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Improving genetic evaluation using a multitrait single-step genomic model for ability to resume cycling after calving, measured by activity tags in Holstein cows

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ABSTRACT

The objective of this study was to evaluate the improvement of the accuracy of estimated breeding values for ability to recycle after calving by using information of genomic markers and phenotypic information of correlated traits. The traits in this study were the interval from calving to first insemination (CFI), based on artificial insemination data, and the interval from calving to first high activity (CFHA), recorded from activity tags, which could better measure ability to recycle after calving. The phenotypic data set included 1,472,313 records from 820,218 cows for CFI, and 36,504 records from 25,733 cows for CFHA. The genomic information was available for 3,159 progeny-tested sires, which were genotyped using Illumina Bovine SNP50 BeadChip (Illumina, San Diego, CA). Heritability estimates were 0.06 for the interval from calving to first insemination and 0.14 for the interval from calving to first high activity, and the genetic correlation between both traits was strong (0.87). Breeding values were obtained using 4 models: conventional single-trait BLUP; conventional multitrait BLUP with pedigree-based relationship matrix; single-trait single-step genomic BLUP; and multitrait single-step genomic BLUP model with joint relationship matrix combining pedigree and genomic information. The results showed that reliabilities of estimated breeding values (EBV) from single-step genomic BLUP models were about 40% higher than those from conventional BLUP models for both traits. Furthermore, using a multitrait model doubled the reliability of breeding values for CFHA, whereas no gain was observed for CFI. The best model was the multitrait single-step genomic BLUP, which resulted in a reliability of EBV 0.19 for CFHA and 0.14 for CFI. The results indicate that even though a relatively

small number of records for CFHA were available, with genomic information and using multitrait model, the reliability of EBV for CFHA is acceptable. Thus, it is feasible to include CFHA in Nordic Holstein breeding evaluations to improve fertility performance.

Key words: genomic prediction, multitrait analysis, reliability, activity tags

INTRODUCTION

Improving fertility in dairy cows is becoming increasingly important throughout the world because it has a substantial effect on the overall profitability of dairy cattle production. Reduced fertility is characterized by increased number of inseminations, more veterinary treatments, longer calving interval, and increased rates of involuntary culling (De Vries, 2006; Sewalem et al., 2008).

The genetic improvement of fertility traits in dairy cows is hindered by low heritability because of the nature of traditionally defined fertility traits, missing and censored records, and farmer's interventions. For example, the interval from calving to first insemination (CFI) is an economically important trait in the Nordic Total Merit index, because it measures the cow's ability to return to cyclic estrus after calving. However, CFI is heavily influenced by the management practices, such as inseminating high-yielding cows later than low-yielding cows or the herd's voluntary waiting period (Andersen-Ranberg et al., 2005; Løf et al., 2012); consequently, the heritability estimate of CFI in Nordic countries is only 0.05 (SEGES, 2015). These factors will result in low accuracy of the EBV, especially for cows and young bulls. Thus, the selection decisions of animals will be based on inaccurate EBV, which decreases the efficiency of selection and increases the number of daughters records required to obtain accurate bull evaluations (Sewalem and Kistemaker, 2008; Sun et al., 2010).

One possible solution to increase accuracy of EBV for fertility traits is to increase the number of daughters

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tested per bull, but that would increase the cost of the breeding program (Veerkamp and Beerda, 2007). Another way to improve the accuracy of selection for fertility is by using more precise phenotypes that directly reflect the cow's physiological or behavioral condition, such as the interval from calving to first high behavioral activity (**CFHA**). The interval from calving to first high behavioral activity is an objective measure of return to cyclic estrus after calving and can be measured by activity tags (Løvendahl and Chagunda, 2010). It has been reported that CFHA has heritability estimates of 0.12 to 0.18, indicating that the inclusion of CFHA in breeding programs would efficiently increase the genetic improvement for a rapid return to cyclicity after calving (Løvendahl and Chagunda, 2009; Ismael et al., 2015).

