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Deterministic models of breeding scheme designs that incorporate genomic selection

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ABSTRACT

A deterministic model to calculate rates of genetic gain and inbreeding was used to compare a range of breeding scheme designs under genomic selection (GS) for a population of 140,000 cows. For most schemes it was assumed that the reliability of genomic breeding values (GEBV) was 0.6 across 4 pathways of selection. In addition, the effect of varying reliability on the ranking of schemes was also investigated. The schemes considered included intense selection in male pathways and genotyping of 1,000 young bulls (GS-Y). This scheme was extended to include selection in females and to include a "worldwide" scheme similar to GS-Y, but 6 times as large and assuming genotypes were freely exchanged between 6 countries. An additional worldwide scheme was modeled where GEBV were available through international genetic evaluations without exchange of genotypes. Finally, a closed nucleus herd that used juvenile in vitro embryo transfer in heifers was modeled so that the generation interval in female pathways was reduced to 1 or 2 yr. When the breeding schemes were compared using a GEBV reliability of 0.6, the rates of genetic gain were between 59 and 130% greater than the rate of genetic gain achieved in progeny testing. This was mainly through reducing the generation interval and increasing selection intensity. Genomic selection of females resulted in a 50% higher rate of genetic gain compared with restricting GS to young bulls only. The annual rates of inbreeding were, in general, 60% lower than with progeny testing, because more sires of bulls and sires of cows were selected, thus increasing the effective population size. The exception was in nucleus breeding schemes that had very short generation intervals, resulting in higher rates of both gain and inbreeding. It is likely that breeding companies will move rapidly to alter their breeding schemes to make use of genomic selection because benefits to the breeding companies and to the industry are considerable.

Key words: genomic selection, breeding program, genetic gain, inbreeding

INTRODUCTION

The potential to make selection decisions on reliable genomic estimated breeding values (**GEBV**) early in the life of animals, rather than waiting for phenotypes to become available, has substantial implications for the design of dairy cattle breeding programs (Schaeffer, 2006).

Genomic estimated breeding values combine genomic and pedigree information (Hayes et al., 2009). The reliability of GEBV in several countries significantly exceeds the reliability of parent average or sire pathway values, but currently is not as high as the reliability achieved in progeny testing (e.g., Harris et al., 2008; Hayes et al., 2009; Moser et al., 2009; VanRaden et al., 2009). Consequently, some breeding companies are in the process of adapting their breeding schemes to incorporate genomic information while continuing to progeny test at the same time (e.g., Harris et al., 2008).

If GEBV are used to make early selection decisions instead of progeny testing, modeling suggests that genetic gains could be increased by 30 to 217% over current rates of genetic gain (Schaeffer, 2006; Harris et al., 2008; König et al., 2009), mainly through reducing generation intervals. Another strategy, recently discussed by König and Swalve (2009), is to use GEBV to reduce the number of progeny-test daughters required. Thus, a desired accuracy is achieved where the reduction in number of progeny required is dependent on the heritability of the trait and the reliability of the GEBV.

The low cost of genotyping relative to progeny testing and the fact that the genomic information can be acquired early in the life of selection candidates make a range of alternative breeding schemes attractive with genomic selection (**GS**). For example, young bulls could be selected as sires of cows using GEBV only, or the number of bulls selected as progeny-test candidates

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could be reduced. These approaches can be extended or redesigned.

One such scheme could take advantage of the fact that dairy cattle breeding is a global industry. Breeding objectives in different countries are currently closely aligned (Miglior et al., 2005) and considerable exchange of genetic material occurs, primarily semen from progeny-tested sires. However, in many cases, it will not be possible for a single country or organization to have a reference population with enough performance records of their sires' daughters in other countries to derive prediction equations for genomic breeding values across all the countries of interest.

If the same SNP panel is used for genomic predictions and free exchange of candidate genotypes occurs between countries, then the same reliability can be achieved for bulls from foreign countries as for domestic sires (within a country). Alternatively, genotypes and phenotypes may not be shared across countries. In this case, GEBV could be converted to domestic scales using an adaptation of traditional multi-trait across-country evaluation (**MACE**) to handle nonindependent data, such as genomic MACE (**GMACE**; VanRaden and Sullivan, 2010). If this were applied, the reliabilities of bulls from foreign countries would be lower than that of domestic sires. Furthermore, the existence of genotype by environment interactions (**G×E**) between countries could mean that some bulls that would not be selected in their country of birth may rank highly in another country. However, it is likely that most animals selected will either come from the country itself or from those countries exhibiting little G×E with the importing country. This type of scheme may also be of interest to countries that have no breeding programs of their own or are importers of semen from countries with similar breeding objectives.

Other possible breeding schemes include nucleus breeding schemes where elite herds of cows are mated to top sires to breed potential future sires. This type of scheme would probably be owned and regulated by breeding companies and is attractive because selection intensities can be increased in both male and female pathways. Such scenarios can also make use of reproductive technologies such as sexed semen or multiple ovulation and embryo transfer (**MOET**). Reproductive technologies may be more effective in achieving high rates of genetic gain in well-organized breeding schemes, rather than in commercial herds, provided that the technology is strategically used. Abdel-Azim and Schnell (2007) explored breeding schemes using MOET and sexed semen in conjunction with marker-assisted selection (but not genomic selection). They found an 11% increase in response to selection. Therefore, the combination of such reproductive technologies and genomic selection could improve the rate of genetic gain.

The classic response to selection (**ΔG**) equation (e.g., Falconer, 1989) modified to include 4 pathways of selection is

$$\Delta G = \frac{\sum_{i=1}^{4} I_i r_i \sigma_A}{\sum_{i=1}^{4} L_i},$$

where L_i is the generation interval in the ith selection pathway, I_i is the selection intensity in the ith pathway of selection, r_i is the accuracy of selection, and σ_A is the genetic standard deviation of selection.

Using this equation, it follows that response to selection is affected by

1) The generation interval (**L**). This is the average age of parents at the birth of their selected progeny (Falconer, 1989). In conventional breeding schemes that use progeny testing to generate data to calculate EBV, the generation interval in male pathways ($\mathrm{L_s}$) is long (e.g., Schaeffer, 2006). By using GEBV, $\mathrm{L_s}$ can be reduced substantially and is dependent on the sexual maturity of bull calves. There is also scope to reduce the generation interval in female pathways ($\mathrm{L_f}$). For example reproductive technologies such as juvenile in vitro fertilization and embryo transfer (**JIVET**) can be used to obtain oocytes before sexual maturity (Raadsma and Tammen, 2005), potentially leading to a large reduction in generation interval.
2) The accuracy of the GEBV. This is mainly dependent on the size of the reference population available (e.g., VanRaden et al., 2009) to derive the GEBV prediction equations. Using current technology, the reliability of GEBV of production traits reported for 4 populations (Australia, New Zealand, the Netherlands, and United States/Canada) range between 0.16 and 0.67 (Harris et al., 2008; Hayes et al., 2009; VanRaden et al., 2009).
3) Selection intensity and the number of animals genotyped. There may be diminishing returns to genotyping more animals if population size is a limiting factor.

The aim of this study was to evaluate a range of alternate breeding program designs incorporating genomic selection and reproductive technologies for both rate

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