Evaluation of genomic selection for replacement strategies using selection index theory

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ABSTRACT

Our objective was to investigate the economic effect of prioritizing heifers for replacement at the herd level based on genomic estimated breeding values, and to compute break-even genotyping costs across a wide range of scenarios. Specifically, we aimed to determine the optimal proportion of preselection based on parent average information for all scenarios considered. Considered replacement strategies include a range of different selection intensities by considering different numbers of heifers available for replacement (15–45 in a herd with 100 dairy cows) as well as different replacement rates (15–40%). Use of conventional versus sexed semen was considered, where the latter resulted in having twice as many heifers available for replacement. The baseline scenario relies on prioritization of replacement heifers based on parent average. The first alternative scenario involved genomic selection of heifers, considering that all heifers were genotyped. The benefits of genomic selection in this scenario were computed using a simple formula that only requires the number of lactating animals, the difference in accuracy between parent average and genomic selection (GS), and the selection intensity as input. When all heifers were genotyped, using GS for replacement of heifers was beneficial in most scenarios for current genotyping prices, provided some room exists for selection, in the sense that at least 2 more heifers are available than needed for replacement. In those scenarios, minimum break-even genotyping costs were equal to half the economic value of a standard deviation of the breeding goal. The second alternative scenario involved a preselection based on parent average, followed by GS among all the preselected heifers. It was in almost all cases beneficial to genotype all heifers when conventional semen was used (i.e., to do no preselection). The optimal proportion

of preselection based on parent average was at least 0.63 when sexed semen was used. Use of sexed semen increased the potential benefit of using GS, because it increased the room for selection. Critical assumptions that should not be ignored when calculating the benefit of GS are (1) a decrease in replacement rate can only be achieved by increasing productive life in the herd, and (2) accuracies of selection should be used rather than accuracies of estimated breeding values based on the prediction error variance and base-generation genetic variance, because the latter lead to underestimation of the potential of GS.

Key words: genomic selection, replacement strategies, selection index theory, sexed semen

INTRODUCTION

Genomic selection (GS) is revolutionizing the design of breeding schemes, especially for dairy cattle (Hayes et al., 2009; Calus, 2010). The fast uptake of GS is a result of its potential to increase genetic gain considerably at an unprecedented rate by reducing generation intervals up to 3 times. Predictions indicate that these decreased generation intervals increase genetic gain by 28 to 108%, when GS replaces progeny testing in dairy cattle breeding schemes (for a review, see Pryce and Daetwyler, 2012). Genomic selection in dairy cattle breeding schemes is currently applied in 3 of the 4 different selection pathways; that is, selection of sires and dams of bulls, and selection of sires of cows. Typically, the effect of selection of dams of cows is expected to have a negligible effect on the realized genetic gain at the level of a commercial dairy herd (Van Tassell and Van Vleck, 1991). Although this indicates that genotyping cows in commercial dairy herds may not directly have an effect on the genetic gain achieved in the population, an indirect benefit may be found by increasing the accuracy of GS through including genotyped cows in the reference population (Mc Hugh et al., 2011).

In addition, it has been shown that GS can yield an economic advantage at the farm level to prioritize heifers for replacement (De Roos, 2011; Pryce and Hayes,

Received December 4, 2014.

Accepted May 20, 2015.

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2012; Weigel et al., 2012), provided that obtaining the genotypes of the heifers is cheap and the accuracy of genomic prediction is high. However, in these aforementioned studies, accuracies of estimated breeding values were used in the calculations, rather than the required accuracies of selection (Bijma, 2012). Accuracies of selection are defined as the correlation between the true and estimated breeding values (Falconer and Mackay, 1996). Accuracies of estimated breeding values are typically computed from the prediction error variance of the mixed model equations and the base-generation additive genetic variance, and are a measure of the standard error of the breeding values (Mrode, 2005). Those 2 types of accuracies are not the same in selected populations (Dekkers, 1992; Bijma, 2012), and in fact may be quite different. Because especially accuracies of parent average breeding values are substantially higher than accuracies of selection based on parent average, using accuracies of breeding values instead of accuracies of selection leads to an underestimation of the potential benefit of GS.

