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Correlations Among First and Second Lactation Milk Yield and Calving Interval

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ABSTRACT

Estimates of genetic correlations were .17 between first lactation milk yield and concurrent calving interval, .10 between second lactation milk yield and first calving interval, and .82 between first and second milk yields. Corresponding phenotypic correlations were .27, .16, and .58. Heritability estimates were .27 and .25 for first and second lactations and .15 for calving interval. Estimates were averages of two samples of 15 New York State herds averaging 144 AI-sired Holstein cows and 30 sires. Milk yields were 305-d, mature equivalent. Calving interval was days between first and second freshening. First milk records without a second freshening were included. Multiple-trait animal model included separate herd-year-season effects for first and second milk yields and calving interval. Numerator relationships among animals within herd, except for daughter-dam relationships, were included. The REML with the expectation-maximization algorithm was used to estimate (co)variance matrices among genetic values and environmental effects for the three traits. Results indicate a need to adjust milk records for the phenotypic effects of current and previous calving interval. The genetic association, however, between fertility and milk yield appears small. Genetic improvement of 450 kg of milk yield may result in 2 added d to first calving interval.

INTRODUCTION

Several reports (1, 3, 6, 7, 8, 11) have estimated the relationship between milk yield and fertility in the same lactation period measured as days open or calving interval. Funk et al. (5) showed the effect of days open on the previous lactation to be linear on milk yield and about half as great as the effect on milk yield in the concurrent lactation.

The objective of this study was to estimate the genetic and phenotypic correlations between calving interval from the first calving to second calving and milk yield in the second lactation period including first lactation milk yield in the analyses as a control for selection on previous milk yield. Consequently, relationships between first lactation milk yield and calving interval and between first and second lactation milk yield also were estimated.

MATERIALS AND METHODS

Two different samples of 15 herds with between 130 and 160 AI-sired Holstein cows were chosen from a population of 585,830 cows that first freshened from January 1, 1976 through December 31, 1987. Characteristics of the two data sets are in Table 1. Cows were required to have a first lactation milk yield. The second lactation yield records were included if present. Calving interval was calculated from the fresh dates for cows with first and second lactation records. Cows with calving intervals less than 300 d or more than 600 d were excluded. Milk records obtained from the Northeast Dairy Records Processing Laboratory were 305-d, mature equivalent. Cows with milk yields less than 1819 kg were excluded as were cows with codes for estimated records, sample days >75 d apart, sick, injured, aborted, or nurse cows. Cows with no second milk yield (and thus no calving interval) were not excluded. Herd sizes were chosen for computational

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TABLE 1. Means and numbers of records associated with two data sets each with 15 herds of New York State AI-sired Holstein cows.

	Data set	
	1	2
First milk yield		
No. of records	2137	2190
Mean, kg	8153	8041
First calving interval		
No. of records	1398	1476
Mean, d	382	386
Second milk yield		
No. of records	1398	1476
Mean, kg	8456	8085
Average		
Cows per herd	142	146
Sires per herd	29	31

reasons with the consequence that the inferences possible from the analyses may be limited.

Restricted maximum likelihood estimates (10) of genetic and residual covariance matrices were obtained for an animal model that included herd-year-season effects (two seasons per year, February through June and July through January) as well as animal additive genetic values and random environmental effects. Covariances were assumed zero between genetic and environmental effects and between all environmental effects for records not on the same animal. The REML procedure is outlined in Henderson (9) and detailed in Swalve and Van Vleck (12) and Dong and Van Vleck (3) for similar models with records on some traits missing, possibly because of selection. Three incidence matrices for herd-year-season effects are needed corresponding to first milk yields only, calving intervals with first milk yields, and second milk yields for cows with first yields and calving interval. Incidence matrices for additive genetic values are identity matrices 1) of order number of cows with first yields only and 2) of order number of cows with first and second yields and calving interval. As with Swalve and Van Vleck (12), additive (numerator) relationships across herds were assumed to be zero to allow inversion of coefficient matrices herd by herd and pooling of quadratics and expectations of quadratics across herds. Within herd, relationships (including sires and base

animals without records) were included in determining the relationship matrix among cows and records. The major exception to using all relationships was that daughter-dam relationships were ignored to create a block diagonal structure of the within-herd coefficient matrices to speed inversion needed for the expectation step. This approach was described by Dong and Van Vleck (3) and discussed by Dong et al. (4). Because the incidence matrices were different for the traits, the usual transformations to speed computations were not possible. Consequently, only 22 rounds of iteration were done for data set 1 and 20 rounds for data set 2. Changes in heritabilities and correlations were slight probably because starting values for data set 2 were round 20 solutions from data set 1 and for data set 1 were from Swalve and Van Vleck (12) for first and second milk yields and Dong and Van Vleck (3) for calving interval and from Dong (2) for the covariance of CI and second lactation milk. Consequently for many of the estimates, accuracy is equivalent to 50 to 60 rounds of iteration.

