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## Estimates of correlations among yield traits and somatic cell score with different models to adjust for bovine somatotropin effects on Holstein dairy cows

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**ABSTRACT.** Records of Holstein cows from the Dairy Records Processing Center at Raleigh, NC were edited to obtain three data sets: 65,720 first, 50,694 second, and 65,445 later lactations. Correlations among yield traits and somatic cell score were estimated with three different models: 1) bovine somatotropin (bST) administration ignored, 2) bST administration as a fixed effect and 3) administration of bST as part of the contemporary group (herd-year-month-bST). Heritability estimates ranged from 0.13 to 0.17 for milk, 0.12 to 0.20 for fat, 0.14 to 0.16 for protein yields, and 0.08 to 0.09 for somatic cell score. Estimates were less for later than first lactations. Estimates of genetic correlations among yields ranged from 0.35 to 0.85 with no important differences between estimates with the 3 models. Estimates for lactation 2 agreed with estimates for lactation 1. Estimates of genetic correlations for later lactations were generally greater than for lactations 1 and 2 except between milk and protein yields. Estimates of genetic correlations between yields and somatic cell score were mostly negative or small (-0.45 to 0.11).

Estimates of environmental correlations among yield traits were similar with all models (0.77 to 0.97). Estimates of environmental correlations between yields and somatic cell score were negative (-0.22 to -0.14). Estimates of phenotypic correlations among yield traits ranged from 0.70 to 0.95. Estimates of phenotypic correlations between yields and somatic cell score were small and negative. For all three data sets and all traits, no important differences in estimates of genetic parameters were found for the two models that adjusted for bST and the model that did not.

**Key words:** Bovine somatotropin, Genetic parameters, Milk yield, Somatic cell score

## INTRODUCTION

Milk, fat, and protein yields are the main economic traits for selection in dairy cattle. Estimates of genetic parameters and genetic correlations between yield traits and somatic cell score (SCS) may be different with different models of analysis. Cue et al. (1987) using a multivariate restricted maximum likelihood algorithm found that genetic and phenotypic correlations between pairs of yield traits were all large and positive. Phenotypic correlations between yield traits and SCS were negative (favorable) but small. Estimates of genetic correlations between yield traits and SCS were positive for milk yield but negative for fat and protein yields. Estimates of heritability for milk, fat and protein yields from that study were relatively large: 0.36, 0.38 and 0.25, respectively. Welper and Freeman (1992) reported estimates of heritability of 0.30, 0.29, 0.27, and 0.16 for milk, fat and protein yields, and SCS, respectively. In that study, estimates of genetic and phenotypic correlations between yield traits were positive and large. Estimates of genetic correlations between yield traits and SCS were positive (unfavorable) and small but estimates of phenotypic correlations were negative (favorable) and small. Dematawewa and Berger (1998) reported estimates of heritability of 0.20, 0.18 and 0.18 for milk, fat and protein yields with large and positive estimates of genetic and phenotypic correlations among the yield traits. Carlen et al. (2004) estimated genetic correlations between lactation, average SCS and yield traits to be small and positive (unfavorable) (0.22, 0.17 and 0.23 for milk, fat and protein yields, respectively).

The United States Food and Drug Administration approved use of bovine somatotropin (bST) for use with dairy cows in 1993. Several studies have shown an increase in milk yield of 10 to 40% from use of bovine somatotropin (Bauman et al., 1985; Peel and Bauman, 1987; Thomas et al., 1991; Bauman, 1992; Tsuruta, 1998; Weigel et al., 1998; Bauman et al., 1999; Al-Jumaah, 2001). Weigel et al. (1998) showed that estimates of heritability for milk yield for records made with or without bST treatment were nearly the same (0.20 and 0.21). Tsuruta et al. (2000) using test day records reported similar estimates of heritability for yield traits for cows treated or untreated with bST. Al-Jumaah (2001), using first-lactation records to compare different models to adjust for bST effects, concluded that estimates of heritability obtained with the different models were almost identical and that estimates of genetic correlations between any

two yield traits were high and positive. In that study, no differences in estimates with different models were reported.

Greater availability for this study of SCS records of cows treated with bST now allows estimation of correlations not only among traditional yield traits but also between individual yield traits and SCS. The objective of the current study was to examine whether use of different models to account for the effect of bST treatment would change estimates of genetic correlations among yield traits and SCS in first, second, and third and later lactations.

