Bivariate analysis of conception rates and test-day milk yields in Holsteins using a threshold-linear model with random regressions

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ABSTRACT

The objective of this study was to estimate genetic correlations between conception rates (CR) and test-day (TD) milk yields in Holsteins for different days in milk (DIM) in small and large herds. The data included 217,213 first-parity service records of 94,984 cows in New York State between 1999 and 2003. The CR was defined as the outcome of a single insemination. Conception rate and TD milk were analyzed using a series of threshold-linear models with fixed effects that included herd-test-date for TD milk and herd-year for CR, age, service month, cubic regressions on DIM using Legendre polynomials and with random effects that included herd $\times$ sire interaction, sire additive genetic and permanent environments with quadratic random regressions on DIM, service sire for CR, and residual. Variance components were estimated using a Bayesian method via Gibbs sampling. Herds were categorized into small (≤ 80 cows) and large operations. Large herds produced a higher TD milk (34.0 vs. 30.8 kg), had lower CR (29.5 vs. 34.4%), began breeding earlier (75 vs. 92 d to first service), and had fewer days open (138 vs. 145 d). The average CR was 20% at 50 DIM, increased to about 38% at DIM 100, and then leveled off. Estimated genetic correlations between CR and TD milk stayed around -0.15 for small herds but changed from positive (0.3) at 60 DIM to negative (-0.3) at 120 DIM for large herds. Genetic correlations for CR between small and large herds were highest at 80 DIM and lowest at 140 DIM. The chi-square test showed that the frequency of service records was significantly different during a given week for 71% of large herds and for 15% of small herds, suggesting more timed artificial insemination services in large herds. For the top 15% of cows for milk, fertility peaked around 100 DIM in large herds and at around 100 and 170 DIM in small herds. It seems that optimum breeding practices in large herds of breeding cows earlier are already followed.

Key words: conception rate, heritability, random regression, threshold model

INTRODUCTION

As production has increased and fertility has deteriorated because of a variety of reasons, reproduction traits have received more attention on the profitability of dairy cows. Lucy (2007) attributes the decline to changes in management and genetics, the latter change mostly due to a negative correlation with production. The genetic improvement of fertility is difficult for several reasons. First, commonly used traits such as days open (DO), nonreturn rate (NR), conception rate (CR), or number of services (NS) have low heritabilities (Jamrozik et al., 2005; González-Recio et al., 2006), and reliability of fertility EBV for bulls with only first-crop daughters is low. Second, fertility traits are subject to differences in management among farms and to censoring. Goodling et al. (2005) reported different heritability estimates that depended on the use of such methods as synchronization treatments, heat detection, and timed breeding. Censored records occur when services continue, when a cow is culled, or when recording of services and pregnancy status is stopped. The CR defined as the proportion of services resulting in pregnancy would be overestimated if those censored records were not included in the analysis. As a result, parameter estimation may be biased. The theory behind analyzing censored records via the Bayesian method was described by Sorensen et al. (1998). Analyses of outcomes of successive services provide a measure of CR that is partly immune to censoring, and a random regression model accounts for intervals between inseminations (Veerkamp et al., 2001).

Hoekstra et al. (1994) and Muir et al. (2004) estimated negative genetic correlations between NR and 305-d milk yield. Pryce et al. (1997) reported a negative genetic correlation between CR at first service and milk yield. Moreover, Kadarmideen et al. (2000), Veerkamp et al. (2001), and González-Recio et al. (2006) reported antagonistic relationships between fertility and milk yields. Windig et al. (2006) showed that genetic cor-

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Table 1. Number of service records (percentage of censored records) by DIM for all, large, and small herds

