

# Including Production in Female Fertility Evaluations

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## Introduction

Milk production and reproductive performance are major factors with respect to overall efficiency and profitability of the dairy industry. For many years, dairy cattle research breeding programs were mainly oriented towards yield traits in most countries. Exceptions were the Scandinavian countries, whose selection indices also included health and reproduction, and North American countries, whose selection indices included conformation together with production. Functional traits, such as fertility, longevity, and health traits, are of increased interest to producers in order to improve herd profitability. Various reports indicated that breeding for increased production in dairy cattle has negative side effects on health and fertility traits (Pryce *et al.*, 2004; Washburn *et al.*, 2002 and de Jong, 2006, Melendez., P and P. Pinedo. 2007; Sewalem *et al.*, 2008). In a review of national selection indices, Miglior *et al.* (2005) indicated that the importance of reproduction traits in dairy cattle breeding programs has dramatically increased in the last five years. Several countries have included fertility traits in their national breeding objectives. However, direct selection for fertility traits may be inefficient because these traits have low heritability values (Jamrozik *et al.*, 2005, and others) resulting in low accuracy of estimated breeding values, especially for cows and young bulls under testing when they get their first proofs. Therefore, decisions that would be made on early selection for these traits are associated with uncertainty. Moreover, selection for milk production has been carried out intensively for a long time and hence genetic evaluation of fertility traits might be biased by not accounting for selection decisions made on correlated traits. Walter and Mao (1985) reported that selection bias in genetic parameter estimates of traits undergoing sequential selection can be reduced if these traits are analyzed simultaneously with traits that did not undergo selection.

Therefore, accounting for milk production in the genetic evaluation for fertility traits may avoid the bias on estimated genetic parameters and may also increase the accuracy of selection. The aim of this study was to assess the influence of including either milk production or heifer non-return rate as a correlated trait on the genetic evaluation of fertility traits in Canadian.

## Materials and Methods

Data were obtained from lactation and reproduction records extracted for genetic evaluation of the Holstein breed with first calving occurring between 1997 and 2007. Traits studied were 56-day non-return rate in cows (**NRR**) and in heifers (**NRRH**), calving to first service (**CTFS**), first service to conception (**FSTC**) and test-day milk yield closest to 90 DIM (**TD90M**). Non-return rate was defined as the percentage of cows which did not return to service within 56 days of first insemination and was recorded as 0 (successful) and 1 (unsuccessful). The data included records of first parity cows only with the exception of NRRH which only included data from virgin heifers.

The traits used were modeled using the following equations:

$$\text{NRR} = \text{RYS} + \text{HY} + \text{HYS} + \text{AMf} + \text{SY} + \text{T} + \text{A} + \text{E}$$

$$\text{NRRH} = \text{RYS} + \text{HY} + \text{HYS} + \text{Mf} + \text{SY} + \text{T} + \text{A} + \text{E}$$

$$\text{FSTC} = \text{RYS} + \text{HY} + \text{HYS} + \text{AMc} + \text{A} + \text{E}$$

$$\text{CTFS} = \text{RYS} + \text{HY} + \text{HYS} + \text{AMc} + \text{A} + \text{E}$$

$$\text{TD90M} = \text{RYS} + \text{HY} + \text{HYS} + \text{AMc} + \text{A} + \text{E}$$

where RYS was a fixed effect of region by year of birth by season of birth; HY was a fixed effect of herd by year of birth, HYS was a random effect of herd by year and season of birth, AMf was a fixed effect of age at previous calving by month of first insemination, Mf was a fixed effect of month

of first insemination, AMc was a fixed effect of age at calving by month of calving, SY was a random effect of service sire by year of insemination; T was a random effect of AI technician; A was a random animal additive genetic effect, and E was a random error term. The three cow fertility traits (NRR, CTFS and FSTC) were each analyzed separately in a single trait analysis and were also analyzed in bi-variate analyses with either TD90M (all three female fertility traits) or NRRH (only with NRR). In each analysis 15,000 records from randomly selected herds were used for parameter estimation. The complete data set containing 1,147,770 animals from 16,373 sires was used to calculate breeding values for each of the models used. The DMU software package for the analysis of multivariate mixed model equations (Madsen and Jensen, 2006) was used for all analysis.

## Results and Discussion

Estimates of heritability for NRR from the uni-variate and bi-variate analyses (with test day milk yield included) were 1.7% and 2.0%, respectively. The corresponding figures for CTFS were 7.0% and 8.0% and for FSTC were 4.9% and 5.0%. Both models provided nearly indistinguishable heritability estimates. These estimates of heritability are somewhat lower than those estimate reported by Jamrozik *et al.* (2005) using 16-traits female reproductive performance. The genetic correlations between NRR and TD90M, CTFS and TD90M and FSTC and TD90M were -0.13, 0.29 and 0.12 respectively. This shows that unfavorable genetic correlations exist between production and fertility traits. This is especially true for CTFS. However, the magnitude of correlations between production and fertility traits found in this study were low compared to other studies (Roxstrom *et al.*, 2001; de Jong, 2007).

Absence of an appreciable correlation between milk production and female fertility traits in Canadian Holsteins compared to other countries may be the result of Canada's longstanding balanced breeding approach that includes selection for high production combined with superior conformation to support such production levels. However, to

warrant this assumption, further studies should be carried out to evaluate the relationship between fertility traits and conformation traits in Canadian dairy breeds.

