

# The Effect of Synchronized Breeding on Genetic Evaluations of Fertility Traits in Dairy Cattle

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## Abstract

Estrus detection is labor-intensive and time-consuming, with decreased expression in many high-producing dairy cows. To overcome this issue, some producers use hormone protocols to synchronize ovulation and perform timed artificial insemination (timed AI). The objective of this study was to assess the potential bias that timed AI might add to the estimated genetic parameters of female reproductive traits. A Holstein population with 400 sires and 3 000 dams was simulated over 20 years, resulting in 30 000 cows randomly distributed in 200 herds. The simulated traits mimicked calving to first service (CTFS), first service to conception (FSTC) and days open (DO), assuming these to be the most affected traits by hormone synchronization. A total of 13 scenarios were tested, changing the percentage of herds and cows that were randomly selected to be under timed AI. To simulate the effect of timed AI, cows had their phenotypes masked by setting CTFS and DO to the mean of CTFS, and FSTC was set to zero. Four parameters were used to indirectly measure the presence of bias: 1) the correlation between true (TBV) and estimated (EBV) breeding values (accuracy); 2) the differences in the mean EBV of top 25, 50, 75 and 100 sires; 3) changes in correlation between TBV's and EBV's ranks; and 4) the changes in the genetic trend. The accuracy within each class of animals (bulls, dams and cows) decreased proportionally with the increase of the use of timed AI. The average EBV of the top sires went toward zero when increasing the number of hormonal synchronized animals. The sires' rank correlation of EBVs and TBVs followed similar behaviour, with smaller correlation for scenarios with more timed AI animals. The genetic trend was also more affected by scenarios that considered more intense use of hormonal synchronization. This simulation study indicated that genetic evaluations that included herds that used timed AI are likely biased, and the amount of bias is proportional to the number of animals on timed AI.

**Keywords:** bias, dairy cattle, fertility, genetics, timed AI

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## Introduction

The success of the fertility performance of dairy farms, especially for artificial insemination (AI) programs, starts with estrus detection (Roelofs et al., 2010; Silper et al., 2017). Detecting estrus can be very labor-intensive, time-consuming, and prone to errors, especially on large farms (Diskin and Sreenan, 2000; Colazo and Mapletoft, 2014). In addition, estrus expression has decreased on high-producing Holstein

cows, with up to 60% of ovulations accompanied by no standing mount (Butler, 2003; Kerbrat and Disenhaus, 2004; Roelofs et al., 2005). The dependency of estrus detection can be overcome by the use of hormonal protocols to synchronize follicle growth, corpus luteum regression, and ovulation. This practice leads to timed AI that facilitates lactating cows to start a new estrous cycle, making ovulation time easier to predict, thereby increasing herds' conception rates (Cerri et al., 2004; Roelofs et al., 2005).

Information about which herds and/or cows are on timed AI is not currently available for most of the genetic programs. However, the phenotypes of these hormonal synchronized cows might be a source of bias for genetic evaluations, and there is a limited number of studies approaching this problem. Therefore, in this study we assessed the effects of timed AI on the estimated genetic effects for female fertility traits in a simulated Canadian Holstein population.

## Materials and methods

### Simulated population

A Holstein population was simulated using a *Fortran 77* program (unpublished) developed by Dr. Larry Schaeffer. A starting population of 400 sires and 3 000 dams was randomly mated for three generations. Subsequently, 17 more generations were used to expand the starting population, resulting in 30 000 cows that were randomly distributed in 200 herds. The traits selected for this study were: calving to first service (CTFS), first service to conception (FSTC), and days open (DO), as these traits are probably the ones more greatly affected by

hormonal synchronization. A fourth unrelated trait representing a production index (PI) was also included, which was used for breeding decisions. Genetic parameters of these traits were obtained from Lactanet and used as input in this simulation. The simulation was replicated 100 times.

### Simulated scenarios

A total of 13 scenarios (named S1 to S13) were tested, where the percentages of herds and cows that were randomly selected to be under timed AI were changed (Table 1). These scenarios were grouped as: A) a control scenario where no synchronization protocols were used, and breeding was based only on natural estrus (S1); B) a combination of natural heat detection and timed AI within herds (S2-S9); C) all cows within herds were hormonal synchronized (S10-S13). The proportion of 25%, 50%, 75% and 100% herds randomly selected were assumed to be on timed AI in groups B and C. In group B, different proportions of animals were also assumed to be on timed AI, with 25% or 50% of cows randomly chosen within a given herd. The hormonal synchronized cows had their phenotypic information masked by setting CTFS and DO to the mean of CTFS (86 days), and FSTC was set to zero.