## MATERIAL AND METHODS

Three different data sets were formed according to parity based on records provided by the Dairy Records Processing Center (DRPC), Raleigh, NC. Data set 1 included only first-lactation records. Data set 2 included only second-lactation records. Data set 3 included records from lactations 3 through 5. Numbers of records and means are shown in Table 1. The three data subsets contained 65,720, 50,694 and 65,445 milk records. There were slightly fewer fat and protein yield records and about 2.6% fewer SCS records. Records consisted of yields preadjusted to 305 day, twice a day milking, and mature equivalent for Holstein cows calving from 1990 through 2001 and of SCS. The SCS is a logarithmic transformation (base 2) of somatic cell count (see Da et al., 1992). Although recording of use of bST by DRPC began in 1994, records of cows born in the period 1990 through 1993 were included to include records of cows receiving bST in later lactations. Approximately 10% of all lactation records included in the data sets were for cows that received bST. Records of cows considered treated with bST had to be coded as injected three or more times during the lactation. Records of cows coded as treated but less than three times during the lactation were not used. Numbers of cows recorded as treated with bST at least three times during the lactation and number of untreated cows are shown in Table 1. Records from herds with less than five cows treated with bST were not included. About 1,000 of the cows in data set 3 that had records with bST treatment also had records without bST treatment.

A two-trait animal model was used to estimate genetic and phenotypic correlations between pairs of yield traits and between each yield trait and SCS for all data sets. In matrix form the model is (for lactations one and two, the permanent environmental effects are not in the model):

$$\begin{bmatrix} \mathbf{y}_i \\ \mathbf{y}_j \end{bmatrix} = \begin{bmatrix} \mathbf{X}_i & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_j \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta}_i \\ \boldsymbol{\beta}_j \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_i & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_j \end{bmatrix} \begin{bmatrix} \mathbf{a}_i \\ \mathbf{a}_j \end{bmatrix} + \begin{bmatrix} \mathbf{W}_i & \mathbf{0} \\ \mathbf{0} & \mathbf{W}_j \end{bmatrix} \begin{bmatrix} \mathbf{c}_i \\ \mathbf{c}_j \end{bmatrix} + \begin{bmatrix} \mathbf{e}_i \\ \mathbf{e}_j \end{bmatrix}$$

where,  $\mathbf{y}_i$  and  $\mathbf{y}_j$  are vectors of lactation records of cows for traits  $i$  and  $j$ ,

$\boldsymbol{\beta}_i$  and  $\boldsymbol{\beta}_j$  are vectors of fixed effects (will change with different models) for traits  $i$  and  $j$ ;

$\mathbf{a}_i$  and  $\mathbf{a}_j$  are vectors of random additive genetic effects for animals for traits  $i$  and  $j$ ;

$\mathbf{c}_i$  and  $\mathbf{c}_j$  are vectors of random permanent environmental effects for cows for traits  $i$  and  $j$  for analysis of data set 3;

$\mathbf{e}_i$  and  $\mathbf{e}_j$  are vectors of random residual effects for traits  $i$  and  $j$ ;

$\mathbf{X}_i$ ,  $\mathbf{Z}_i$ , and  $\mathbf{W}_i$  are known design matrices for trait  $i$ , and

$\mathbf{X}_j$ ,  $\mathbf{Z}_j$ , and  $\mathbf{W}_j$  are known design matrices for trait  $j$ .

**Table 1.** Summary of data for analyses of milk yield, fat yield, protein yield, and somatic cell score (SCS) for lactations 1, 2 and 3 to 5<sup>a</sup> with three models<sup>b</sup>.