The potential additional revenues generated by using GS to select replacement heifers depends on several factors, including the cost of genotyping, the economic value of one genetic standard deviation of the breeding goal, the accuracy of selection based on GS compared with selection based on parent average, the replacement rate (i.e., the percentage of the dairy cows in a herd replaced by heifers on a yearly basis), and the number of available heifers. The number of heifers available for replacement may be increased up to 2-fold by use of sexed semen. If a large difference is present between the number of heifers available and the number of heifers required for replacement, an important question is whether all heifers should be genotyped, or whether first a preselection based on pedigree information should be performed. It has been suggested that optimal application of GS at the level of the breeding program involves genotyping a fraction of the selection candidates that are preselected based on other information sources (Henryon et al., 2012), and more specifically for dairy cattle breeding programs it has been shown that such strategies with a preselection step for bull dams are close to optimal (Wensch-Dorendorf et al., 2011). When using GS to select heifers for replacement, it has also been shown that a preselection step based on parent average information increases marginal revenues (Weigel et al., 2012).

Most of the studies thus far that have aimed to investigate the effect of GS at farm level, due to genotyping of animals within the herd, have been based on stochastic simulations. One of the major benefits of stochastic simulations is that the dynamics of replace-

ment in the herds can be modeled in detail. In addition, stochastic simulations yield not only point estimates of, for instance, genetic gain per scenario, computed as the average across replicates, but also uncertainty of those predictions, computed from the standard deviation across replicates. Such stochastic simulations, however, can be computationally quite intensive. An alternative is to model the scenarios at a more abstract level using selection index theory, which yields deterministic predictions of the evaluated variables (Schrooten et al., 2005; Dekkers, 2007). Such simulations are computationally inexpensive, which enables evaluation of a large number of different scenarios at low cost.

Our objective was to investigate the potential economic effect of prioritizing heifers for replacement at the herd level based on genomic estimated breeding values (**GEBV**), and to compute break-even genotyping costs across a range of scenarios. In those scenarios, the following factors were considered: different replacement rates, different numbers of heifers available, use of conventional or sexed semen, and genotyping of all versus a portion (based on parent average information) of heifers. Specifically, we aimed to determine the optimal proportion of preselection based on parent average information for all scenarios considered. The baseline scenario was represented by prioritization based on pedigree index. All comparisons were conducted based on deterministic predictions using selection index theory that predicts response to selection.

MATERIALS AND METHODS

Selection Response Due to Within-Herd Selection

The effect of the pathway to select dams to breed cows on the response to selection in the breeding program, which typically takes place within herds, is generally negligible compared with the other 3 selection pathways that typically take place in the overall breeding program (Van Tassell and Van Vleck, 1991). In our simulations, we therefore assumed that in applications of GS for replacement of heifers at the herd level, the achieved gain due to replacement strategies is not “cumulative,” in contrast to the genetic gain achieved at the level of the breeding program. Consider that the genetic level of animals in a commercial herd consistently lags behind the genetic level of the breeding program (Bichard, 1971; Elsen, 1993); for example, it takes ~3 yr before daughters of a bull start to produce after the bull has been first recognized to be a valuable breeding animal. Selecting the best heifers for replacement helps to temporarily decrease the genetic lag between the breeding program and the herd

during the productive lifetime of the selected heifers. Maintaining this reduced genetic lag relative to the breeding program in the long term requires continuous GS of replacement heifers in the herd. Thus, the use of GS for the selection of replacement heifers generates a once-off revenue. This also implies that the additional cost for genotyping needs to be earned solely from the additional revenue due to being better able to identify the best heifers for replacement.

Parent Average Versus Genomic Selection

In our study, several different scenarios were considered; see Table 1 for a summary of the considered values for the input parameters. All scenarios were evaluated both using selection on parent average and GS. The only differences between using parent average and GS are accuracies of selection, and the additional cost for genotyping. In the base line scenario, replacement rates of cows ranged from 15 to 40% (i.e., 15 to 40% of the cows in the herd were replaced by heifers on a yearly basis). Considering a herd of 100 dairy cows, the (average) productive life (**PL**; in years) of a heifer can be computed from the replacement rate (RR; expressed as a proportion) as

$$PL = \frac{1}{RR}. \quad [1]$$

The considered range for PL was therefore 2.5 to 6.67 yr, including for instance the average PL of 1,284 d or 3.52 yr in the Netherlands in 2014 (CRV, 2014). Equation 1 shows that to reduce the replacement rate, which is desirable to reduce rearing costs or to increase intensity of selecting replacements, herd life should be improved.

