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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; i.e., 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,

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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 replacement 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