Trait/Item <sup>c</sup>	Lactation 1		Lactation 2		Lactation 3 <sup>a</sup>	
	No.	Mean	No.	Mean	No.	Mean
<b>Milk (kg)</b>						
Records	65,720	10,301	50,694	10,529	65,445	9,906
bST	4,740	11,414	3,944	11,573	4,490	10,883
non-bST	60,980	10,214	46,750	10,441	60,955	9,884
CC 1, 2	18,326	–	18,065	–	19,380	–
CC 3	18,835	–	18,554	–	20,152	–
<b>Fat (kg)</b>						
Records	65,621	361.5	50,665	364.6	65,415	348.6
bST	4,740	396.6	3,944	395.1	4,489	380.3
non-bST	60,881	358.7	46,721	362.0	60,926	346.2
CC 1, 2	18,803	–	18,056	–	19,369	–
CC 3	18,812	–	18,545	–	20,140	–
<b>Protein (kg)</b>						
Records	65,532	314.8	50,569	321.8	65,259	305.0
bST	4,740	344.2	3,943	351.1	4,489	332.3
non-bST	60,792	312.5	46,626	319.3	60,770	302.9
CC 1, 2	18,268	–	18,010	–	19,307	–
CC 3	18,777	–	18,498	–	20,078	–
<b>SCS (score)</b>						
Records	63,912	2.775	49,253	3.018	63,768	3.692
bST	4,733	2.666	3,940	2.964	4,488	3.610
non-bST	59,179	2.784	45,313	3.023	59,280	3.698
CC 1, 2	17,936	–	17,662	–	18,933	–
CC 3	18,441	–	18,145	–	19,696	–

<sup>a</sup>Number of cows with lactations 3 to 5: milk, 44,405; fat, 44,380; protein, 44,278; SCS, 43,524.

<sup>b</sup>Model 1 ignored bovine somatotropin (bST) treatment but included as a fixed factor contemporary group (herd-year-month of calving). Model 2 included contemporary groups for Model 1 and a fixed factor for bST or no bST treatment. The contemporary groups for Model 3 were herd-year-month of calving - bST treatment.

<sup>c</sup>CC 1, 2: Number of contemporary groups (herd-year-month of calving) for Models 1 and 2; CC 3: Number of contemporary groups for Model 3.

The first moments for all traits were assumed to be  $E(y) = X\beta$ .

$$\text{For } \mathbf{a} = \begin{bmatrix} \mathbf{a}_i \\ \mathbf{a}_j \end{bmatrix}, \mathbf{c} = \begin{bmatrix} \mathbf{c}_i \\ \mathbf{c}_j \end{bmatrix} \text{ and } \mathbf{e} = \begin{bmatrix} \mathbf{e}_i \\ \mathbf{e}_j \end{bmatrix},$$

the first moments and second moments about the mean for random effects for data sets 1 and 2 for animals with one record each were assumed to be:

$$\mathbf{E} \begin{bmatrix} \mathbf{a} \\ \mathbf{c} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} \quad \text{and} \quad \mathbf{Var} \begin{bmatrix} \mathbf{a} \\ \mathbf{c} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{G}_0 \otimes \mathbf{A} & \mathbf{0} \\ \mathbf{0} & \mathbf{R}_0 \otimes \mathbf{I}_N \end{bmatrix}$$

The moments for data set 3 were assumed to be:

$$\mathbf{E} \begin{bmatrix} \mathbf{a} \\ \mathbf{c} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix} \quad \text{and} \quad \mathbf{Var} \begin{bmatrix} \mathbf{a} \\ \mathbf{c} \\ \mathbf{e} \end{bmatrix} = \begin{bmatrix} \mathbf{G}_0 \otimes \mathbf{A} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{C}_0 \otimes \mathbf{I}_c & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{R}_0 \otimes \mathbf{I}_N \end{bmatrix}$$

where  $\otimes$  is the right direct product operator,

$\mathbf{A}$  is the matrix of numerator relationships among animals,

$\mathbf{G}_0$  is the matrix of additive genetic variances and covariance,

$\mathbf{C}_0$  is the matrix of permanent environmental variances and covariance,

$\mathbf{I}_c$  is an identity matrix with order equal to the total number of cows with records,

$\mathbf{R}_0$  is the matrix of residual variances and residual covariance (if a trait is missing,  $\mathbf{R}_0$  is reduced accordingly),

$\mathbf{I}_N$  is an identity matrix with order equal to number of records for a trait if both traits measured for that lactation,

$\sigma_{a_i}^2$  and  $\sigma_{a_j}^2$  are the additive genetic variances for traits  $i$  and  $j$ ,

$\sigma_{a_i a_j}$  is the additive genetic covariance between traits  $i$  and  $j$ ,

$\sigma_{c_i}^2$  and  $\sigma_{c_j}^2$  are the permanent environmental variances for traits  $i$  and  $j$  for a cow,

$\sigma_{c_i c_j}$  is the permanent environmental covariance between traits  $i$  and  $j$ ,

$\sigma_{e_i}^2$  and  $\sigma_{e_j}^2$  are the residual variances for traits  $i$  and  $j$ , and

$\sigma_{e_i e_j}$  is the residual environmental covariance between records for traits  $i$  and  $j$  for a lactation.