The selection intensity was calculated as outlined by Falconer and Mackay (1996) using the number of

available heifers and the number of heifers required for replacement (i.e., $RR \times 100$). Considering a herd of 100 lactating dairy cows, a sex ratio of the calves of 50/50, and that at maximum 90% of the female calves survive the first 2 yr of life, the maximum number of heifers available was 45. In the baseline scenario with the use of conventional semen, we assumed that the number of heifers available was at least equal to the required number for replacement, and therefore used ranges of 15 to 45 heifers being available for replacement. Reducing the numbers of heifers available for replacement from 45 to 15 considers scenarios in which an increasingly larger proportion of female calves was sold at early age or an increasingly smaller proportion of cows was mated to a dairy bull. Those numbers result in selection intensities (i) ranging from 0 (when all available heifers were used as replacements) to 1.09 (when RR was equal to 15 when 45 heifers were available for replacement).

In the scenarios with use of sexed semen, the maximum number of heifers available was twice the maximum number in the baseline scenario, resulting in 15 to 90 heifers available in those scenarios. Considering replacement rates of 15 to 40%, results in selection intensities ranging from 0 (when all available heifers were used for replacement) to 1.50 (when RR was equal to 15 when 90 heifers were available for replacement).

One-Stage Selection

To evaluate the considered selection strategies, we used deterministic simulations. The response of each of the considered replacement strategies was predicted as (Hazel, 1943)

$$R = i r_{IH} \sigma_H, \quad [2]$$

where i is the selection intensity (reflecting the proportion of heifers selected as explained previously), r_{IH} is

Table 1. Overview of the considered values for the input parameters across all scenarios

Parameter	Value
Herd size	100 lactating cows
Replacement rate (RR)	15–40%
Productive life (= $1/RR$)	2.50–6.67 yr
Semen used	Conventional or sexed
Numbers of heifers available	15–45 (conventional semen) 15–90 (sexed semen)
Selection intensities	0–1.01 (conventional semen) 0–1.44 (sexed semen)
Selection criterion to select heifers for replacement	Parent average (PA) Genomic estimated breeding value (GS)
Accuracy of selection	0.15–0.26 (PA) 0.69 (GS)

the accuracy of selection, and σ_H is the standard deviation of the breeding goal. It is important to note that r_{IH} is the accuracy of selection being the correlation between true and estimated breeding values, which in selected populations is not the same as the accuracy of breeding values computed from the prediction error variance and the base-generation additive genetic variance (Bijma, 2012). The primary aim of our study was to compare scenarios where heifers in a herd were selected for replacement either using parent averages or GS. To compare both approaches and considering that σ_H is expressed on a per lactation basis, the revenue due to GS per replaced heifer per year is

$$R_{\text{heifer,year}} = i(r_{IH(GS)} - r_{IH(PA)})\sigma_H, \quad [3]$$

where $r_{IH(GS)}$ is the accuracy of GS, and $r_{IH(PA)}$ is the accuracy of selection based on parent average information.

The revenue of GS compared with selection based on parent average at the herd level across the lifetime of the replaced heifers was computed as

$$R_{\text{add}} = PL \times \#h \times i(r_{IH(GS)} - r_{IH(PA)})\sigma_H, \quad [4]$$

where PL is the productive life in years, and $\#h$ is the number of replaced heifers in the herd in a particular year. The term $PL \times \#h$ is the total expected number of productive years of the heifers that have been used in the herd for replacement per year, which is equal to the number of lactating cows per herd (i.e., 100 in our case). The expression to compute the revenue due to GS can therefore be simplified to

$$R_{\text{add}} = 100 \times i(r_{IH(GS)} - r_{IH(PA)})\sigma_H. \quad [5]$$

Comparing equations 3 and 5 shows that for the considered scenarios the revenue due to GS per replaced heifer per year is 1% of the total revenue at the herd level across the productive life of the replaced heifers.

The accuracy of selection based on parent average information within a commercial dairy herd ($r_{IH(PA)}$), was computed as outlined by Bijma (2012). In these calculations, we assumed for the sires of the replacement heifers a selected proportion of 0.02 yielding a selection intensity of 2.42 (Pryce and Daetwyler, 2012). Assuming that the number of heifers required for replacement and the number available is constant within a herd across years, the selected proportion of the dams of the heifers is equal to the ratio of both numbers, which was used to compute the selection intensity for dams across the scenarios considered. Using these selection