RESULTS AND DISCUSSION

Estimates of heritability and genetic and phenotypic correlations are in Table 2. Scaled (to about unity for phenotypic variance) residual and phenotypic variances are also in Table 2. Estimates of heritability are somewhat smaller for milk yield than those reported by Swalve and Van Vleck (12) in agreement with Dong et al. (4) who found smaller estimates of genetic variances as more relationships were ignored.

Heritability estimates for calving interval in this study average the same as those of Dong and Van Vleck (3) for two different data sets (herd sizes ranged from 180 to 220) with first milk yield and calving interval for a similar REML analysis with an animal model and from daughter on dam regression (11) but are larger than from analyses of days open with sire models (.03 to .05) (1, 7, 11).

In the comparison of analyses with full relationships and with some relationships ignored, Dong et al. (4) found no important differences in genetic or phenotypic correlations.

The genetic and phenotypic correlations between first and second milk yields agree almost

TABLE 2. Estimates of parameters for first and second lactation milk yield and calving interval (CI) from two data sets.

Estimates	Data set		
	1	2	Avg.
Heritabilities			
First milk	.28	.25	.27
CI	.16	.15	.15
Second milk	.27	.24	.25
Genetic correlations			
First milk, CI	.18	.16	.17
First milk, second milk	.82	.83	.82
Second milk, CI	.12	.09	.10
Phenotypic correlations			
First milk, CI	.29	.25	.27
First milk, second milk	.56	.60	.58
Second milk, CI	.17	.14	.16
Residual variances			
First milk, kg/1364 ²	.64	.72	.68
CI, d/60 ²	.54	.57	.56
Second milk, kg/1364 ²	.75	.86	.80
Phenotypic variances			
First milk, kg/1364 ²	.89	.96	.92
CI, d/60 ²	.65	.67	.66
Second milk, kg/1364 ²	1.02	1.14	1.08

exactly with those from a similar analysis by Swalve and Van Vleck (12). The phenotypic correlations between first milk yield and concurrent calving interval agree with similar analyses (3) and with results using sire models with days open (7, 11).

The estimates of genetic correlations between first milk yield and calving interval averaged .17 in this study as compared with .09 to .16 from previous analyses with an animal model (3). However, sire analyses with days open (1, 7, 11) have resulted in much larger estimates of genetic correlations as have daughter-dam analyses (11). The difference in heritability of .03 versus .15 for calving interval could account for more than a twofold increase in the genetic correlation because of the same covariance and a much smaller genetic variance in the denominator of the correlations, $.03^{1/2}$ versus $.15^{1/2}$.

In agreement with studies to estimate adjustment factors for first calving interval on second lactation milk (5), both the genetic and phenotypic correlations between second milk yield and previous calving interval are about 40% less than between first milk yield and concur-

rent calving interval. In fact, the phenotypic regression coefficient of yield on first calving interval is about 60 to 64% for second lactation milk yield as compared with first lactation milk yield from data set 1 (4.75 kg/d CI versus 7.80 kg/d CI) and from data set 2 (4.27 kg/d CI versus 6.68 kg/d CI).

CONCLUSIONS

Calving interval as a measure of fertility appears to have a larger heritability ($\sim .15$) as estimated from an animal model in this study and in (3) than does days open ($\sim .03$) as estimated from sire models (1, 7, 11). The difference cannot be explained by the higher heritability usually associated with gestation length because the variance for days open dominates the variance of the sum of days open and gestation length. The increase in heritability with estimates of genetic variance from the animal model may explain much of the disparity in genetic correlations between days open and milk yield in the first lactation ($\sim .40$ to $.60$) from a sire model (1, 7, 11) and between calving interval and milk yield in the first lactation ($\sim .10$ to $.15$) from an animal model. Studies of reasons for the different estimates of heritability and genetic correlations with calving interval from analyses with animal models and sire models are needed.

The expected genetic change in calving interval for change in milk yield due to selection on milk yield can be calculated if the genetic variances and covariances are known. Calculations based on the estimates of the genetic correlation between calving interval and first milk yield (.17), heritabilities of .27 and .15 for yield and calving interval, and corresponding phenotypic variances of 1,700,000 kg² and 2400 d² resulted in expected genetic increase of 2.1 d for a genetic increase of 450 kg of milk. Smaller estimates of heritability for calving interval would reduce the expected change in calving interval, and larger estimates of the genetic correlation would increase the expected correlated change in calving interval due to selection for milk yield. The economic value of the increased milk yield greatly exceeds the economic value of the decreased fertility as measured by increased calving interval.

The genetic and phenotypic correlations of second lactation milk yield with first calving

interval are about 60% as large as those for first lactation milk yield with first calving interval. The phenotypic regressions suggest that 2 to 3% of the variation in second lactation milk yield can be accounted for by the previous calving interval. In agreement with Funk et al. (5), adjustment for previous days open or calving interval seems desirable as well as adjustment of yield for days open or calving interval associated with the same lactation.

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