Class, DIM	All	Large	Small
≤50	7,342 (3.3)	4,118 (3.4)	3,224 (3.3)
51–71	46,914 (4.2)	28,717 (3.9)	18,197 (4.8)
72–92	47,492 (5.4)	25,845 (4.9)	21,647 (5.9)
93–113	37,651 (6.8)	19,547 (6.2)	18,104 (7.6)
114–134	31,165 (8.3)	16,011 (7.6)	15,154 (9.7)
135–155	24,355 (10.5)	12,213 (9.7)	12,142 (11.3)
156–176	18,589 (12.9)	9,052 (12.3)	9,537 (13.5)
177–197	14,379 (14.8)	7,060 (14.6)	7,319 (14.9)
198–218	10,660 (17.4)	4,894 (16.4)	5,766 (18.3)
219–239	8,132 (20.4)	3,727 (19.4)	4,405 (21.3)
≥240	18,414 (29.2)	7,951 (27.8)	10,463 (30.4)
Total	265,093 (9.8)	139,135 (8.6)	125,958 (11.1)

relations between milk and NS were influenced by herd environments. However, fertility is partly influenced by body condition (Wall et al., 2007) and thus varies with DIM. If there is an interaction between fertility as a function of DIM and management, specific ranges of DIM may exhibit higher fertility, and these ranges may be different for different managements. Perhaps the simplest way to differentiate environments is by herd size. Whereas small farms are likely to be family farms with more expertise and more attention to individual animals, large farms would rely more on technology. In particular, estrus detection can be more successful with small farms, whereas large farms would be more likely to use some form of estrus synchronization.

The objective of this study was to estimate genetic correlations between CR and TD milk yields over DIM in large and small Holstein herds and to estimate genetic correlations for CR and TD milk between large and small herds using a threshold-linear random regression model.

MATERIALS AND METHODS

Data

Data files for service records and test-day records were provided by Dairy Record Management Systems (Raleigh, NC). Service records were extracted that included first-parity cows in New York State that calved between 1999 and 2003. Conception was confirmed by a veterinarian or by the next calving. Service records with days to service from calving before 21 d were discarded. Days to service of 50 d was set for service records between 21 and 50 d, and service records after 250 d were discarded. The total number of records was 265,093 for 116,985 cows; 25,893 service records for cows that did not have subsequent calving dates and no confirmation of pregnancy were considered censored. Each service record was matched to a closest TD record for milk. Three times more TD milk records without

corresponding service records were available. However, their inclusion would require creating 3 times more missing records for CR. Inclusion of many missing records would make convergence very slow. Therefore, only TD milk records with service records were used. In addition, our analysis via a Gibbs sampling approach would not reach convergence within a reasonable time using this large data set and our computing resources. It is unclear what effect this might have on the results when excluding those TD milk records in this analysis due to the selection implemented. The data set was divided into 2 subsets according to herd size (large: ≥80 cows; small: <80 cows). The numbers of records by DIM with 21-d intervals are presented in Table 1 for large and small herds (139,135 and 125,958, respectively). The percentage of censored records was 2.5% higher in large herds than in small herds. More censored records accumulated in the later stages of lactation. The censored records were treated as no conception in this study. The average herd sizes for large and small herds were 198 and 27 cows, respectively (Table 2). The pedigree file contained 12,126 sires and dams. The CR was defined as the outcome of an insemination as a binary trait when estimating parameters using the following model.

Threshold-Linear Random Regression Model

Four traits, CR and TD milk in small and large herds, were analyzed using a multiple trait threshold-linear model. The threshold-linear sire model with random regressions on DIM was defined as follows:

$$\begin{bmatrix} \mathbf{1} \\ \mathbf{y} \end{bmatrix} = \begin{bmatrix} \mathbf{X}\boldsymbol{\beta} + \mathbf{W}_1\mathbf{s} + \mathbf{W}_2\mathbf{h} + \mathbf{Z}_1\mathbf{u} + \mathbf{Z}_2\mathbf{p} + \mathbf{e} \\ \mathbf{X}\boldsymbol{\beta} + \mathbf{W}_2\mathbf{h} + \mathbf{Z}_1\mathbf{u} + \mathbf{Z}_2\mathbf{p} + \mathbf{e} \end{bmatrix},$$

where $\mathbf{1}$ = vectors of unobserved liabilities for service records in small and large herds from a binary outcome (no conception or conception); $\mathbf{y}$ = vectors of observations for TD milk in small and large herds as a continu-

Table 2. Means (SD) of fertility traits, test-day milk yield, and herd size for all, large, and small herds