intensities for sires and dams, the equilibrium accuracies of selecting sires (r_s) and dams (r_d) were computed using the program SelAction (Rutten et al., 2002). [The equilibrium refers to the Bulmer effect and the accumulation of pedigree information; see Dekkers (1992) and Bijma and van Arendonk (1998) for more details]. The values for r_d were computed assuming that each dam had one own performance record for the overall index with a heritability of 0.2. Alternatively, the value for r_d was assumed to be 0.69, considering genomic selection based on low density genotypes. The value for r_s was assumed to be 0.73, considering genomic selection based on 50k genotypes. These accuracies for genomic selection are clarified below. The values for r_s and r_d were then used to compute $r_{IH(PA)}$ as (Bijma, 2012):

$$r_{IH(PA)} = \sqrt{\frac{1}{4}(1 - k_s)r_s^2 + \frac{1}{4}(1 - k_d)r_d^2}, \quad [6]$$

where k_d and k_s represent the proportional reduction in the variance of the selection criterion used for dams and sires, respectively, due to their selection intensities; $0 < k_s, k_d < 1$. For instance, the value k_s is computed from the selection intensity for sires i_s and the truncation points of the standard normal distribution corresponding to the selected proportion (x_s) as $k_s = i_s(i_s - x_s)$ (Tallis, 1961).

The accuracy of genomic selection based on 50k genotypes was considered to be 0.73, following the average value reported for the Dutch/Flemish situation using the EuroGenomics reference population (Lund et al., 2011). In this scenario, we assumed that the accuracy of GS in heifers is $r_{LD} = r_{\text{imp}}r_{50k}$, where r_{LD} is the accuracy of selection using GEBV based on low density (LD) genotypes followed by imputation to 50k SNP, and r_{imp} is the accuracy of imputing 50k genotypes for heifers that were genotyped with the LD chip, measured as the correlation between the true and the imputed genotypes. The imputation accuracy r_{imp} was assumed to be 0.95, which is reported on average across several studies (for a review, see Calus et al., 2014). Using 0.73 for r_{50k} yields that $r_{LD} = 0.69$. Thus, a value of 0.69 was used for $r_{IH(GS)}$.

The computed revenue due to GS can be translated into the break-even cost of genotyping a heifer. The break-even cost is simply computed by dividing the revenue due to GS by the number of genotyped heifers, and is expressed in the Results section in standard deviation units of the breeding goal. The break-even cost represents the genotyping cost where the cost due to genotyping is equal to the revenue of using GS. When the actual genotyping cost is lower than the break-even cost, then genotyping heifers for prioritization for

replacement generates additional revenue at the farm level.

Two-Stage Selection

An important question is whether all heifers need to be genotyped to capture (most of) the marginal revenue realized with GS. To investigate this, a scenario with 2-stage selection was considered, where based on parent average information the best proportion p_1 of the heifers was selected to be genotyped. From these preselected heifers, another proportion (p_2) was selected based on GEBV. The total proportion of heifers selected is $P = p_1 p_2$. Similar to the approach used in Schrooten et al. (2005), the response for the 2-stage selection scenarios was computed using the exact method developed by Ducrocq and Colleau (1986), which is based on principles described by Tallis (1961) and Dutt (1973).

For 2-stage selection, the marginal revenue minus the marginal cost of using 2-stage selection at the herd level across the productive life of the replaced heifers is obtained by

$$(R_{2\text{-stage}} - R_{\text{par}})E - p_1 \times \#h \times C_{\text{genotyping}}, \quad [7]$$

where $R_{2\text{-stage}}$ and R_{par} are, respectively, the response from 2-stage selection and selection based on parent average expressed in standard deviation of the breeding goal, E is the economic value of one standard deviation of the breeding goal, and $C_{\text{genotyping}}$ is the cost for genotyping one heifer. Note that $R_{2\text{-stage}}$ is computed at the herd level across the productive life of the replaced heifers. Similarly, R_{par} was computed as

$$R_{\text{par}} = 100i_{\text{IH(PA)}}\sigma_{\text{H}}. \quad [8]$$

Note that for a given RR and number of heifers available, i.e., for a constant intensity of selection, R_{par} is a constant in equation 7. Thus, when deriving the optimal value of p_1 by finding the maximum value for equation 7, the result is not affected by the value of R_{par} . To compute the optimal value of p_1 , we assumed that the ratio of E and $C_{\text{genotyping}}$ (i.e., $E/C_{\text{genotyping}}$) was either 2 or 4. The ratio of 2 reflects for instance the current Dutch situation, where E is considered to be 100 (De Roos, 2011) and the genotyping cost per heifer is €50. The ratio of 4 represents a scenario where the current genotyping costs are halved. Note that the results can be used for any other situation where the same ratios apply.