Table 1 – Simulate scenarios (S) considering different proportion of herds (Pherd) and different proportion of cows (Pcow) under hormonal synchronization.

	S1	S2	S3	S4	S5	S6	S7	S8	S9	S10	S11	S12	S13
<b>Pherd (%)</b>	0	25	50	75	100	25	50	75	100	25	50	75	100
<b>Pcow (%)</b>	0	25	25	25	25	50	50	50	50	100	100	100	100

### Statistical Model

Breeding values were estimated for all animals (sires, dams and cows) by the following multi-trait animal model:

$$y = Xb + Za + Wh + e$$

where  $y$  is the vector of observations (CTFS, FSTC, and PI);  $b$  is the vector of the fixed effect year of calving;  $a$  is the vector of random

additive genetic effects;  $h$  is the vector of random herd-year born-season effects;  $e$  is the vector of random residual effects;  $X$ ,  $Z$  and  $W$  are design matrices relating observations in  $y$  to factors in the model. Four seasons of calving were defined as: January-March, April-June, July-September, and October-December. The covariance matrix was defined as:

$$\begin{bmatrix} \mathbf{a} \\ \mathbf{h} \\ \mathbf{e} \end{bmatrix} \sim MVN \left( \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \mathbf{G} \otimes \mathbf{A} & 0 & 0 \\ 0 & \mathbf{I} \otimes \mathbf{H} & 0 \\ 0 & 0 & \mathbf{I} \otimes \mathbf{R} \end{bmatrix} \right),$$

where  $\mathbf{G}$  is the covariance matrix of random additive genetic effects,  $\mathbf{H}$  is the covariance matrix of herd-year random effect, and  $\mathbf{R}$  is residual covariance matrix. The  $\mathbf{A}$  matrix represents the additive relationship matrix; and  $\mathbf{I}$  is an identity matrix. Days open components were derived from CTFS and FSTC results.

### Assessing timed AI effect

Four criteria were used to measure the impact of timed AI on the predicted breeding values:

- 1) Correlation between TBV and EBV (accuracy);
- 2) Differences in the mean EBV of top 25, 50, 75 or 100 sires;
- 3) Changes in correlation between TBV's and EBV's ranks;
- 4) Changes in the genetic trend over 20 years;

### Results and Discussion

The accuracy (correlation between TBV and EBV) within each class of animals (bulls, dams and cows) decreased proportionally with the increase of the use of timed AI. On average, EBVs of sires were less affected than cows and dams, with an average accuracy (CTFS) of 0.44, 0.37, and 0.35, respectively. This was expected since sires have multiple daughters contributing to their predicted breeding values (BV), with cows both on and off treatment (Dassonneville et al., 2012).

The average EBV of the top (best 25, 50, 75 or 100) sires went toward zero for the analyzed traits when increasing the number of treated animals. This is probably an effect due to the reduction of variance created by the use of hormonal synchronization. The average EBV differences from S1 and S10 were -0.23 and -0.14 SD for CTFS when considering top 25 and top 100, respectively.

The sire rank correlation between EBVs of the simulated scenarios and the TBVs followed

a similar pattern to the previously described results, with a smaller correlation for scenarios with more synchronized animals. The sire rank correlation varied from 0.67 (S1) to 0.16 (S13) for CTFS and from 0.56 (S1) to 0.12 (S13) for FSTC. Important sire re-ranks were observed; especially as timed AI was used more intensively.

The genetic trend for female reproduction traits was also most affected by scenarios that considered more intensive use of hormonal synchronization. The overall EBV mean of CTFS over the last five simulated generations differed considerably when compared to S1, whereby S5 decreased by 0.72 days while S10 increased by 0.13 days. Similar patterns were observed in FTCS and DO. Although the genetic trends were quite similar in the first four generations, the long-term use of hormonal synchronized cows clearly affected the genetic trend of the population.

### Conclusions

All measures used to assess the effect of timed AI changed unfavorably and proportionally to the increased of its use. The long term use of hormonal synchronized cows in the genetic evaluation has impacted the genetic trends of female reproductive traits. Information about which animals were on timed AI should be available for genetic programs, which could be used to model its effect on the female fertility phenotypes.

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