With model 1, the only fixed factor was the contemporary group (herd-year-month (HYM) of calving) with bST treatment ignored. With model 2, the two fixed factors were the contemporary group (HYM) and bST treatment (treated or not treated). With model 3, bST treatment or no bST treatment was used to form the contemporary group to be HYM-bST treatment which was the only fixed factor.

Variance components for random effects were estimated using a derivative-free REML algorithm (Graser et al., 1987) with the computer programs (MTDFREML) developed by Boldman et al. (1995). Local convergence was considered to be met if the variance of the -2 log likelihoods in the simplex was less than  $1 \times 10^{-6}$ . After first convergence, restarts were made to find global convergence with convergence declared when the values of -2 log likelihood did not change to the second decimal.

A weakness of MTDFREML (Boldman et al., 1995) has been the inability to estimate standard errors of estimates of genetic parameters for multiple-trait models when not all traits were measured on each animal with records. In this study, standard errors of estimates of

heritability and of genetic correlations were estimated by using the Kachman and Van Vleck procedure (Kachman SD and Van Vleck LD, personal communication, 2005). The data file was changed to add a new dummy fixed factor for each trait with a unique level of the dummy factor assigned to each record when the trait was missing with the indicator of the missing value included in the analysis as if it were an actual record.

## RESULTS AND DISCUSSION

Estimates of heritability for milk, fat and protein yields and SCS are listed in Table 2 for three models from analyses of first-lactation records. Estimates for lactation one were 0.17, 0.20, 0.16 and 0.09, respectively, with standard errors of 0.01 for all models. Estimates for second lactations were generally slightly smaller and slightly more variable by model than for first lactations. Records of cows in data set 3 resulted in slightly smaller estimates than for first- or second-lactation records with estimates for milk, fat and protein yields of 0.14, 0.12 and 0.14 with Model 3. The average estimates of heritability for SCS were similar for the three data sets and three models (0.08-0.11). Dematawewa and Berger (1998) obtained estimates of heritability of milk, fat and protein yields of 0.19, 0.17 and 0.17, respectively. Tsuruta (1998) reported estimates of heritability for milk, fat and protein yields and SCS of 0.29, 0.26, 0.25 and 0.06 for first-lactation records. Al-Jumaah (2001) estimated heritabilities of milk, fat and protein yields for first-lactation records to be 0.15, 0.26 and 0.20, respectively. Estimates from this study also were in the range of estimates by DeGroot et al. (2002), Sawalha (2004) and Carlen et al. (2004).

Table 2 also shows estimates of correlations estimated from first-lactation records. Estimates of genetic correlations among yield traits ranged from moderately to strongly positive with the three models. These estimates are generally consistent with previous studies (Cue et al., 1987; De Jager and Kennedy, 1987; Dong and Van Vleck, 1988; Welper and Freeman, 1992; Dematawewa and Berger, 1998; Veerkamp et al., 2001; Al-Jumaah, 2001; Tsuruta et al., 2004; Carlen et al., 2004). There were no important differences for estimates of genetic correlations among yield traits for the three models for first-lactation records. Estimates of the genetic correlation between milk yield and SCS were small and negative with the three models: -0.03, -0.04 and -0.03 for Models 1, 2 and 3, respectively. Estimates between fat yield and SCS were small and positive: 0.11, 0.12 and 0.10 for Models 1, 2 and 3, respectively. Estimates between protein yield and SCS were also positive but smaller: 0.03, 0.02 and 0.03.

Estimates of environmental correlations among yield traits for first lactations were in agreement with those found in previous studies (Dematawewa and Berger, 1998; Al-Jumaah, 2001; Veerkamp et al., 2001; Carlen et al., 2004; Tsuruta et al., 2004). Estimates from this study were large and positive and the same to two decimal places with the three models: 0.77 between milk and fat yields, 0.96 between milk and protein yields, and 0.78 between fat and protein yields. Estimates of environmental correlations between yield traits and SCS were small and negative and similar for each of the three models: -0.15 to -0.17 between milk yield and SCS, -0.20 between fat yield and SCS, and -0.14 between protein yield and SCS.

Table 3 shows that estimates of phenotypic correlations among yield traits for first lactations were large and positive and were the same with the three models: 0.70 between milk and fat yields, 0.92 between milk and protein yields, and 0.74 between fat and protein yields. Estimates between yield traits and SCS were small and negative, ranging for -0.10 to -0.17.