The optimum value of p_1 ; that is, the value that maximizes marginal revenue minus marginal cost, has

a value in the range of p to 1.0. If p_1 is equal to 1.0, this scenario reduces to a scenario where all heifers available for replacement are genotyped and selection is in one stage. Consequently, the obtained response is equal to the response of that scenario. When p_1 decreases, both the genotyping cost and the revenue decrease. The optimum value of p_1 across the range of p to 1 was identified by evaluating marginal revenue minus marginal cost across this range while increasing p_1 with steps of 0.1.

RESULTS

Accuracy of Selection Based on Parent Average

Accuracy of selection based on parent average relies on the accuracy and intensity of selection of bulls, which were assumed fixed, and on the selection intensity of dams within herds, which depends on the proportion of available dams that are selected to generate the replacement heifers. Assuming that this proportion is the same as the RR and that the dams have one own performance record equaling one observation at the level of the overall index, the accuracy of the parent average ranged from 0.15 to 0.26 across the considered scenarios (Figure 1). When the dams would have genotypes instead, the values would range from 0.17 to 0.35. The accuracy of the parent-average increases when selection in the females becomes weaker (Figure 1), and is therefore dependent on the RR. Note that the accuracy of the parent-average for within-herd selection is higher than the accuracy of the parent-average in a breeding

Figure 1. Accuracy of within-herd selection of replacement heifers based on the parent-average (PA) EBV, as function of the within-herd selected proportion of dams, assuming that dams either have own performance information (black solid line) or genomic information (red dashed line). Color version available online.

program (where it is ~ 0.15 , Bijma, 2012) because selection of females for within-herd replacement is weaker than selection of females in a breeding program.

Revenues of GS

The revenues of using GS to prioritize heifers for replacement, compared with using parent average, computed at the herd level across the productive life of the replaced heifers, are shown in Figure 2 for use of conventional semen, and in Figure 3 for use of sexed semen. Note that the considered herd has 100 cows, and therefore the number of heifers available for replacement is equal to the RR expressed as a percentage. Using GS compared with parent average for replacement can yield revenues of 4.7 to 10.6 standard deviation units of the breeding goal if only 2 more heifers are available than required, both for scenarios with conventional and sexed semen. The value of 10.6 is obtained when 17 heifers are available for replacement, whereas 15 are required. The value of 4.7 is obtained when 42 heifers are available for replacement, whereas 40 are required. The corresponding values per replaced heifer per year are, respectively, 0.047 and 0.106 standard deviation units, when 2 more heifers are available than required. Revenues from using GS compared with parent average for replacement ranged from 18.8 to 32.9 standard deviation units of the breeding goal if 10 more heifers were available than required. The revenues of using sexed semen, comparing scenarios with sexed semen with twice the number of heifers as in scenarios with conventional semen are at least 1.4 times those obtained with conventional semen. This ratio increases considerably if the difference between the numbers of heifers available and those required for replacement decreases, indicating that the additional benefit of sexed semen along with GS is largest when the number of available heifers is low compared with the number of heifers required for replacement.

Break-Even Genotyping Cost

Break-even costs of genotyping were calculated to indicate the maximum cost of genotyping per individual that would be compensated by additional revenues. Genotyping costs below the break-even cost enable farmers to make a profit from genotyping their replacement heifers. Both for use of conventional and sexed semen, the maximum break-even cost was reached with the lowest RR, being slightly higher than 1.3 standard deviation units of the breeding goal (Figures 4 and 5). Both for use of conventional and sexed semen, break-even costs of 0.11 to 0.62 standard deviation units of the breeding goal were reached when 2 more heifers

Figure 2. The total revenue due to selecting heifers based on genomic breeding values instead of parent average, expressed as standard deviation units of the breeding goal, computed at the herd level across the productive life of the replaced heifers, in a scenario with use of conventional semen. The total revenue is shown as a function of the replacement rate and the number of heifers available. Scenarios where the number of heifers required for replacement was smaller than the number available were not considered and are indicated in white. Color version available online.

were available than required and break-even costs of 0.42 to 1.31 standard deviation units were reached when 10 more heifers were available than required.

Two-Stage Selection

Across scenarios with different numbers of heifers available and different RR, the optimum proportion of

Figure 3. The total revenue due to selecting heifers based on genomic breeding values instead of parent average, expressed as standard deviation units of the breeding goal, computed at the herd level across the productive life of the replaced heifers, in a scenario with use of sexed semen. The total revenue is shown as a function of the replacement rate and the number of heifers available. Scenarios where the number of heifers required for replacement was smaller than the number available were not considered and are indicated in white. Color version available online.

