Estimation of (Co)Variances of Test Day Yields for First Lactation Holsteins in the United States

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ABSTRACT

(Co)variance components for milk, fat, and protein yields during first lactation were estimated from data for test days from 23,029 Holstein cows from 37 herds in Pennsylvania and Wisconsin. Four lactation stages of 75 d were defined, and the test day nearest the center of each interval was used. In four analyses, a lactation stage was added, and observations with missing values were deleted; 17,190 observations were available for the final analysis of lactations with test days in all lactation stages. Missing values were deleted because a canonical transformation was used for estimation of (co)variance matrices. Heritability estimates were similar across analyses, which indicated little effect from selection. Heritabilities usually increased with lactation stage and were highest for milk; mean heritability estimates were 0.19 for milk, 0.14 for fat, and 0.16 for protein. Phenotypic and genetic correlations were higher between milk and protein than between milk and fat. Within a yield trait, genetic correlation declined from 0.90 for adjacent stages to 0.75 for milk and protein and to 0.82 for fat between initial and final lactation stages. Within lactation stage, mean genetic correlations were 0.40 between milk and fat, 0.78 between milk and protein, and 0.56 between fat and protein; corresponding mean phenotypic correlations were 0.64, 0.91, and 0.66. The effect of solving the model iteratively was examined with records that had been adjusted using solutions from fitting the full model. Heritabilities for the beginning of lactation increased slightly with the iterative solution, which indicated a better model fit.
(**Key words**: (co)variance component estimation, test day model, multitrait evaluation, heritability)

INTRODUCTION

Current systems for genetic evaluation are based on yields observed during the first 305 d of lactation. Lactation yields typically are estimated from monthly measurements of milk volumes and analysis of milk samples for fat and protein percentages (33). In recent years, several studies (20, 28, 30) have confirmed that environmental effects can be accounted for with greater precision when an effect for test day is included. Interest in the development and implementation of test day models is increasing worldwide, and many countries are conducting research to develop genetic evaluation systems that use test day data.

Two approaches have been investigated for the use of test day information (29): 1) direct use by fitting a model to test day data and 2) indirect use based on correction for environmental influences on test day yields and aggregation of test day data into a lactation measure for later processing. The indirect approach is being used routinely in genetic evaluation systems of several countries by adjusting test day data and then combining them into a lactation measure (1, 3, 11, 12). The objective of both approaches is to provide a more accurate accounting of environmental effects because lactation records of contemporaries often do not include all of the same test dates. Inclusion of an effect for test day in a model enables accounting for the effects of environment on a specific day of production. Direct use of test day data also is desirable to accommodate the less frequent measurement that has resulted from efforts to reduce the cost of milk recording and the associated loss of information that is available for computation of 305-d yields. Regardless of the length of the interval between tests, a test day model can appropriately weight the recorded test day information by considering the covariances between test days. The use of test day data also allows relaxation of traditional restrictions on the length of intervals between tests and the number of DIM at first test.

Two methods are being studied for direct inclusion of test day data in a model. The first method is based on analysis of test day data with a model that estimates fixed regression coefficients for lactation curves within fixed effects of parity, calving age, and calving season. Many studies (5) have found genetic differences in persistencies of yield traits for dairy cattle. To allow for those differences, regression coefficients of the lactation curve can be fitted for each animal as random effects (8, 9, 10). This method is partially used in Canada for yield traits of dairy goats (27). Simplified versions that include a single genetic effect have been applied in Germany (22) and in Canada for SCS of dairy cattle (21). Theoretically, the complete method can be implemented for more than one yield trait or more than one parity through a multitrait approach, as was done to predict genetic merit for yield traits of German Holsteins (22). A complete model has been proposed for yield traits of dairy cattle in Canada (10).

A second method to include test day information directly is to apply a multitrait approach in which different test day yields are treated as different traits. Australia and the US are among the countries developing a test day model for multiple parities that considers the test day yields during first parity and the test day yields during later parities as separate traits (34).

The primary challenge in the development of test day models is the estimation of genetic parameters that are required for the implementation of an evaluation system (4, 8, 15, 18, 19, 23, 32). If a random regression model is used, the underlying model is not intuitive and is complex (10). For random regression and multitrait models, the number of genetic parameters is large, especially if milk, fat, and protein are considered together for more than just first parities.