**Table 2.** Estimates of phenotypic standard deviations and estimates and standard errors for heritability (diagonal), genetic correlations (above diagonal) and environmental correlations (below diagonal) among yield traits and somatic cell score (SCS) for first-lactation records with Models 1<sup>a</sup>, 2<sup>b</sup> and 3<sup>c</sup>.

Trait	SD <sup>d</sup>	Milk	Fat	Protein	SCS
Model 1					
Milk (kg)	1,587	<b>0.17 ± 0.01</b>	0.35 ± 0.03	0.85 ± 0.01	-0.03 ± 0.06
Fat (kg)	50	0.77 ± 0.01	<b>0.20 ± 0.01</b>	0.52 ± 0.03	0.11 ± 0.06
Protein (kg)	46	0.96 ± 0.01	0.78 ± 0.01	<b>0.16 ± 0.01</b>	0.03 ± 0.06
SCS	1.3	-0.15 ± 0.01	-0.20 ± 0.01	-0.14 ± 0.01	<b>0.09 ± 0.01</b>
Model 2					
Milk (kg)	1,583	<b>0.17 ± 0.01</b>	0.35 ± 0.03	0.85 ± 0.01	-0.04 ± 0.06
Fat (kg)	50	0.77 ± 0.01	<b>0.20 ± 0.01</b>	0.52 ± 0.03	0.12 ± 0.06
Protein (kg)	46	0.96 ± 0.01	0.78 ± 0.01	<b>0.16 ± 0.01</b>	0.02 ± 0.06
SCS	1.3	-0.15 ± 0.01	-0.20 ± 0.01	-0.14 ± 0.01	<b>0.09 ± 0.01</b>
Model 3					
Milk (kg)	1,570	<b>0.17 ± 0.01</b>	0.35 ± 0.03	0.84 ± 0.01	-0.03 ± 0.06
Fat (kg)	50	0.77 ± 0.01	<b>0.20 ± 0.01</b>	0.52 ± 0.03	0.10 ± 0.06
Protein (kg)	45	0.96 ± 0.01	0.78 ± 0.01	<b>0.16 ± 0.01</b>	0.03 ± 0.06
SCS	1.3	-0.17 ± 0.01	-0.20 ± 0.01	-0.14 ± 0.01	<b>0.09 ± 0.01</b>

<sup>a</sup>Model 1, bovine somatotropin (bST) treatment ignored in model but included contemporary groups for herd-year-month of calving.

<sup>b</sup>Model 2, bST treatment used as fixed effect and with same contemporary groups as Model 1.

<sup>c</sup>Model 3, bST treatment part of contemporary group.

<sup>d</sup>SD, estimate of phenotypic standard deviation calculated from sum of estimates of additive genetic and residual components of variance.

**Table 3.** Estimates of phenotypic correlations<sup>a</sup> among yield traits and somatic cell score (SCS) for first-lactation records with Models 1, 2 and 3<sup>b</sup>.

Model	M, F	M, P	M, S	F, P	F, S	P, S
1	0.70	0.92	-0.14	0.74	-0.16	-0.10
2	0.70	0.92	-0.14	0.74	-0.17	-0.10
3	0.70	0.92	-0.14	0.74	-0.16	-0.10

<sup>a</sup>M, F: phenotypic correlation between milk and fat yield; M, P: phenotypic correlation between milk and protein yield; M, S: phenotypic correlation between milk yield and SCS; F, S: phenotypic correlation between fat yield and SCS; P, S: phenotypic correlation between protein yield and SCS.

<sup>b</sup>Model 1, bovine somatotropin (bST) treatment ignored in model; Model 2, bST treatment used as fixed effect; Model 3, bST treatment was part of the contemporary group.

Estimates of genetic and environmental correlations from second-lactation records are shown in Table 4. Estimates of genetic correlations among yield traits were in agreement with estimates for first-lactation records. Estimates ranged from moderately to strongly positive with the three models. Differences were small between estimates with the three models. Estimates with Models 1, 2 and 3 were 0.44, 0.44 and 0.42 for milk and fat yields; 0.85, 0.85 and 0.83 for milk and protein yields, and 0.62, 0.63 and 0.60 for fat and protein yields. Estimates between



yield traits and SCS for the three models were small and negative. Estimates with Models 1, 2, and 3 were the same between milk yield and SCS (-0.03) and between protein yield and SCS (-0.02). Estimates between fat yield and SCS were negative but larger in magnitude than for milk and protein yields with SCS (-0.12, -0.24 and -0.23).