Break-even cost genotyping - conventional semen

Figure 4. Break-even cost for genotyping replacement heifers, expressed as standard deviation units of the breeding goal, as a function of the replacement rate and the number of heifers available, in a scenario with use of conventional semen. Scenarios where the number of heifers required for replacement was smaller than the number available were not considered and are indicated in white. Color version available online.

Break-even cost genotyping - sexed semen

Figure 5. Break-even cost for genotyping replacement heifers, expressed as standard deviation units of the breeding goal, as a function of the replacement rate and the number of heifers available, in a scenario with use of sexed semen. Scenarios where the number of heifers required for replacement was smaller than the number available were not considered and are indicated in white. Color version available online.

preselection was evaluated for use of conventional and sexed semen. This was done for 2 scenarios, where the ratio of the economic value of one standard deviation unit of the breeding goal to the genotyping cost of a single heifer was either 2 or 4. When using conventional semen, the optimum proportion of preselection was 1.0 in most scenarios considered with a minimum value of 0.97 (results not shown); that is, it was almost always beneficial to genotype all the heifers available for replacement.

For the scenarios with use of sexed semen, the optimum proportions of preselection are presented in Figures 6 and 7, for a ratio of the economic value of one standard deviation unit of the breeding goal to the genotyping cost for a single heifer of 2 and 4, respectively. Across all scenarios with sexed semen, the lowest optimal proportion of preselection was 0.63 when the ratio of the economic value of one standard deviation unit of the breeding goal to the cost for genotyping a single heifer was 2:1 (Figure 6). This value increased to 0.88, when the relative cost of genotyping was halved (Figure 7). In summary, also when sexed semen is used, in most scenarios genotyping all heifers is beneficial, unless the number of available heifers is much larger than the number of heifers required for replacement.

DISCUSSION

The objective of our paper was to investigate the economic effect of prioritizing heifers for replacement based on GEBV, at the herd level, and to determine optimal proportions of preselection based on par-

ent average. We demonstrated that in the context of targeting heifers for replacement, predictions based on selection index theory can be used to derive the revenue due to GS, break-even genotyping cost, and the optimum proportion of preselection based on parent average. As shown, the adopted calculations to quantify the revenue due to selecting all heifers based genomic selection compared with parent average can be performed with a simple formula that only requires the

Optimal proportion pre-selection - sexed semen

Figure 6. Optimal proportion of preselection based on parent average, as a function of the numbers of heifers available and the replacement rate, when using sexed semen. The ratio of the economic value of one standard deviation unit of the breeding goal to the costs for genotyping a single heifer was assumed to be 2:1. Evaluated scenarios were required to have at least 2 heifers more available than the number required for replacement. Other scenarios, as well as scenarios where the total genotyping costs exceeded the revenues, are indicated in white. Color version available online.

Figure 7. Optimal proportion of preselection based on parent average, as a function of the numbers of heifers available and the replacement rate, when using sexed semen. The ratio of the economic value of one standard deviation unit of the breeding goal to the costs for genotyping a single heifer was assumed to be 4:1. Evaluated scenarios were required to have at least 2 heifers more available than the number required for replacement. Other scenarios, as well as scenarios where the total genotyping costs exceeded the revenues, are indicated in white. Color version available online.

number of lactating animals, the difference in accuracy between parent average and genomic selection, and the selection intensity as input (equation 5). This implies that calculations based on selection index theory can easily be performed across a wide range of different parameters, as also described by Dekkers (2007) in a more general framework, and are computationally much less demanding than stochastic simulations.

Optimal proportions of preselection based on parent average were always 1.0 with conventional semen, and tended to be quite high (>0.63) with use of sexed semen as well. This indicates that genotyping (almost) all heifers was generally the best GS strategy. However, it should be noted that whether or not those optimal GS strategies are economically viable depends on the actual genotyping price. When considering the current Dutch situation [i.e., cost of genotyping one individual of approximately €50 and a considered economic value of approximately €100 (De Roos, 2011) for one standard deviation of the breeding goal], then indeed our results show that using GS to target heifers for replacement leads to increased income for the farmer in almost all scenarios. If the economic value of one standard deviation of the breeding goal is considerably lower, then the number of scenarios in which GS is beneficial reduces quickly. For instance, considering a scenario where genotyping costs are equal to the economic value of one standard deviation of the breeding goal, the area with values greater than 1 in Figures 4 and 5 shows that in less than half of the evaluated scenarios GS is beneficial.