Statistic	All	Large	Small
Days open, d	142 (64)	138 (64)	145 (64)
Days to first service, d	85 (35)	75 (25)	92 (40)
Days to second service, d	125 (45)	114 (37)	136 (50)
Days to third service, d	161 (51)	150 (44)	174 (54)
Conception rate, %	31.9	29.5	34.4
Conception rate at first service, %	31.5	28.1	34.2
Conception rate at second service, %	32.8	30.4	34.9
Conception rate at third service, %	31.0	28.9	33.2
Test-day milk yield, kg	32.5 (7.0)	34.0 (7.0)	30.8 (6.7)
Herd size, n	50 (78)	198 (140)	27 (16)

ous trait; β = vectors of fixed effects of herd-test-date for TD milk and herd-year for CR, and age group, month of service, and cubic regressions on DIM (from 50 to 250 d) using third-order Legendre polynomials for both traits; $\mathbf{s}$ = vector of random service sire effects used only for CR; $\mathbf{h}$ = vector of random herd $\times$ sire ($\mathbf{H} \times \mathbf{S}$) interaction with quadratic regressions on DIM using second-order Legendre polynomials; $\mathbf{u}$ = vector of random sire effects with quadratic regressions on DIM using second-order Legendre polynomials; $\mathbf{p}$ = vector of random permanent environmental effects for cows with quadratic regressions on DIM using second order Legendre polynomials; $\mathbf{e}$ = vector of random residual effects; $\mathbf{X}$, $\mathbf{W}_1$, $\mathbf{W}_2$, $\mathbf{Z}_1$, and $\mathbf{Z}_2$ = incidence matrices for β , $\mathbf{s}$, $\mathbf{h}$, $\mathbf{u}$ and $\mathbf{p}$, respectively. The variances are defined as

$$\text{Var} \begin{bmatrix} \mathbf{s} \\ \mathbf{h} \\ \mathbf{u} \\ \mathbf{p} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{S} \otimes \mathbf{I}_s & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{H} \otimes \mathbf{I}_h & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{G} \otimes \mathbf{A}_u & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{P} \otimes \mathbf{I}_p & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{R} \otimes \mathbf{I}_n \end{bmatrix}$$

where $\mathbf{S} = 2 \times 2$ service sire variance matrix for CR; $\mathbf{I}_s$ = identity matrix for s service sires; $\mathbf{H} = 12 \times 12$ matrix for $H \times S$; $\mathbf{I}_h$ = identity matrix for h levels of $H \times S$; $\mathbf{G} = 12 \times 12$ additive genetic (co)variance matrix for sires with the third-order Legendre polynomials for CR and TD milk; $\mathbf{A}_u$ = additive genetic relationship matrix for u sires; $\mathbf{P} = 12 \times 12$ permanent environmental variance matrix for cows; $\mathbf{I}_p$ = identity matrix for p cows; $\mathbf{R} = 4 \times 4$ residual variance matrix; $\mathbf{I}_n$ = identity matrix for n records; and $\otimes$ = direct matrix product. The $H \times S$, additive sire, and permanent environmental effects were considered random regressions on DIM using the second-order Legendre polynomials. Although the $H \times S$ effect is not usually included in analyses of fertility, in our preliminary study, the addition of this effect resulted in smaller fluctuations of additive sire

variances along DIM and in higher heritability for CR. Uniform prior distributions for β , the univariate normal prior distribution for $\mathbf{s}$, and multivariate normal prior distributions for $\mathbf{h}$, $\mathbf{u}$, and $\mathbf{p}$ were assumed. Scaled inverted Wishart prior distributions were assigned to (co)variance matrices for $\mathbf{H}$, $\mathbf{U}$, $\mathbf{P}$, and $\mathbf{R}$, and the scaled inverted chi-square distributions were assigned to the variance for $\mathbf{S}$.

For a combined analysis using all data from small and large herds, the same multiple trait model was used except for 2 traits (TD milk and CR) instead of 4 traits (TD milk and CR in small and large herds). Therefore, the matrix sizes were 2×2 for $\mathbf{S}$ (including zeros for TD milk), 6×6 for $\mathbf{H}$, 6×6 for $\mathbf{G}$, 6×6 for $\mathbf{P}$, and 2×2 for $\mathbf{R}$.

