J. Dairy Sci. 92:5292–5303
doi:10.3168/jds.2009-2232

Application of selection index calculations to determine selection strategies in genomic breeding programs

S. König*[1] and H. H. Swalve†
*Institute of Animal Breeding and Genetics, University of Göttingen, 37075 Göttingen, Germany
†Institute of Agricultural and Nutritional Sciences, University of Halle, 06099 Halle, Germany

ABSTRACT

The availability of genomic estimated breeding values (GEBV) allows for possible modifications to existing dairy cattle breeding programs. Selection index calculations including genomic and phenotypic observations as index sources were used to determine the optimal number of offspring per genotyped sire with a focus on functional traits and the design of cooperator herds, and to evaluate the importance of a central station test for genotyped bull dams. Evaluation criteria to compare different breeding strategies were correlations between index and aggregate genotype (r_{TI}), and the relative selection response percentage (RSR) of an index without single nucleotide polymorphism information in relation to a single nucleotide polymorphism-based index. The number of required daughter records per sire to achieve a predefined r_{TI} strongly depends on the accuracy of GEBV (r_{mg}) and the heritability of the trait. For a desired r_{TI} of 0.8, $h^2 = 0.10$, and $r_{mg} = 0.5$, at least 57 additional daughters have to be included in the genetic evaluation. Daughter records of genotyped sires are not necessary for optimal scenarios where r_{mg} is greater than or equal to r_{TI}. There still is a substantial need for phenotypic daughter records, especially for low-heritability functional traits and $r_{mg} < 0.7$. Phenotypic records from genotyped potential bull dams have no relevance for increasing r_{TI}, even with a low value for r_{mg} of 0.5. Hence, genomic breeding programs should focus on recording functional traits within progeny groups, preferably in cooperator herds. For low-heritability traits and with $r_{mg} > 0.7$, the RSR of conventional breeding programs was only 10% of RSR from genomic breeding strategies. As shown in scenarios including 2 traits in the index as well as in the aggregate genotype, the availability of highly accurate GEBV for production traits and low-accuracy GEBV for functional traits increased the risk of widening the gap between selection responses in production and functionality. Counteractions are possible, such as via higher economic weights for low-heritability functional traits. Finally, an alternative selection strategy considering only 2 pathways of selection for genotyped male calves and for cow dams was evaluated. This strategy is competitive with a 4-pathway genomic breeding program if the fraction of selected male calves for the artificial insemination program is below 1% and if selection is focused on functionality, thus pointing to substantial insufficiencies caused by low reliabilities of breeding values for cows for such traits in conventional bull dam selection schemes.

Key words: genomic selection, breeding program, selection index

INTRODUCTION

Genetic selection in livestock populations, and especially in dairy cattle breeding programs, can currently be based on estimates of the association between large numbers of SNP and phenotypic information. This new technology is called genome-wide selection (**GS**) and is revolutionizing dairy cattle breeding programs (Hayes et al., 2009). Meuwissen et al. (2001) showed by simulation that this approach would be feasible and would yield correlations between true and SNP-based breeding values high enough to eliminate the necessity for traditional methods of breeding value estimation based on progeny testing in dairy cattle. Schaeffer (2006) outlined forms of a breeding program that apply this new technology. However, as several authors (e.g., Hayes et al., 2009; König et al., 2009; VanRaden et al., 2009) have pointed out, the magnitude of the correlation between the true breeding value and the genomic EBV (**GEBV**) is of crucial interest. In fact, this correlation, also referred to as the accuracy of GEBV ($\boldsymbol{r_{mg}}$), may determine the extent to which genomic selection will be applied, and hence will be the crucial factor determining future breeding programs in dairy cattle.