The scenarios with preselection involved selecting a proportion of the best animals based on parent average to be genotyped. As pointed out by Hjortø et al. (2015), this strategy may be suboptimal, if the best animals based on parent average are among those that would be selected for replacement based on genomic selection. An alternative strategy is to genotype heifers that have parent averages centered around the level of parent average above which heifers would be selected for replacement, which may increase the benefit of genotyping for replacement by reducing the total genotyping costs (Hjortø et al., 2015). Whether this leads to a further increase of the revenues due to genotyping likely depends on accuracy achieved for selection based on parent average.

Depending on the considered genotyping cost and the considered economic value, our results suggest that use of GS for replacement is beneficial in more scenarios, compared with other studies (De Roos, 2011; Pryce and Hayes, 2012; Weigel et al., 2012; Hjortø et al., 2015). Our results are somewhat different from those of others for 2 main reasons. First, we used accuracies of selection in our computations, which should be used when evaluating selection response, whereas in the other studies accuracies of EBV were used. The difference is that accuracies of EBV are a measure of the standard error of EBV, whereas the accuracy of selection represents the correlation between estimated and true breeding values. Those values are not the same in populations under selection (Bijma, 2012), in the sense that accuracies of EBV are higher than accuracies of selection. The difference between accuracies of genomic EBV versus accuracies of genomic selection is expected to be relatively small. However, as pointed out by Bijma (2012), the difference between accuracies of a parent average (i.e., an EBV based only on EBV of the parents) and accuracy of selection based on parent average is substantial. The accuracy of a parent average may for instance be 0.51 when the sire and dam EBV have accuracies of, respectively, 0.9 and 0.5. The accuracy of selection based on parent average, however, is only ~ 0.15 (Bijma, 2012). In this example, using the accuracy of EBV of 0.51, compared with using the accuracy of selection of 0.15, leads to an overestimation of the accuracy of selection based on parent average of 0.36. As can be derived from equation 5, for the ranges of selection intensities considered in our study, this leads to an underestimation of the benefit of using GS for replacement of up to 51.84 standard deviation of the breeding goal, or €5,184, considering an economic value of one standard deviation of the breeding goal of €100. This example clearly shows that using accuracies of EBV instead of accuracies of selection, when

comparing the potential of genomic to traditional selection, can lead to considerable underestimation of the potential of genomic selection. It should be noted that perhaps in a few years' time, when genotyping of cows is abundant, the accuracy of parent average may increase somewhat due to the genomic information available for dams (Figure 1). The values used for selection based on parent average, ranging from 0.15 to 0.26, may then increase to 0.17 to 0.35. Because these increases are limited, their effect on the reported differences between selecting replacement heifers based on parent average or genomic selection is also expected to be limited.

The second reason why our results are more in favor of genomic selection compared with the results of some other studies, is that we considered that low replacement directly results in a longer productive life of the heifers in the herd (equation 1). In some other studies, this relationship between RR and productive life was not considered (De Roos, 2011; Pryce and Hayes, 2012), whereas this relationship is implicitly included in stochastic simulations that consider a constant herd size over time (Weigel et al., 2012). The relationship between RR and productive life decreases the break-even costs considerably at low RR (Figures 4 and 5), compared with, for instance, assuming that each heifer stays in the herd for 3 lactations. The most extreme RR of 15 and 40%, imply that heifers stay, respectively, 6.7 and 2.5 yr in the herd. So, with a lower RR the break-even genotyping costs are considerably lower, because the revenues are generated across a greater number of lactations.

The revenue achieved through genotyping of replacement heifers may be further increased by several future developments, possibly leading to widespread genotyping in dairy herds the next 5 to 10 yr. Expected further reductions in genotyping cost is the most important one. In addition, making use of the genomic data for other purposes than prioritization of heifers for replacement will reduce the anticipated break-even cost. This may include (Pryce and Hayes, 2012) selling pedigree heifers at a premium, using mating plans to optimize rates of genetic gain while controlling inbreeding and avoiding mating of carriers of genetic defects, parentage verification, and use of further integrated management systems that use information from genomic tests to optimize herd management at the level of individual animals.

