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Relationship between female fertility and production traits in Canadian Holsteins

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ABSTRACT

The objectives of this study were a) to estimate the genetic correlation between milk production and some female fertility traits such as 56-d nonreturn rate in cows (NRRC), calving to first service (CTFS), and first service to conception (FSTC); b) to assess the influence of including milk production as a correlated trait on the genetic evaluation of these traits in Canadian Holsteins; and c) to determine if using heifer nonreturn rate (NRRH) had a similar effect as using milk production on cow NRRC evaluation. The data included fertility and production records of first-parity Holstein cows. Genetic parameters were estimated using uni- and bivariate analyses in which milk production at around 90 DIM (TD90M) was included as a correlated trait to NRRC, CTFS, and FTSC. A bivariate analysis was also carried out in which NRRH was included as a correlated trait to NRRC. The models were compared by genetic trend (NRRC, CTFS, and FSTC) and cross-validation and predictability (NRRC). The heritability estimates for NRRC from the uni- and bivariate analyses were 0.017 and 0.020, respectively. The corresponding figures for CTFS were 0.07 and 0.08 and for FSTC were 0.049 and 0.05. The genetic trends for NRRC of the 2 models (NRRC+TD90M and NRRC+NRRH) gave very similar results. However, when milk production was included in the genetic evaluation of CTFS and FSTC, the genetic trends of the 2 fertility traits were higher compared with the univariate analysis. In NRRC evaluation by cross-validation and predictability, the bivariate analyses were more consistent and gave a better predictability than the univariate analysis. However, there was no major difference between the 2 models. Consequently, it might be worth including milk production or heifer fertility as correlated traits in the genetic evaluation of female fertility traits.

Key words: fertility, accounting for selection, multiple-trait analysis

INTRODUCTION

Reproductive performance is one of the major factors that influences the overall efficiency and profitability of the dairy industry. Nonetheless, for many years, dairy cattle research breeding programs were mainly oriented toward yield traits. This was true for most countries with the exception of Scandinavian countries, whose selection indices also included health and reproduction, and North American countries, whose selection indices included conformation together with production (Miglior et al., 2005). Functional traits such as fertility, longevity, and health traits have a considerable effect on the overall efficiency of dairy cattle production. Consequently, these traits are of increasing interest to producers to improve herd profitability. Even so, various reports indicate that breeding for increased production in dairy cattle has negative side effects on health and fertility traits because of antagonistic genetic correlations between production and reproduction traits (Veerkamp et al., 2001; Kadarmideen et al., 2003; Pryce et al., 2004; Melendez and Pinedo, 2007) and production and health traits (Kadarmideen et al., 2000).

Generally, selection for increased production reduces reproductive efficiency (Grosshans et al., 1997; Dematawewa and Berger, 1998; Castillo-Juarez et al., 2000) and increases susceptibility to some diseases and the risk of culling due to diseases and other abnormalities (Simianer et al., 1991; Dematawewa and Berger, 1998; Sewalem et al., 2006). Inadequate herd reproductive performance (manifested in prolonged calving intervals), increased forced culling, or both, can result in less milk and fewer calves per cow per year, less volunteer culling and therefore increased replacement cost, and ultimately, lower net returns (Wall et al., 2003; Gonzalez-Recio et al., 2004, 2006). High-producing cows tend to be less fertile, and this prolongs the length of calving interval, as well as the rate of involuntary culling. In addition, less fertile cows have decreased longevity (Sewalem et al., 2008) and their lifetime production can be less than that of cows with adequate fertility (González-Recio et al., 2004). Hence, a balance between production and functional

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traits must be pursued, and proper economic weights must be applied to every trait.

In a review of national selection indices in several countries, Miglior et al. (2005) indicated that the importance of reproduction traits in dairy cattle breeding programs has increased dramatically in the last 10 yr. Several countries have included fertility traits in their national breeding objectives. However, others may argue that direct selection for fertility traits may be inefficient because these traits have low heritability (Kadarmideen et al., 2003; Jamrozik et al., 2005) resulting in low accuracy of EBV, especially for cows and young bulls. Hence, selection decisions for these traits often involve a great deal of uncertainty.

