Genetic architecture of fertility traits in hormonally synchronized and heat detected dairy cows

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Abstract

Ovulation synchronization is becoming a popular alternative to estrus detection in the dairy industry. Accurate heat detection (HD) can be challenging and because of this, ovulation synchronization in combination with artificial insemination, known as timed artificial insemination (TAI), has become a management tool for producers. In addition to overcoming reproductive inefficiencies, TAI can be used to reduce the interval between calving and conception. Previous research has shown that using TAI affects accuracy of genetic evaluations for fertility traits. Moreover, bulls ranked differently for fertility traits under TAI and HD scenarios, suggesting that selection for fertility traits without differentiating between breeding methods might lead to potential bias within genetic evaluations. The objectives of this study were to estimate genetic correlations between fertility traits measured under TAI and HD in Canadian Holstein cows. Lactanet provided data containing 3 842 breeding protocol descriptions, of which 2 002 were classified as TAI and 1 840 as HD. First parity cows were included in the dataset, excluding heifers due to a low frequency of TAI usage in this category. Calving to first service (CTFS), first service to conception (FSTC), and days open (DO) were the fertility traits considered. The final dataset included 228 744 records from 152 104 cows. The genotype dataset included 6 985 genotyped cows with records for FSTC and DO and 7 220 genotyped cows with records for CTFS. Variance components were estimated using a Bayesian single-step GBLUP multiple-trait animal model adapted from models used by Lactanet in the genetic evaluations for fertility traits. The heritability estimates were slightly different between HD and TAI (FSTC (0.02, 0.03), CTFS (0.02, 0.01), and DO (0.03 and 0.04), with all the posterior standard deviation (PSD) values < 0.003) and were in the range of those in the literature. The additive genetic correlation ($\pm$ PSD) between HD and TAI were 0.73 $\pm$ 0.04, 0.89 $\pm$ 0.03 and 0.91 $\pm$ 0.01 for FSTC, CTFS and DO, respectively. The genetic correlations less than unity suggest the phenotypic expression of two different traits. In the next step, we will explore the potential different genetic backgrounds between HD and TAI traits by performing genome-wide association studies.

Key words: Heat detection, timed artificial insemination, genetic correlation, days open, calving to first service, first service to conception

Introduction

Estrus detection is required for successful artificial insemination (AI), which can represent a challenge for some herds. Studies have revealed that high-producing cows may display a shortened and less obvious estrus, making detection difficult (MacMillan, 2010; Walsh et al., 2011; Wiltbank et al., 2011). With the use of hormonal synchronization combined with AI in a technique known as timed AI (TAI), estrus detection has become much simpler as it results in a more predictable estrus. Additionally, TAI has been applied to improve breeding outcomes in dairy cows with poor fertility (Wiltbank et al., 2011) and to reduce the interval between calving and conception (MacMillan, 2010).

Oliveira Junior et al. (2021a) investigated multiple parameters to indirectly measure bias when using TAI records on genetic evaluations of fertility traits. The results of their study found that as the usage rate of TAI increased, there were unfavourable changes in all analyzed parameters for female reproductive traits. Lynch et al. (2021) analyzed real fertility data from Canadian Holstein cows and concluded that the use of TAI affects the accuracy of genetic evaluations for fertility traits in dairy cattle, which corroborated the results of Oliveira Junior et al. (2021a). Lynch et al. (2021) observed a large re-ranking of bulls when comparing TAI against heat detection (HD) records, suggesting that TAI and HD records might provide information of genetically different traits.

The objective of this study was to estimate the genetic correlation (r_g) between fertility traits measured on both TAI and HD records in Canadian Holstein cows.

Material and Methods

Breeding data

Data were provided by Lactanet (Guelph, Ontario, Canada), and contained 3 842 breeding protocol descriptions, of which 2 002 records were classified as TAI, and 1 840 as HD. Traits were measured in first parity cows, with heifers not being included given the low frequency of TAI usage in this category (Lynch et al., 2021).

The following fertility traits were analyzed: (i) calving to first service (CTFS), defined as the number of days between calving and first insemination; (ii) first service to conception (FSTC), defined as the number of days between the first insemination and the insemination that resulted in a calf; and (iii) days open (DO), defined as the number of days from calving to conception. This resulted in a dataset with six fertility traits, whereby each trait was split by whether HD or TAI was used, for instance CTFS_HD was CTFS measured on cows using heat detection, and CTFS_TAI was measured on cows where TAI was used. Three hundred and five-day milk yield (MILK) was also

included in analyses as a reference trait and to help with analyses convergence.

Contemporary groups (CG) were formed by the concatenation of herd and year born. Groups with less than five animals, as well as disconnected CG (Roso et al., 2004) were removed. The description of the final dataset is presented on Table 1.

Table 1. – Descriptive statistics of records in the edited dataset for fertility traits measured on heat detection (HD) or on timed artificial insemination (TAI) cows

Traits	Cows	Mean	SD
FSTC_HD	52 789	19.85	31.98
FSTC_TAI	27 523	17.57	33.45
CTFS_HD	58 923	76.48	25.55
CTFS_TAI	31 366	79.75	18.29
DO_HD	52 789	95.12	40.66
DO_TAI	27 523	96.32	37.35
MILK	85 549	9 417.90	1 667.41

FSTC: first service to conception; CTFS: calving to first service; DO: days open; MILK: 305-day milk yield (kilograms).