Variance components were estimated with the THRGIBBS1F90 program (Misztal et al., 2002) via the Bayesian approach using Gibbs sampling for threshold and linear models. For each analysis, 30,000 Gibbs samples were discarded as burn-in, and 270,000 samples were saved every 10th to calculate posterior means and standard deviations for (co)variance component, correlation, and heritability estimates. The convergence was visually determined by plotting Gibbs samples. All parameter estimates for CR were on a liability scale.

RESULTS AND DISCUSSION

CR and TD Milk Yields

Table 2 shows the means and standard deviations of DO; days to first, second, and third services; overall CR; CR at first, second, and third services; TD milk yields; and herd size in large and small herds. Here, the definition of CR is the proportion of successive services to the total number of services. The CR (34.4%) in small herds was 4.9 percentage units higher than that (29.5%) in large herds. This may be due to AI conducted in earlier stages of lactation for large herds, resulting in shorter DO; the first insemination is 17 d earlier and DO is 7 d shorter in large herds than in small herds.

Figure 1. Conception rates (CR, ●), corresponding test-day milk yields (▲), and all test-day milk yields (no symbols) across DIM for all (dotted), large (■), and small (▲) herds, respectively.

Calculating from these CR, the average numbers of services were 2.9 and 3.4 for small and large herds, using up to 10 and 14 service records per cow, respectively. The intervals from first to second and from second to third insemination were 39 and 36 d in large herds and 44 and 38 d in small herds, respectively. The reasons for inconsistency between these intervals and the 21-d estrus cycle may include timed AI programs, low or erroneous heat detection or expression, and recording errors. The reproductive performance in large herds appears better than in small herds because of the shorter DO, even though the CR in some stages of lactation is low. The TD milk yield was 3.2 kg less in small herds (30.8 kg) than in large herds (34.0 kg).

Figure 1 shows phenotypic CR and TD milk yields over DIM for large and small herds. Although daily milk yields were higher for all stages of lactation in large herds, CR were always higher for small herds. Assuming that cows express heat equally on any day, the chi-square test may provide evidence of timed AI during a week when a null hypothesis of no timed AI was

used. The chi-square test indicated that the frequency of service records during a week was significantly different for 71% of large herds and for 15% of small herds ($P < 0.05$), suggesting more frequent timed AI services in large herds. This hypothesis is supported by a study by Norman et al. (2008). They reported that cows following timed AI programs had more services and lower CR but also lower DO because of fewer days at first service.

When including all TD milk records regardless of whether there are corresponding CR records, lactation curves for large and small herds were similar to typical lactation curves in the first lactation for high- and low-producing cows, suggesting that essentially the same results would be obtained when all TD milk or only TD milk with corresponding service records were used. Cows with service records produced greater milk yields except for peak milk yields over DIM than did all lactating cows, indicating that cows without sufficient energy balance to produce milk and express heat had fewer chances to be inseminated.

Table 3. Averages of posterior means (upper) and SD (lower) for (co)variance components of conception rate (CR) and test-day (TD) milk yield during lactation from 50 to 250 DIM for all, large, and small herds ($\times 100$ for variances of CR and covariances, Cov)

Effect	All			Large			Small		
	CR	TD milk	Cov	CR	TD milk	Cov	CR	TD milk	Cov
Service sire	4.6 0.3	—	—	4.0 0.4	—	—	5.2 0.4	—	—
Sire genetic	1.2 0.2	1.3 0.1	-2.1 1.3	2.8 0.5	1.8 0.2	-3.3 2.4	2.0 0.4	1.3 0.1	-1.3 1.9
Permanent environmental	3.6 0.9	21.3 0.2	-0.4 3.6	5.4 1.2	24.5 0.4	-0.4 5.8	27.4 2.9	17.9 0.3	-6.1 6.4
Herd $\times$ sire	3.2 0.4	0.5 0.4	0.7 0.3	4.1 0.7	0.8 0.2	0.8 2.9	3.1 0.8	0.8 0.2	1.8 3.3
Residual	100.0 0.1	11.0 0.1	-8.6 1.8	100.0 0.1	12.4 0.1	-6.4 2.7	100.0 0.1	8.9 0.1	-9.4 2.6

The CR increased from 19 to 31% and from 23 to 36% for large and small herds, respectively, and stabilized or slightly decreased after 90 DIM. There may be several reasons for different CR in large and small herds: days to each service is longer for small herds, which could result in a lower CR; milk production is lower in small herds; and heat detection may be easier in small herds although reproduction management may be superior in large herds (Lucy, 2001). Although large herds may receive good management such as timed AI programs, they require more labor. Spalding et al. (1975) reported similar days to first, second, and third services and higher CR in small herds in New York State; however, the CR were higher than those obtained in this study.