The inclusion of genomic information in dairy cattle breeding programs should be viewed within the framework of other improvements. Current ideas for improvements of existing dairy cattle breeding programs in Germany are partly based on the establishment of

---

Received March 22, 2009.
Accepted July 9, 2009.
[1] Corresponding author: skoenig2@gwdg.de

central station tests for potential bull dams (König et al., 2007a) and on cooperator herds for progeny testing (Gernand et al., 2007). Central station tests for potential bull dams, although creating substantial additional costs, are mainly implemented to prevent biases in EBV caused by preferential treatment (Kuhn et al., 1994), or to avoid the impact of heterogeneous variances in different environments (e.g., Garrick and van Vleck, 1987). Both the central station test of bull dams and progeny testing in selected cooperator herds generate additional advantages when the focus is on detailed recording of functional or health traits (König and Swalve, 2006; Swalve and König, 2007). An example is the application of selection indices to determine the genetic improvement of hoof health traits for different breeding strategies. König and Swalve (2006) found that the selection response for reducing incidences of laminitis per generation as well as the accuracy of EBV of bulls for laminitis could be doubled if direct observations on the laminitis status of 50 daughters were included as index sources. Their suggestion was to install cooperator herds for progeny testing to enable the routine recording of various types of disorders. Swalve (2008) gave an extended overview of the necessity of cooperator herds in dairy cattle breeding programs by considering aspects from data recording of functional traits up to aspects of the logistical advantages in the era of genomic selection. Recording of functional traits on a national scale is difficult to implement when daughters of young bulls are distributed over 49,202 dairy cattle farms (ADR, 2007) that keep registered herdbook cows.

However, both innovations (i.e., the implementation of a station test for bull dams and contracting cooperator herds for progeny testing) do not substantially alter the genetic framework of conventional dairy cattle breeding schemes, as suggested by Henderson (1964) or by Skjervold and Langholz (1964). A substantial modification of current dairy cattle progeny-testing programs seems to be possible through the application of GS. Schaeffer (2006) assumed an accuracy of 0.75 for GEBV and applied the general formula proposed by Rendel and Robertson (1950) for calculating annual genetic gain. Annual genetic gain was doubled because of a substantial reduction inof generation intervals, and the costs of proving bulls were reduced by 92% because of the elimination of progeny testing. König et al. (2009) used the same design for a genomic breeding program, but considered discounted costs and discounted returns over a whole investment period of 15 yr. For accuracies of GEBV above 0.70, a distinct economic advantage of genomic breeding programs, compared with progeny-testing programs, of up to a factor of 2.59 was found. However, current practical results for estimated accuracies of GEBV (e.g., VanRaden et al., 2009) lagged behind the theoretical expectations obtained from simulation studies (e.g., Meuwissen et al., 2001). Especially for low-heritability functional traits, gain from genomic prediction compared with the parent average was relatively low (VanRaden et al., 2009). In this study, genomic information improved the accuracies of genetic values equivalent to 11 daughter records for traits with moderate heritability. These results imply continued progeny testing to ensure reliable genetic evaluations, as well as greater efforts in recording reliable phenotypes of functional traits for the derivation of SNP effects. Schaeffer (2006) suggested implementing a system of cooperator herds as a substantial tool for generating accurate phenotypes and genotypes, which could be financed by the $23 million savings generated by using the GS strategy in the Canadian Holstein population.

From the current point of research (Hayes et al., 2009), the most likely breeding strategy remains a combination of both GS and progeny testing. The mixture of SNP information and phenotypic performance implies the need for an evaluation or even a modification of breeding strategies related to bull dam selection and progeny testing. Another even more progressive idea in the context of genomic breeding programs is a shift from bull dam selection schemes toward direct selection of genotyped male calves. This approach implies a 2-pathway selection scheme (i.e., the selection of male calves for AI and dams of cows within farms) instead of the classical 4-pathway strategy (Robertson and Rendel, 1950).

For dairy cattle breeding organizations, several questions arise when implementing genomic selection in breeding programs. In Germany, some of these questions are 1) the optimal size of progeny groups, especially when attempting to focus on the documentation of health traits in cooperator herds, 2) the abundance or the necessity of a central station test for potential bull dams, and 3) the possibility of a substantial shift from bull dam selection (2-step selection strategy) toward the direct selection of genotyped male calves as cow sires for AI. To answer these questions with a focus on functional traits, the aim of our study was to extend the calculations done by König and Swalve (2006) by integrating genomic information via selection index calculations. König and Swalve (2006) compared the genetic gain of direct selection strategies on health traits with conventional indirect approaches via indicator traits. Currently, an extension of such strategies is possible via genomic information. Results from different scenarios were used to recommend a suitable breeding strategy for a genomic breeding program.