Genomic data

The imputed genotype data (50K SNP) were provided by Lactanet and included 6 985 cows with records for FSTC and DO, and 7 220 cows with records for CTFS. All genotype data were 50K or imputed to 50K density and were mapped to the ARS-UCD1.2 bovine assembly. Genotype quality control consisted of removing markers with a minor allele frequency lower than 0.05 and removing markers with a call rate less than 90%. Also, animals with a genotype call rate less than 90% were removed. A total of 44 819 SNP remained for further analyses, and all animals passed quality control.

Variance components

Variance components were estimated in single-step GBLUP (ssGBLUP) three-trait animal models using Bayesian methodology implemented in the GIBBS1F90 software (Misztal et al., 2002). Besides the fertility traits measured in TAI and HD cows, MILK was included as an additional trait in the three-trait models as its genetic parameters are well-known in the literature (Oliveira Junior et al.,

2021b). The trait-specific statistical model equations used in this study were adapted from those used by Lactanet (Guelph, Ontario, Canada) in their genetic evaluations (Oliveira Junior et al., 2021b). The general model equation for fertility traits was defined as:

$$y_{ijkl} = \mu + RYM_i + AM_j + H_k + a_l + e_{ijkl}$$

where y_{ijkl} were the observed phenotypes (e.g., CTFS_TAI, CTFS_HD, MILK) of the lth cow, RYM_i was the fixed effect of the ith region-year-month born, AM_j was the fixed effect of the jth age of previous calving-month of previous calving for DO and CTFS, while for FSTC, AM_j was the fixed effect of the jth age of previous calving-month of first service, H_k was the random effect of the kth herd-year born, a_i was the random additive genetic effect of the lth cow and e_{ijkl} was the vector of random residuals. The covariance matrix (V) was defined as:

$$V = var \begin{bmatrix} a \\ h \\ e \end{bmatrix} = \begin{bmatrix} G \otimes H & 0 & 0 \\ 0 & HY \otimes I & 0 \\ 0 & 0 & R \otimes I \end{bmatrix}$$

assuming that $\begin{bmatrix} a \\ h \\ e \end{bmatrix} \sim N(0, V)$, for additive genetic ($G$), herd-year ($HY$) and residual ($R$) covariance matrices among traits, H was the genetic relationship matrix, and I was an identity matrix. The inverse of H (Aguilar et al., 2010) was defined as:

$$H^{-1} = A^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & G_{22}^{-1} - A_{22}^{-1} \end{bmatrix}$$

where subscript 2 refers to genotyped animals, A^{-1} was the inverse of the pedigree relationship matrix and G_{22}^{-1} was the inverse of the genomic relationship matrix, as described by VanRaden (2008).

A Gibbs chain of 1 005 000 iterations was generated with an initial burn-in of 5 000 and a sampling interval of 100. Therefore, the posterior mean and posterior standard deviation (PSD) of the estimated heritability, covariances, and correlations were calculated with the remaining 10 000 samples.

Results & Discussion

The heritability estimates were in agreement with the range of values found in the literature (Oliveira Junior et al., 2021b). Genetic correlation that substantially deviated from unity between the same fertility trait under HD and TAI may indicate that they are genetically different traits (Table 2).

Table 2. Posterior means (±PSD) of heritability, and genetic correlation for fertility traits measured on heat detection (HD) or on timed artificial insemination (TAI) cows

Traits	Heritability	Genetic correlation
FSTC_HD	0.02 ± 0.002	0.73 ± 0.04
FSTC_TAI	0.03 ± 0.002	
CTFS_HD	0.02 ± 0.002	0.89 ± 0.03
CTFS_TAI	0.01 ± 0.001	
DO_HD	0.03 ± 0.002	0.91 ± 0.01
DO_TAI	0.04 ± 0.003	
MILK	0.28[1]	

[1] Mean heritability from the three multiple trait analysis (SD < 0.001). FSTC: first service to conception; CTFS: calving to first service; DO: days open; MILK: 305-day milk yield (kilograms).

These findings, in conjunction with conclusions from Oliveira Junior et al. (2021b) and Lynch et al. (2021), support the hypothesis that fertility traits measured under the use of TAI are genetically different from those recorded in cows where HD is used. Genome-wide association studies could further resolve the different genetic backgrounds between fertility traits recorded in HD and TAI cows.

Technologies, such as TAI, have improved animal breeding efforts, by decreasing generation interval and increasing selection intensity (Gengler and Druet, 2001). As these new technologies and management strategies are adopted by the dairy industry, their effects on an animal breeding program should be closely monitored.

Conclusions

The genetic correlations less than unity between fertility traits measured on heat

detection and hormonal synchronized cows suggests the phenotypic expression of two different traits. Further investigation on the genetic background of this difference is warranted.

Acknowledgements

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