(Co)variance Estimates

Table 3 shows the averages of posterior means and the SD of (co)variance components for CR and TD milk from 50 to 250 DIM in large and small herds using the 4-trait model and for CR and TD milk in all herds with the combined data using the 2-trait model. Additive genetic and $H \times S$ variances for CR were larger in large herds than in small herds, but service sire and permanent environmental variances were smaller for large herds. For TD milk, all variance estimates except for $H \times S$ variance were larger in large herds. Average covariance estimates between CR and TD milk for additive genetic, permanent environmental, and residual effects were negative for both herds although these antagonistic relationships were not strong. Most of the estimates in all herds were in between the estimates in large and in small herds.

Heritability and Correlation Estimates

Table 4 shows the averages of posterior means and the SD for proportions of additive genetic, permanent environmental, and $H \times S$ variances to the total

variance for CR and TD milk from 50 to 250 DIM in large and small herds using the 4-trait model and for CR and TD milk in all herds using the 2-trait model. The proportion of permanent environmental variance in small herds for CR was 0.15 higher than that in large herds. One explanation for this large permanent environmental variance of CR in small herds may be due to the higher proportion of censored service records used in small herds. Another possibility could be that the additional variance accounts for variability associated with expression of estrus in mostly small herds; large herds were mostly synchronized and therefore the expression of estrus was unimportant. The average heritability estimate for CR in large herds was slightly lower than that in small herds (0.052 and 0.057, respectively). These heritability estimates were higher than the 0.0224 calculated by Weller and Ron (1992). Using a threshold model, González-Recio et al. (2006) also used censored fertility traits and reported heritability estimates of DO and NS to conception as 0.05 and 0.04 (0.10 and 0.07 for repeatability; 0.04 and 0.05 for herd variance ratio).

Figure 2 shows posterior means and SD of heritability estimates of CR for different herd sizes using the 4-trait model. For large herds, they ranged from 0.02 to 0.07, dropping once and increasing after 90 DIM. On the other hand, for small herds, they increased gradually from 0.03 to 0.10 along with DIM. The differences in the later stages of lactation between heritability estimates in large and small herds were not significant. The heritability estimate for pregnancy rate at 120 DIM reported by Goodling et al. (2005) was 3 times higher than our result at 120 DIM and their result for DO. The heritability estimates (not shown in Figure 2) using the combined data in all herds increased from 0.03 to 0.7 over DIM and were similar to those calculated by Averill et al. (2006) using the Ali-Schaeffer function.

Figure 3 shows posterior means and SD of genetic correlations between CR and TD milk across DIM

Figure 2. Posterior means and SD (with bars) for heritability estimates of conception rates across DIM for large and small herds.

Figure 3. Posterior means and SD (with bars) for genetic correlations between conception rates and test-day milk yields across DIM for large and small herds.

using the 4-trait model. For small herds, the genetic correlations were close to zero; however, for large herds, they changed from positive (0.3) at 60 DIM to negative (-0.3) at 120 DIM, implying that in large herds, cows that produce more (less) milk have better (worse) reproduction performance in the early stages of lactation but not in the later stages. The positive genetic correlation in the early stages of lactation may indicate that only cows with genetic potential for sufficient energy for both production and reproduction had been inseminated as mentioned before. Also, the positive genetic correlation may be due in part to the use of only TD milk records with corresponding CR because only cows that expressed heat in the early stages of lactation may have been selected for sufficient energy balance to produce more milk and ova, according to Figure 1.