Intensive selection for milk production has been carried out for a long time and hence genetic evaluation of fertility traits might be biased by not accounting for the early selection decisions that were made (Kadarmideen et al., 2003). 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. Pollak and Quaas (1981), using a simulation study, demonstrated that a single trait evaluation was biased by selection and the bias was removed by including records upon which the selection decision was made. Kadarmideen et al. (2003) recommended a joint evaluation of fertility traits and milk yield using a multiple trait approach. However, they did not test a joint evaluation of heifer and cow fertility traits. In Canada, Canadian Dairy Network (CDN) runs the official evaluation for reproduction using a multiple-trait animal model, which includes heifer and cow fertility and calving traits (Van Doormaal et al., 2007).

The objectives of this study were a) to estimate the genetic correlation between milk production and some female fertility traits; b) to assess the influence of including milk production as a correlated trait on the genetic evaluation of cow fertility traits; and c) to determine if using heifer 56-d nonreturn rate had a similar effect as using milk production on cow 56-d nonreturn rate evaluation.

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-d nonreturn rate in heifers (**NRRH**) and in cows (**NRRC**), days from calving to first service (**CTFS**), days from first service to conception (**FSTC**), and test-day milk yield closest to 90 DIM (**TD90M**), which is the average interval from calving to first service in first-lactation Holstein cows. Nonreturn rate was defined as a cow or heifer that did not return in heat within 56 d of first insemination and was recorded as 0 (unsuccessful) or 1 (successful). For FTSC, a recorded subsequent calving was required. The data included records of first-parity cows with the exception of NRRH, which only included data from virgin heifers. Genetic parameters were estimated using univariate and bivariate analyses in which milk production (TD90M) was included as a correlated trait for all 3 female fertility traits. A bivariate analysis was also carried out in which NRRH was included as a correlated trait in evaluation of NRRC.

The traits were modeled using the following equations:

$$\begin{aligned}\mathrm{NRRC} &= \mathrm{RYS} + \mathrm{HY} + \mathrm{RYSH} + \mathrm{AcMf}\\ &\quad + \mathrm{SSY} + \mathrm{TID} + \mathrm{A} + \mathrm{E},\end{aligned}$$

$$\begin{aligned}\mathrm{NRRH} &= \mathrm{RYS} + \mathrm{HY} + \mathrm{RYSH} + \mathrm{Mf} + \mathrm{SSY}\\ &\quad + \mathrm{TID} + \mathrm{A} + \mathrm{E},\end{aligned}$$

$$\mathrm{FSTC} = \mathrm{RYS} + \mathrm{HY} + \mathrm{RYSH} + \mathrm{AcMc} + \mathrm{A} + \mathrm{E},$$

$$\mathrm{CTFS} = \mathrm{RYS} + \mathrm{HY} + \mathrm{RYSH} + \mathrm{AcMc} + \mathrm{A} + \mathrm{E},$$

$$\mathrm{TD90M} = \mathrm{RYS} + \mathrm{HY} + \mathrm{RYSH} + \mathrm{AcMc} + \mathrm{A} + \mathrm{E},$$

where RYS was a fixed effect of region (5 regions) by year of birth by season of birth (4 seasons: January to March, April to June, July to September, and October to December); HY was a fixed effect of herd by year of birth; RYSH was a random effect of region by herd by year by season of birth; AcMf was a fixed effect of age at calving by month of first insemination; Mf was a fixed effect of month of first insemination; AcMc was a fixed effect of age at calving by month of calving; SSY was a random effect of service sire by year of insemination; TID was a random effect of AI technician; A was a random animal additive genetic effect; and E was a random error term.

In matrix form, the multiple-trait model can be described as

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z}_1\mathbf{r} + \mathbf{Z}_2\mathbf{s} + \mathbf{Z}_3\mathbf{t} + \mathbf{Z}_4\mathbf{a} + \mathbf{e},$$

where $\mathbf{y}$ is a vector of observations, $\mathbf{b}$ is a vector of all fixed effects, $\mathbf{r}$ is a vector of HRYS effects, $\mathbf{s}$ is a vector of service sire effects, $\mathbf{t}$ is a vector of AI technician (TID) effects, $\mathbf{a}$ is a vector of animal additive genetic effects (A), $\mathbf{e}$ is a vector of residuals, and $\mathbf{X}$ and $\mathbf{Z}_i$ ($i = 1, 4$) are respective incidence matrices.