However, the possibility to achieve accurate EBV for CFHA is hindered by the limited numbers of the phenotypic records available, mainly because of the limited number of farms using activity tags to detect estrus and their ability to automatically store the physical activity data in central databases. To increase reliability of EBV for a trait with small number of phenotypic records, a multitrait model to use additional information of the correlated traits could be a good approach. Moreover, genomic selection could be a promising tool to improve the accuracy of estimation of breeding values of fertility traits.

Genomic selection refers to selection based on genomic EBV instead of the traditional selection using information on phenotypes and pedigrees to predict breeding values (Meuwissen et al., 2001). Genomic selection may result in higher rates of genetic gain over traditional selection using BLUP-EBV because genomic EBV have higher reliabilities, especially for young animals that do not have daughter records. As accurate selection can be performed early in life, genomic selection can greatly reduce evaluation cost and generation interval compared with the traditional progeny test schemes (Schaeffer, 2006; Boichard et al., 2016).

Various models have been used for genomic prediction to use phenotypic information as much as possible for genomic prediction. Misztal et al. (2009) proposed that the genomic breeding values can be obtained in a single-step genomic BLUP (**ssGBLUP**) including phenotypic, pedigree, and genomic information, where a pedigree-based relationship matrix (**A**) in the evaluation procedure is replaced by a matrix (**H**) that combines **A** and a genomic relationship matrix (**G**) (Christensen and Lund, 2010; Christensen, 2012). The same procedure also applied by Aguilar et al. (2011), who reported a 3× increase of reliability of EBV prediction by using ssGBLUP instead of traditional BLUP estimation of breeding values for conception rate in US

Holstein. Furthermore, studies on Nordic Holstein and Red cattle indicated that ssGBLUP can provide more accurate and simpler estimation of genomic breeding values compared with the multistep genomic prediction methods (Gao et al., 2012; Su et al., 2012b). The objective of our study was to improve reliability of EBV for CFI and CFHA using information of correlated traits and genomic markers, and assess whether it is feasible to include CFHA in the Nordic Holstein breeding program, given the current relatively small number of phenotypic records.

MATERIALS AND METHODS

Phenotypic and Genotypic Data

Female fertility traits in the present study were CFHA (Løvendahl and Chagunda, 2010; Ismael et al., 2015), and CFI. The CFHA was based on data from physical activity meters; physical activity data were collected from 55,627 Danish Holstein cows during the period from January 2010 to May 2016. The cows were housed in 176 commercial dairy herds with automatic milking systems and electronic activity tags were fitted on neckbands (Lely Qwes-H or -HR, Lely Industries BV, Maassluis, the Netherlands). Cows' physical activity was measured as the number of electronic impulses per 2-h bin initiated by changes in acceleration due to head and neck movements. Data were edited using the procedure as described by Ismael et al. (2015). Only records from cows in parities 1 to 3 were included in the analysis. To be eligible for inclusion in the analysis, physical activity had to be recorded within the period from 15 to 155 d postpartum. Within this period, every cow had to have at least 45 consecutive days of recorded activity; this rule was applied because different farms had different start times for physical activity recording. Furthermore, only records for cows from genotyped sires were included in the analysis. After editing, the final phenotypic records of CFHA contained 36,504 records from 25,733 Holstein cows that came from 1,611 genotyped sires and were housed in 144 commercial dairy herds. For CFI, the insemination records for the Holstein cows were obtained from the Nordic Cattle Genetic Evaluation (NAV; SEGES, Aarhus, Denmark). The CFI data included Holstein cows that calved between January 2010 and March 2016. The raw data were edited using Nordic cattle genetic evaluation rules (NAV, 2013). Furthermore, only records in parities 1 to 3 were kept, and cows that moved to other herds during the insemination period were removed. Cows with CFI outside the range of 20 to 230 d were excluded from the analysis. After editing, the final CFI data set contained 1,472,313 records from 820,218 Holstein

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