dairy Science. 2019;102: 9971–9982.

[4] Wiggans GR, Cole JB, Hubbard SM, Sonstegard TS. Genomic Selection in Dairy Cattle: The USDA Experience. Annu Rev Anim Biosci. 2017;5: 309–327.

[5] Mrode RA. Linear Models for the Prediction of Animal Breeding Values. Second edition. Wallingford, UK; Cambridge, MA: CABI, 2005.

[6] Daetwyler HD, Villanueva B, Woolliams JA. Accuracy of Predicting the Genetic Risk of Disease Using a Genome-Wide Approach. PLoS ONE. 2008;3: e3395.

[7] Goddard M. Genomic selection: prediction of accuracy and maximisation of long term response. Genetica. 2009;136: 245–257.

[8] Habier D, Tetens J, Seefried F-R, Lichtner P, Thaller G. The impact of genetic relationship information on genomic breeding values in German Holstein cattle. Genetics Selection Evolution. 2010;42: 5.

[9] Clark SA, Hickey JM, van der Werf JHJ. Different models of genetic variation and their effect on genomic evaluation. Genet Sel Evol. 2011;43: 18.

[10] Goddard ME, Hayes BJ, Meuwissen THE. Using the genomic relationship matrix to predict the accuracy of genomic selection. *J* Anim Breed Genet. 2011;128: 409–421.

[11] Calus MPL. Genomic breeding value prediction: methods and procedures. Animal. 2010;4: 157–164.

[12] Wolc A, Arango J, Settar P, Fulton JE, O'Sullivan NP. Persistence of accuracy of genomic estimated breeding values over generations in layer chickens. Genetics Selection Evolution. 2011;43: 23.

[13] Van Grevenhof EM, Van Arendonk JAM, Bijma P. Response to genomic selection: the Bulmer effect and the potential of genomic selection when the number of phenotypic records is limiting. Genet Sel Evol. 2012;44: 26.

[14] Gonzalez-Recio O, Coffey MP, Pryce JE. On the value of the phenotypes in the genomic era. Journal of Dairy Science. 2014;97: 7905–7915.

[15] Gao H, Christensen OF, Madsen P, Nielsen US, Zhang Y, Lund MS, et al. Comparison on genomic predictions using three GBLUP methods and two single-step blending methods in the Nordic Holstein population. Genetics Selection Evolution. 2012;44: 8.

[16] Gray KA, Cassady JP, Huang Y, Maltecca C. Effectiveness of genomic prediction on milk flow traits in dairy cattle. Genetics, Selection, Evolution. 2012;44: 24.

[17] Lourenco D a. L, Tsuruta S, Fragomeni BO, Masuda Y, Aguilar I. Genetic evaluation using single-step genomic best linear unbiased predictor in American Angus. J Anim Sci. 2015;93: 2653–2662.

[18] International Committee for Animal Recording. Section 02 - Cattle Milk Recording. Overview. In: ICAR Guidelines. Rome: ICAR, 2017.

[19] Misztal I, Tsuruta S, Strabel T, Auvray B, Druet T, Lee DH. BLUPF90 and related programs (BGF90). In: Proceedings of 7th World Congress on Genetics Applied to Livestock Production: 19-23 August 2001; Montpellier, France.

Figures

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Additional file 1 Table S1

Format:

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Additional file 2 Figure S1

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Description:

Conventional selection, BLUP simulation, 100 sires						
Number of records	Number of daughters / sire	Accuracy for sires	Accuracy for cows	Accuracy for non-phenotyped animals	Total number of phenotyped cows	Total number of phenotypes
Variable resources for phenotyping						
1	100	0.93	0.62	0.56	10,000	10,000
2	100	0.96	0.70	0.59	10,000	20,000
5	100	0.97	0.81	0.64	10,000	50,000
10	100	0.98	0.89	0.66	10,000	100,000
Fixed resources for phenotyping						
1	1000	0.99	0.63	0.59	100,000	100,000
2	500	0.99	0.71	0.61	50,000	100,000
5	200	0.99	0.82	0.64	20,000	100,000
10	100	0.98	0.89	0.66	10,000	100,000
Genomic selection						
Variable resources for phenotyping						
1	-	-	0.62	0.53	10,000	10,000
2	-	-	0.70	0.58	10,000	20,000
5	-	-	0.81	0.64	10,000	50,000
10	-	-	0.89	0.68	10,000	100,000
Fixed resources for phenotyping						

1	-	-	0.63	0.91	100,000	100,000
2	-	-	0.71	0.86	50,000	100,000
5	-	-	0.82	0.77	20,000	100,000
10	-	-	0.89	0.68	10,000	100,000

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