Estimated Breeding values for NRR, CTFS and FSTC in first lactation from a total of 2,939 sires born between 1995 and 2002 with at least 50 daughters with records were selected. The estimated breeding values were averaged by year of birth to estimate genetic trends. The resulting genetic trends, expressed as genetic standard deviations for NRR, CTFS and FSTC, from a single trait and a bi-variate analysis including TD90M as a correlated trait are shown in Figures 1, 2 and 3, respectively. The genetic trend, expressed as genetic standard deviations for NRR from a bi-variate analysis including NRRH as a correlated trait is presented in Figure 4.

Figure 1 shows the genetic trends for 56-day non-return rate. Trends were more or less flat over the years. The genetic trend from uni-variate analysis was slightly higher in the last 2 years than the preceding years. This shows the inclusion of milk production in the model for the analysis of NRR has little influence on genetic trend.

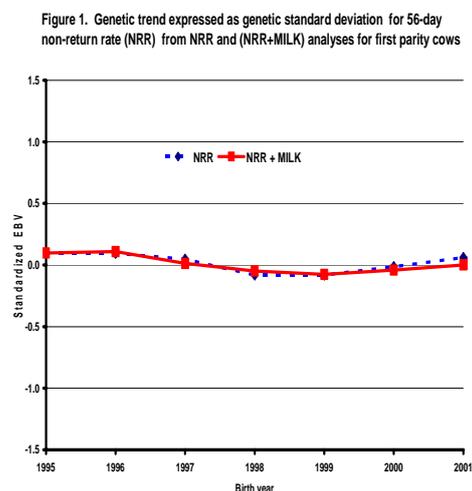
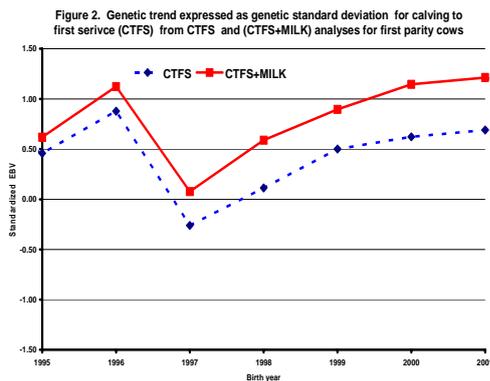


Figure 2 shows that the genetic trend for CTFS in the uni-variate analysis had an irregular but flat trend over time. However, the inclusion of milk yield in the model has increased the trend by 0.07 of a genetic standard deviation per year.



The genetic trend for first service to conception (FSTC) is shown in Figure 3. Similar to CTFS, the inclusion of milk yield in the model increased the genetic trend but for FSTC the increase is only 0.02 of a genetic standard deviation per year.

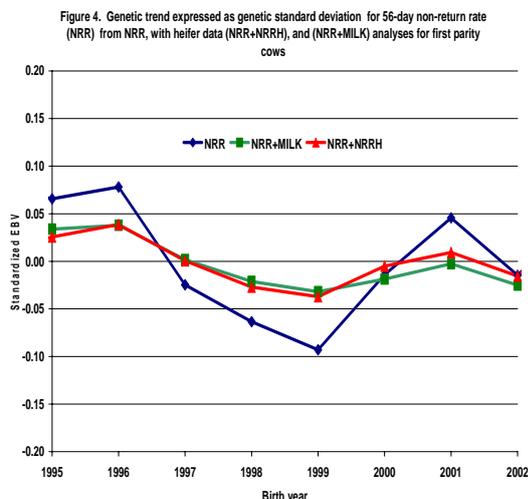
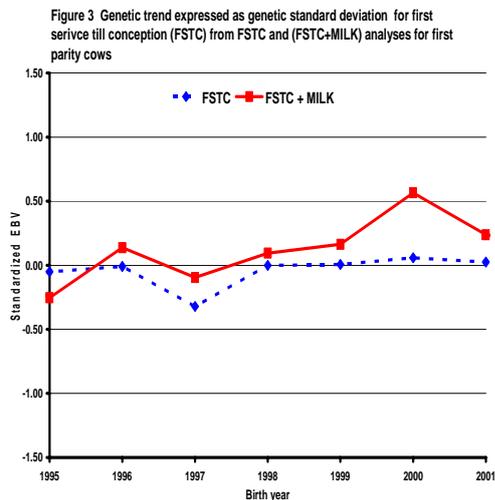


Figure 4 shows that including heifer non-return (NRRH) rate as a correlated trait had a similar impact on genetic trend for NRR as did including TD90M as the correlated trait. Calculating the correlation between the breeding values for NRR obtained from the three models showed that including TD90M or NRRH as a correlated trait resulted in similar breeding values for the selected bulls (correlation is 0.98). Correlations between breeding values from the single trait model and the two multi trait models were 0.90 and 0.91 when using NRRH and TD90M as correlated traits, respectively.

The result found in this study indicate that including heifer non-return rate or milk production as a correlated trait had an impact on estimated breeding values that is very similar. Including one of these effects may help to account for selection and avoid bias on the estimated genetic parameters and also may increase the accuracy of selection. However, further studies should be carried out to verify the results and determine if there is an increase in the accuracy of breeding values.

## Conclusions

In this study, minimal differences in the heritability of female fertility traits were obtained between uni-variate and bi-variate analyses in which milk production was included as a correlated trait. Genetic trends for female fertility traits found in this study were lower than results reported elsewhere. Adding milk production as a correlated trait in the genetic evaluation for NRR had little effect on the genetic trend of NRR. Including heifer non-return rate as a correlated trait in the genetic evaluation of cow non-return rate had a similar effect as including production. However, including production as a correlated trait in the genetic evaluation of CTFS and FSTC increased the genetic trend for these traits over time. Further studies should be carried out to confirm if the inclusion of milk production as a correlated trait influences the accuracy of the genetic evaluations for female fertility traits evaluation and whether inclusion of heifer non-return rate can be used instead.

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