Higher heritability for CR at higher DIM suggests that breeding cows later would increase the accuracy of the genetic evaluation. However, the negative genetic

correlation between CR and TD milk at higher DIM especially for productive cows in large herds would make later inseminations less successful. Also, changes in heritability across DIM as estimated may be partly artifacts of the random regression model and peculiarities of the data.

Selected reports for genetic correlations between fertility and milk production traits are presented in Table 5. Berger et al. (1981) and Dematawewa and Berger (1998) estimated that genetic correlations between milk yield and reproductive performance were 0.4 to 0.6. Hoekstra et al. (1994) and Pryce et al. (1997) reported that genetic correlations of milk yield with NR 56 and with milk and conception to first service were -0.26 and -0.19 , respectively. Kadarmideen et al. (2000) and Veerkamp et al. (2001) reported that the genetic correlations with NS per conception and with conceived to first service were 0.41 and -0.42 , and 0.48 and -0.49 , respectively. Muir et al. (2004) also estimated

Table 4. Averages of posterior means (upper) and SD (lower) for proportions of additive genetic (heritability), permanent environmental, and herd $\times$ sire interaction variances to the total variance for conception rate (CR) and test-day (TD) milk yield and for correlations (COR) between the 2 traits during lactation from 50 to 250 DIM for all, large, and small herds

Variance	All			Large			Small		
	CR	TD milk	COR	CR	TD milk	COR	CR	TD milk	COR
Service sire	0.040 0.003	—	—	0.028 0.003	—	—	0.042 0.003	—	—
Sire genetic	0.043 0.009	0.149 0.013	-0.182 0.099	0.052 0.017	0.178 0.018	-0.151 0.100	0.057 0.012	0.177 0.019	-0.102 0.115
Permanent environmental	0.032 0.008	0.624 0.005	0.003 0.051	0.046 0.010	0.619 0.006	0.021 0.062	0.196 0.016	0.619 0.009	-0.027 0.033
Herd $\times$ sire	0.028 0.004	0.016 0.004	0.048 0.159	0.035 0.006	0.021 0.005	0.043 0.127	0.022 0.006	0.025 0.007	0.169 0.193
Residual	0.889	0.323 0.003	-0.026 0.005	0.824	0.311 0.003	-0.018 0.008	0.711	0.312 0.004	-0.031 0.008

Figure 4. Genetic correlations between conception rates at 50, 100, 150, and 200 DIM for all herds and all other DIM using combined data for all herds.

genetic correlations of 0.02 for NR 56 with 305-d milk. Using censored records, González-Recio et al. (2006) estimated genetic correlations of 0.63 and 0.23 with DO and NS, respectively. Although most of these studies showed antagonistic or very weak genetic relationships between milk production and fertility, Berry et al. (2003) concluded that the genetic correlation between test-day milk yield and fertility traits changes during the lactation. Those results support our finding that genetic correlations change during lactation. Cows in large herds are more likely to experience good management, and high-producing cows may have good energy balance for reproduction (Lucy, 2001). Figure 4 shows the genetic correlations among CR at 50, 100, 150, and

200 DIM and other DIM for combined data in all herds using the 2-trait model. The correlations among CR at different DIM were close to zero or even negative when the distance was 100 d or larger. This may indicate that various genes control female fertility in the different stages of lactation, or it may be a consequence of using a random regression model with low accuracy.

Environmental correlations between CR and TD milk changed from positive to negative for both herds during lactation and to rather positive in the later stages of lactation (Figure 5) although the average correlations were close to zero: 0.02 and -0.03 for large and small herds, respectively (Table 4). The positive correlations in the early stages of lactation for large herds and in the later stages of lactation for small herds suggest that producers in large herds may have received better reproduction management plans such as timed AI or synchronization, especially for high-producing cows in the early stages of lactation. A possible explanation for this occurrence is that cows in large herds are more likely to have phenotypically better energy balance for both reproduction and milk production in the early stages of lactation but worse balance in the later stages of lactation. Lucy (2001) summarized the negligible effects of milk production on reproductive efficiency: higher producing herds generally have better reproductive performance. The highest producing cows do not necessarily have the greatest negative energy balance or the lowest BCS. First-lactation cows have lower energy balance because they require energy for growth in addition to lactation. This lower energy balance is associated with delayed intervals to first ovulation. An alternative explanation for negligible environmental correlations in large herds and increasingly negative correlations in

