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Improving accuracy of bulls' predicted genomic breeding values for fertility using daughters' milk progesterone profiles

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ABSTRACT

The main objective of this study was to investigate the benefit of accuracy of genomic prediction when combining records for an intermediate physiological phenotype in a training population with records for a traditional phenotype. Fertility was used as a case study, where commencement of luteal activity (C-LA) was the physiological phenotype, whereas the interval from calving to first service and calving interval were the traditional phenotypes. The potential accuracy of across-country genomic prediction and optimal recording strategies of C-LA were also investigated in terms of the number of farms and number of repeated records for C-LA. Predicted accuracy was obtained by estimating population parameters for the traits in a data set of 3,136 Holstein Friesian cows with 8,080 lactations and using a deterministic prediction equation. The effect of genetic correlation, heritability, and reliability of C-LA on the accuracy of genomic prediction were investigated. When the existing training population was 10,000 bulls with reliable estimated breeding value for the traditional trait, predicted accuracy for the physiological trait increased from 0.22 to 0.57 when 15,000 cows with C-LA records were added to the bull training population; but, when the interest was in predicting the traditional trait, we found no benefit from the additional recording. When the genetic correlation was higher between the physiological and traditional traits (0.7 instead of 0.3), accuracy increased less when adding the 15,000 cows with C-LA (from 0.51 to 0.63). In across-country predictions, we observed little to no increase in accuracy of the intermediate physiological phenotype when the training population from Sweden was large, but when accuracy increased the training population was small (200 cows), from 0.19 to 0.31 when 15,000 cows were added from the Netherlands (genetic correlation of 0.5 between countries), and from

0.19 to 0.48 for genetic correlation of 0.9. The predicted accuracy initially increased substantially when recording on the same farm was extended and multiple C-LA records per cow were used in prediction compared with single records; that is, accuracy increased from 0.33 with single records to 0.38 with multiple records (on average 1.6 records per cow) from 2 yr of recording C-LA. But, when the number C-LA per cow increased beyond 2 yr of recording, we noted no substantial benefit in accuracy from multiple records. For example, for 5 yr of recording (on average 2.5 records per cow), accuracy was 0.47; on doubling the recording period to 10 yr (on average 3.1 records per cow), accuracy increased by 0.07 units, whereas when C-LA was recorded for 15 yr (on average 3.3 records per cow) accuracy increased only by 0.05 units. Therefore, for genomic prediction using expensive equipment to record traits for training populations, it is important to optimize the recording strategy. The focus should be on recording more cows rather than continuous recording on the same cows.

Key words: multitrait genomic prediction, milk progesterone, dairy cattle, accuracy

INTRODUCTION

Although milk progesterone (**P4**) levels have been widely accepted as valid indicators of fertility in dairy cows, their application in routine genetic evaluation schemes has been constrained by the high cost associated with collecting sufficient samples per cow. Endocrine fertility traits derived from milk P4 levels have been recommended as indicators for fertility in dairy cows because they are physiological phenotypes that more directly reflect parts of a cow's reproductive physiology (Bulman and Lamming, 1978; Lamming and Darwash, 1998; Darwash et al., 1999). For example, the interval from calving to first ovulation as determined by P4 levels in milk could be used as a direct indicator of a cow's ability to return to luteal activity after calving, instead of an indirect indicator such as the interval from calving to first service (**CFS**). Several studies have revealed that endocrine fertility traits yield higher

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heritability estimates than traditional fertility traits derived from calving and insemination data. Notably, for the interval from calving to commencement of luteal activity (**C-LA**), heritability estimates of 0.15 to 0.28 have been reported (Darwash et al., 1997; Veerkamp et al., 1998; Petersson et al., 2007; Tenghe et al., 2015). Furthermore, examining the phenotypic correlation of C-LA with traditional fertility traits showed that early reestablishment of cyclic activity in postpartum cows increases the probability of an early insemination after calving, shortens the interval from calving to conception, increases conception rate, and reduces the number of services per conception (Darwash et al., 1997). These observations further suggest that early reestablishment of cyclic activity is an important prerequisite for good fertility.

Until recently, methods to measure milk P4 levels were labor intensive. They often entailed manually taking several milk samples per cow, analyzing, and recording the results. However, inline technology such as the Herd Navigator (DeLaval Int., Tumba, Sweden) now exists to measure P4 levels on individual cows during each milking, making it possible to sample a larger number of animals at a reasonable cost. But because few herds currently have the inline recording system, endocrine fertility traits that are defined from milk P4 levels would be most useful in a genomic selection scheme, where cows from contract herds form the reference population. In comparison, traditional fertility traits are routinely measured on a large scale, are more practical phenotypes for fertility, and are still useful target traits in national genetic evaluations. Therefore, combining (genomic predictions for) endocrine and traditional fertility traits may provide a more accurate prediction of fertility. In a previous study, using real data, the improvement in accuracy achievable from using endocrine fertility traits concurrent with a traditional traits (CFS) in genomic prediction of fertility was quantified (Tenghe et al., 2016a). However, the extent of exploring the effect of number of cows with endocrine traits in the training population in that study was limited by the data size. In the current study, the limitation was overcome by using a deterministic prediction equation to evaluate accuracy of prediction.

The main objective of our study was to investigate the benefit on accuracy of genomic prediction when combining records for an intermediate physiological phenotype in a training population with records for a traditional phenotype. Fertility was used as a case study, where the endocrine trait C-LA was a physiological or biological phenotype, whereas CFS and calving interval (**CInt**) were traditional phenotypes currently used in selection for fertility breeding values. The main

objective was achieved by (1) evaluating the potential accuracy of different scenarios when combining a cow training population measured for the endocrine fertility trait C-LA with a training population of bulls with daughter observations for traditional fertility traits in multitrait genomic prediction of fertility; (2) evaluating the potential accuracy of across-country genomic prediction; (3) investigating recording strategies that optimally use the Herd Navigator for genomic prediction in terms of the number of farms and number of lactations per cow. For our objectives, predicted accuracy was obtained by estimating population parameters for the traits in a data set of Holstein Friesian cows and using a deterministic equation (Wientjes et al., 2016) that uses actual population parameters to predict the accuracy of genomic breeding values when different populations are combined in 1 training population. The effect of different factors such as genetic correlation between populations, heritability, and reliability of the physiological phenotype on the accuracy of genomic prediction were investigated.

MATERIALS AND METHODS

To obtain potential accuracy of predicting genomic breeding values using the deterministic equation, 3 steps were involved. In the first step, the available phenotypes and genotypes were used to estimate population parameters. The phenotypes were used to estimate genetic parameters (heritability and genetic correlations) in a mixed model, whereas the genotypes were used to estimate the effective number of chromosome segments (**Me**). In the second step, the population parameters were used in the deterministic equation to predict potential accuracy for different scenarios of genomic selection. In the last step, recording strategies for endocrine fertility traits were investigated.

Phenotypes

The phenotype data consisted of inline P4 records from 15 commercial herds in the Netherlands. In total, phenotypic data were available for 8,080 lactations on 3,136 Holstein Friesian cows. Milk sampling, measuring and recording of P4 level was performed with the Herd Navigator (DeLaval Int.) on all farms. Sampling frequency for P4 measurement was based on a biological model (Friggens et al., 2008), but on average was undertaken every 2 d. The endocrine fertility trait investigated was C-LA, which was defined as the number of days between day of calving and first day on which milk P4 level was elevated ≥ 5 ng/mL. The traditional fertility traits were CFS and CInt.

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