**Table 4.** Estimates of phenotypic standard deviations and estimates and standard errors for heritability (diagonal), genetic correlations (above diagonal) and environmental correlations (below diagonal) among yield traits and somatic cell score (SCS) for second-lactation records with Models 1<sup>a</sup>, 2<sup>b</sup> and 3<sup>c</sup>.

Trait	SD <sup>d</sup>	Milk	Fat	Protein	SCS
Model 1					
Milk (kg)	1,821	<b>0.16 ± 0.01</b>	0.44 ± 0.05	0.85 ± 0.01	-0.03 ± 0.08
Fat (kg)	58	0.77 ± 0.01	<b>0.15 ± 0.01</b>	0.62 ± 0.04	-0.12 ± 0.08
Protein (kg)	52	0.95 ± 0.01	0.78 ± 0.01	<b>0.15 ± 0.01</b>	-0.02 ± 0.08
SCS	1.4	-0.14 ± 0.01	-0.20 ± 0.01	-0.15 ± 0.01	<b>0.08 ± 0.01</b>
Model 2					
Milk (kg)	1,817	<b>0.17 ± 0.01</b>	0.44 ± 0.05	0.85 ± 0.01	-0.03 ± 0.08
Fat (kg)	58	0.77 ± 0.01	<b>0.15 ± 0.01</b>	0.63 ± 0.04	-0.24 ± 0.08
Protein (kg)	52	0.95 ± 0.01	0.78 ± 0.01	<b>0.16 ± 0.01</b>	-0.02 ± 0.08
SCS	1.4	-0.16 ± 0.01	-0.16 ± 0.01	-0.15 ± 0.01	<b>0.08 ± 0.01</b>
Model 3					
Milk (kg)	1,806	<b>0.14 ± 0.01</b>	0.42 ± 0.05	0.83 ± 0.01	-0.03 ± 0.08
Fat (kg)	58	0.77 ± 0.01	<b>0.12 ± 0.01</b>	0.60 ± 0.04	-0.23 ± 0.08
Protein (kg)	52	0.95 ± 0.01	0.80 ± 0.01	<b>0.14 ± 0.01</b>	-0.02 ± 0.08
SCS	1.4	-0.17 ± 0.01	-0.16 ± 0.01	-0.15 ± 0.01	<b>0.11 ± 0.01</b>

<sup>a</sup>Model 1, bovine somatotropin (bST) treatment ignored in model but included contemporary groups for herd-year-month of calving.

<sup>b</sup>Model 2, bST treatment used as fixed effect and with same contemporary groups as Model 1.

<sup>c</sup>Model 3, bST treatment part of contemporary group.

<sup>d</sup>SD, estimate of phenotypic standard deviation calculated from sum of estimates of additive genetic and residual components of variance.

Estimates of environmental correlations among the yield traits for second lactations agreed with estimates for first lactations. Estimates were large and positive, and the same or similar for the three models: 0.77 between milk and fat yields, 0.95 between milk and protein yields, and 0.78, 0.78 and 0.80 between fat and protein yields. Estimates between yield traits and SCS were small and negative. Estimates with the three models were: -0.14, -0.16 and -0.17 between milk yield and SCS; -0.20, -0.16 and -0.16 between fat yield and SCS, and the same with the three models between protein yield and SCS (-0.15).

Estimates of phenotypic correlations among yield traits for second lactations (Table 5) were similar to those for first lactations. Estimates were the same for each of the three models between milk and fat yields (0.72) and between milk and protein yields (0.92) and were similar (0.76, 0.76 and 0.73) between fat and protein yields. Small and negative estimates of phenotypic correlations between yield traits and SCS were also similar for each of the three models: -0.15 between milk yield and SCS; -0.16, -0.17 and -0.17 between fat yield and SCS; and -0.13 between protein yield and SCS.

**Table 5.** Estimates of phenotypic correlations<sup>a</sup> among yield traits and somatic cell score (SCS) for second-lactation records with Models 1, 2 and 3<sup>b</sup>.