Table 5. Genetic correlations between fertility and milk production traits reported in literature¹

Reference	Genetic correlation between fertility and milk production traits
Berger et al. (1981)	0.47 (DO, 60-d milk) 0.44 (NS, 60-d milk) 0.62 (DO, 305-d milk) 0.62 (NS, 305-d milk)
Hoekstra et al. (1994)	-0.26 (NR56, 305-d milk)
Pryce et al. (1997)	-0.19 (CR at first service, 305-d milk)
Dematawewa and Berger (1998)	0.55 (DO, 305-d milk) 0.53 (NS, 305-d milk)
Kadarmideen et al. (2000)	0.41 (NS, 305-d milk) -0.42 (CR, 305-d milk)
Veerkamp et al. (2001)	0.48 (NS, 305-d milk) -0.49 (CR at first service, 305-d milk)
Berry et al. (2003)	Negative except in early lactation (PR, TD milk)
Muir et al. (2004)	0.02 (NR56, 305-d milk)
González-Recio et al. (2006)	0.63 (DO, 305-d milk) 0.23 (NS, 305-d milk)

¹DO = days open; NS = number of services; CR = conception rate; PR = pregnancy rate; NR56 = nonreturn rate in 56 d; TD = test day.

Figure 5. Posterior means and SD (with bars) for environmental correlations between conception rates and test-day milk yields across DIM for large and small herds.

small herds is that large herds continuously attempt to breed their most productive cows, whereas small herds concentrate their efforts on cows with the highest probability of conception.

Figure 6 shows genetic correlations for CR and TD milk between small and large herds. The genetic correlations for TD milk were almost constant, ranging from 0.77 to 0.97 (0.89 on average). These correlations for CR were highest (0.72) at 80 DIM and lowest (0.37) at 140 DIM and increased to 0.63 later (0.53 on average). In small and large herds, CR are genetically similar in early stages of lactation, but they become very different in the middle of lactation, when the majority of the lactating cows conceive. This suggests that genes for CR could be influenced more by environment compared

Figure 6. Posterior means and SD (with bars) for genetic correlations of conception rates (CR) and test-day milk yields between small and large herd environments across DIM.

Figure 7. Phenotypic conception rates for top 15% milk producing cows across DIM for large and small herds.

with those for TD milk, indicating a higher degree of genetic-environment interaction. The same reproductive performance would be expected when breeding sires in the early stage in small and large herd environments, but daughters of the same sires may not express good fertility in the later stages.

When analyses are conducted with 2 data sets (i.e., data for small and large herds and combined data for all herds), the results from the combined analysis are expected to be between those obtained from small and large herds. However, this behavior was not always seen in this study. For CR, some estimates from the combined analyses were smaller or larger than estimates from the separate analyses. Such disparity can be caused by sampling errors or by inconsistency in the definition of traits used in the separate analyses. In particular, the CR could be different in large versus small farms or under timed AI versus traditional conditions.

Figure 7 presents phenotypic CR for top 15% milk producing cows in small and large herds. Although the curve for the large herds has a single peak around 90 DIM, the curve for small farms has an additional peak at about 170 DIM. There is a possibility that high-producing cows in small farms recover faster from the negative energy balance partly because of their lower production compared with cows in large farms, and because different management on small farms (including little timed AI but more accurate heat detection) results in better CR around 170 DIM.

CONCLUSIONS

Conception rate for cows improves up to about 110 DIM in small herds and until about 90 DIM in large herds. Then it declines but a second peak is present at

about 170 DIM for the most productive cows in small herds only. In small herds, the conception rate seems to be barely affected by test-day milk yield through lactation, but in large herds it is negatively affected past 100 DIM with the most negative correlation at 190 DIM. In production systems similar to those in small herds, the chance of pregnancy is maximized by breeding past 90 to 100 DIM. On the other hand, in large herds, the chance of pregnancy for more productive cows is maximized by breeding within the interval of about 70 to 150 DIM. It appears that those recommendations have already been implemented based on a summary of available statistics.

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