Moment of Selection

In our study, we assumed that heifers were selected for replacement within the herd closely before their first calving and did not consider the potential effect of

selecting females at a different stage of their life. The moment of selection could of course be shifted back in time. Genomic tests could, for instance, be performed at the moment a heifer calf is born. Weigel et al. (2012) showed that genotyping is clearly more beneficial for heifer calves and yearling heifers, compared with first and higher parity cows, because phenotypic information is already available from lactating animals, which reduces the relative added value of a genomic test. Arguably, prioritizing heifer calves or replacement heifers leads to similar results, although prioritizing heifer calves may be a better strategy if the revenue of selling surplus heifers is lower than the rearing costs.

Preselection based on parent averages can already be applied when performing the matings that will yield the next generation of replacement heifers. It should be noted that calves can be genotyped, whereas genotyping of the calves is not possible at the mating stage. This implies that selecting at the mating stage can only be done using parent average information, and possibly optimal replacement strategies for heifers are based on a preselection step based on parent average at mating and based on genomic tests applied to calves or heifers. Selecting at the mating stage does open up several opportunities to generate additional economic benefits. For instance, those cows whose offspring are not expected to be considered for replacement could be mated with a beef bull, whereas the other cows could be inseminated with sexed semen of a dairy bull. This leads to an immediate decrease in genotyping costs, because the number of dairy heifer calves decreases, but may also reduce the potential effect of genomic testing if the number of heifers raised is very close to the number of heifers needed for replacement.

Use of Sexed Semen

In our scenarios, the use of sexed semen increased the potential benefit of using GS, simply because it increased the room for selection. In terms of additional costs of the various scenarios, the fact that using sexed semen is more expensive than conventional semen was not considered. The price of sexed semen does not affect the outcome of our comparisons because we always compared 2 scenarios that either both used conventional, or both used sexed semen, such that use of sexed semen did not result in additional costs between compared scenarios. Nevertheless, acknowledging that sexed semen is more expensive than conventional semen can lead to practical schemes where the best heifers and cows are inseminated with sexed semen, whereas the others are inseminated with conventional semen of a dairy or beef bull. Such scenarios can also be modeled

using selection index theory by considering selection of heifers and dams to be inseminated with sexed semen as a first selection step, and selection of the resulting heifer calves as a second selection step. Fine tuning of such specific scenarios will likely lead to increases of the revenue due to the combined use of sexed semen and GS to target heifers for replacement.

Sensitivity to Accuracies of Selection

In our study, we used accuracies of selection based on parent average ranging from 0.15 to 0.26 (ρ_{PA}) and an accuracy of 0.69 (ρ_{GS}) for genomic tests, respectively. An important question is how the results are changed when the considered accuracy of genomic tests is smaller or larger than 0.69. Considering that the accuracy of selection based on parent average is approximately unaffected by the size of the reference population, our results in terms of revenue and break-even genotyping cost are simply affected by a factor of $(\rho_{GS}^* - \rho_{PA})/(\rho_{GS} - \rho_{PA})$. So a change in accuracy of GS of 0.1 yields changes of 18.5 to 23.3% compared with our reported results.

CONCLUSIONS

Our results show that using GS for replacement of heifers is beneficial in most scenarios at current genotyping prices, provided some room is available for selection, in the sense that at least 2 more heifers are available than needed for replacement. In those scenarios, minimum break-even genotyping costs are equal to half the economic value of a standard deviation of the breeding goal. Use of sexed semen increased the potential benefit of using GS because it increased the room for selection. Furthermore, 2-stage selection, including a first preselection of heifers based on parent average and a final selection step based on GS, proved to be beneficial in a limited number of scenarios when using sexed semen and when the number of heifers available was considerably larger than the number required for replacement because this reduces the genotyping relatively more than it reduces the revenue due to suboptimal prioritization of heifers for replacement. Critical assumptions for the calculations are 1) a decrease in replacement rate leads to an increased productive life in the herd, and 2) accuracies of selection should be used and not accuracies of (genomic) breeding values that are computed from the prediction error variance of the mixed model equations and the base-generation additive genetic variance. Using accuracies of breeding values can lead to considerable underestimation of the potential of genomic selection. Finally, using selection

index theory was shown to be a convenient tool to evaluate the effect of genomic selection versus use of parent averages to target heifers for replacement.

ACKNOWLEDGMENTS

The authors acknowledge financial support from the Dutch Ministry of Economic Affairs, Agriculture, and Innovation (The Hague, the Netherlands; public-private partnership “Breed4Food” code KB-12-006.03-004-ASG-LR).

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