Model	M, F	M, P	M, S	F, P	F, S	P, S
1	0.72	0.92	-0.15	0.76	-0.16	-0.13
2	0.72	0.92	-0.15	0.76	-0.17	-0.13
3	0.72	0.92	-0.15	0.73	-0.17	-0.13

<sup>a</sup>M, F: phenotypic correlation between milk and fat yield; M, P: phenotypic correlation between milk and protein yield; M, S: phenotypic correlation between milk yield and SCS; F, S: phenotypic correlation between fat yield and SCS; P, S: phenotypic correlation between protein yield and SCS.

<sup>b</sup>Model 1, bovine somatotropin (bST) treatment ignored in model; Model 2, bST treatment used as fixed effect; Model 3, bST treatment was part of the contemporary group.

Table 6 contains estimates with Models 1, 2 and 3 of correlations estimated from records for lactations three, four and five. Estimates of genetic correlations between milk and fat yields and between fat and protein yields were considerably larger than for lactations one and two and slightly smaller between milk and protein yields. Estimates between yield traits and SCS for the three models were more negative than for lactations one and two.

**Table 6.** Estimates of phenotypic standard deviations and estimates and standard errors for heritability (diagonal), genetic correlations (above diagonal) and environmental correlations (below diagonal) among yield traits and somatic cell score (SCS) for third, fourth and fifth lactation records with Models 1<sup>a</sup>, 2<sup>b</sup> and 3<sup>c</sup>.

Trait	SD <sup>d</sup>	Milk	Fat	Protein	SCS
<b>Model 1</b>					
Milk (kg)	1,895	<b>0.13 ± 0.01</b>	0.53 ± 0.04	0.80 ± 0.01	-0.23 ± 0.08
Fat (kg)	65	0.82 ± 0.01	<b>0.12 ± 0.01</b>	0.70 ± 0.03	-0.34 ± 0.08
Protein (kg)	56	0.97 ± 0.01	0.81 ± 0.01	<b>0.15 ± 0.01</b>	-0.23 ± 0.08
SCS	1.6	-0.22 ± 0.01	-0.23 ± 0.01	-0.22 ± 0.01	<b>0.08 ± 0.01</b>
<b>Model 2</b>					
Milk (kg)	1,889	<b>0.13 ± 0.01</b>	0.55 ± 0.05	0.82 ± 0.01	-0.23 ± 0.08
Fat (kg)	65	0.81 ± 0.01	<b>0.12 ± 0.01</b>	0.72 ± 0.04	-0.34 ± 0.08
Protein (kg)	56	0.97 ± 0.01	0.82 ± 0.01	<b>0.15 ± 0.01</b>	-0.23 ± 0.08
SCS	1.6	-0.22 ± 0.01	-0.23 ± 0.01	-0.22 ± 0.01	<b>0.08 ± 0.01</b>
<b>Model 3</b>					
Milk (kg)	1,879	<b>0.14 ± 0.01</b>	0.55 ± 0.04	0.80 ± 0.04	-0.23 ± 0.08
Fat (kg)	65	0.82 ± 0.01	<b>0.12 ± 0.01</b>	0.70 ± 0.04	-0.34 ± 0.08
Protein (kg)	56	0.97 ± 0.01	0.80 ± 0.01	<b>0.14 ± 0.01</b>	-0.23 ± 0.08
SCS	1.6	-0.22 ± 0.01	-0.23 ± 0.01	-0.22 ± 0.01	<b>0.11 ± 0.01</b>

<sup>a</sup>Model 1, bovine somatotropin (bST) treatment ignored in model but included contemporary groups for herd-year-month of calving.

<sup>b</sup>Model 2, bST treatment used as fixed effect and with same contemporary groups as Model 1.

<sup>c</sup>Model 3, bST treatment part of contemporary group calculated from sum of estimates of additive genetic, permanent environmental and residual components of variance.

<sup>d</sup>SD, estimate of phenotypic standard deviation calculated from sum of estimates of additive genetic, permanent environmental and residual components of variance.

Estimates of environmental correlations among yield traits for lactations 3-5 were slightly larger than for lactations one and two. Estimates with the three models were: 0.82, 0.81 and 0.82 between milk and fat yields; 0.97 for all models between milk and protein yields, and 0.81, 0.82, and 0.80 between fat and protein yields. Estimates of environmental correlations between yield traits and SCS were small and slightly more negative than for lactations one and two: -0.22, -0.23 and -0.22 between SCS and milk, fat and protein yields for each of the three models.

As with estimates of heritability, estimates of repeatability from lactations 3-5 were nearly the same for the three models ranging only from 0.34 to 0.36 for milk yield and 0.35 to 0.36 for protein yield and with estimates of 0.33 for fat yield and 0.40 for SCS for all three models. Similarly, estimates of permanent environmental correlations were almost identical for the three models: about 0.72 for milk and fat yields, 0.95 for milk and protein yields, 0.77 for fat and protein yields and nearly zero (-0.01 to -0.04) between the yield traits and SCS.

Estimates of phenotypic correlations among yield traits for the later lactations were similar to those for first and second lactations (Table 7). Estimates were the same for each of the three models: 0.75 between milk and fat yields, 0.95 between milk and protein yields, and 0.78 between fat and protein yields. Small and negative estimates of phenotypic correlations between yield traits and SCS were also the same for each of the three models: -0.15 between milk yield and SCS, -0.20 between fat yield and SCS, and -0.13 between protein yield and SCS.

**Table 7.** Estimates of phenotypic correlations<sup>a</sup> among yield traits and somatic cell score (SCS) for later lactations (3, 4 and 5) with Models 1, 2 and 3<sup>b</sup>.

Model	M, F	M, P	M, S	F, P	F, S	P, S
1	0.75	0.95	-0.15	0.78	-0.20	-0.13
2	0.75	0.95	-0.15	0.78	-0.20	-0.13
3	0.75	0.95	-0.15	0.78	-0.20	-0.13

<sup>a</sup>M, F: phenotypic correlation between milk and fat yield; M, P: phenotypic correlation between milk and protein yield; M, S: phenotypic correlation between milk yield and SCS; F, S: phenotypic correlation between fat yield and SCS; P, S: phenotypic correlation between protein yield and SCS.

<sup>b</sup>Model 1, bovine somatotropin (bST) treatment ignored in model; Model 2, bST treatment used as fixed effect; Model 3, bST treatment was part of the contemporary group.

The estimates of heritability for SCS 0.09 were larger than the estimate of heritability of incidence of mastitis reported by Carlen et al. (2004) of 0.01 who concluded that the strong genetic correlation between the two traits indicated that SCS may serve as an indicator trait for mastitis in breeding programs. The small but generally favorable negative estimates of genetic correlations, except for some for the first lactation, between yield traits and SCS from the current study, suggest that little selection emphasis on yield traits would need to be sacrificed to make genetic progress in decreasing SCS. The standard errors of estimates of genetic correlations were relatively small which indicates that those estimates could be used in setting up multiple-trait evaluations and indexes including yield traits and SCS.

These analyses show that with these data whether or how the bST effect is modeled had little effect on the estimates of genetic parameters. This result might not hold if a higher proportion of the records were from cows treated with bST. For these analyses, the percentage of records with bST treatment was only about 7%.

An even more important point that was not the goal of this study is what the effect would be on ranking of sires and cows based on estimated breeding values with the different models. Obviously, Model 1, which ignores bST treatment, could result in serious biases in estimates of breeding values of sires and especially of cows. Further study is needed to determine whether Models 2 and 3 would result in similar rankings for breeding values even though estimates of genetic parameters were similar for both models for these data.

## CONCLUSIONS

Estimates of heritability for yield traits and SCS were similar for each of the three models for records in first, second, and third and later lactations. Estimates of heritability for yield traits obtained in this study ranged from 0.12 to 0.20. Estimates of heritability for SCS were identical for each of the three models and ranged only from 0.08 to 0.09 for different lactations. Estimates of genetic correlations between pairs of yield traits ranged from 0.35 to 0.85 and were similar for the three models over all lactations. Estimates of genetic correlations between milk and fat yields increased from lactation one (0.35) to lactation two (about 0.43) to later lactations (about 0.54). The increase in estimates between fat and protein yields followed a similar pattern (0.52 to about 0.63 to about 0.71). Estimates of genetic correlations between yield traits and SCS in first lactation were smaller in magnitude: -0.03 to 0.12 than the small but favorable estimates for later lactations of -0.23 to -0.32.

For the three sets of lactations used in this study, no important differences in estimates of genetic parameters were found among the three models: the model unadjusted for bST treatment and for two models that adjusted for bST. Slight to no differences between estimates with different models within lactations indicate that adjustment for bST has negligible effects on estimates of heritability and genetic, permanent environmental, and temporary (residual) environmental correlations.

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