Veerkamp and Goddard (32) used many bivariate analyses to calculate the components of (co) variance matrices. Multitrait random regression and bivariate analyses often produce nonpositive definite matrices or correlations that are improper. Fortunately, multitrait models can be simplified with canonical transformation (14), and variance components can be estimated using these uncorrelated traits (16). However, a canonical transformation requires complete data.

Recently, canonical transformation was extended to allow missing values when genetic evaluations are computed by estimating the missing values at each round of iteration (2). However, this extension is not usable for the estimation of (co)variance components because that estimation requires the (co)variance matrices. One solution is to eliminate records with missing data and to apply a canonical transformation to the remaining data. The objectives of this study were to estimate variance components for a multitrait test day model using canonical transformation and to determine the impact of selection during lactation on the estimates.

MATERIALS AND METHODS

Data

First lactation records were analyzed for 23,029 Holstein cows that calved from 1990 through 1996 in 37 large herds from Wisconsin (261 cows per herd) and Pennsylvania (287 cows per herd). The dairy records processing centers in those states have historically supplied monthly records in progress to the Animal Improvement Programs Laboratory, ARS, USDA (Beltsville, MD); therefore, available test day data were nearly complete. Initial data for test days consisted of milk yields and fat and protein percentages. Four lactation stages of 75 d each were defined starting with d 6. The test day that was nearest to the center of the lactation stage (d 43, 118, 193, or 268) was retained. Only four lactation stages were defined to increase the likelihood of observations in all stages. Associated fat and protein yields were computed from milk yields and component percentages. Milk, fat, and protein yields that were recorded during the four lactation stages were the 12 traits analyzed.

Complete data were required to estimate the full set of genetic parameters. Lactation stages were added progressively, and records with missing values were deleted so that the effect of selection could be estimated; 17,190 records with test days in all lactation stages were available for final analysis.

Model

Because a test day could occur on any day within the 75-d stage, a model that adjusted for the shape of the lactation curve was necessary. A model based on those of Guo and Swalve (7) and Wiggans and Goddard (34) was used:

$$y_{ijklmno} = HTF_j + AS_k + AS_k(b_1)z_{1l} + AS_k(b_2)z_{2l} + HYS_{im} + C_{in} + a_{io} + e_{ijklmno}$$

where $y_{ijklmno}$ = test day record for milk, fat, or protein yield of cow o for lactation stage i; class j for herd, test day, and milking frequency (HTF); major class k for calving age and season (AS) across lactation stages; DIM l; class m for herd, year, and calving season (HYS); and minor class

n for calving age (C) in months within lactation stage; b = regression coefficient; $z_{1l} = (DIM_l)^{0.5}$ and $z_{2l} = \log(DIM_l)$ (7); a = animal effect (breeding value); and e = residual effect. Milking frequency for HTF classes was two or three times daily, and HTF classes were required to have at least three records. Calving ages for major AS classes were 20 to 23, 24 to 25, 26 to 27, 28 to 31, and 32 to 35 mo. Starting with January, six 2-mo calving seasons were defined for AS and HYS effects. Because of the impact of calving age and season on yield and persistency (20), AS was included in the model along with regressions on a function of DIM that were nested within AS. Defining the HYS effect within trait and lactation stage (in contrast to HTF, which is defined across lactation stage) allowed the consideration of different effects of environment by lactation stage. The effect of minor classes for calving age (C) within trait and lactation stage was included to account for differences by age in persistency that were not accounted for by nesting regressions within AS. Of the models compared by Guo and Swalve (7) with three parameters, a mixed log model was selected to represent the lactation curve because of good overall fit for milk, fat, and protein yields. A model with three parameters was adequate for this test day study because lactation curves were fit within four lactation stages rather than over all 305 d.

Analysis

Canonical transformation requires that the same model apply to all traits. However, traits from different lactation stages necessarily occur on different test days. Therefore, the model was analyzed in two steps that were similar to the procedure proposed by Wiggans and Goddard (34).

Step 1 estimated effects that were not specific to lactation stage (HTF and AS) for the shape of the lactation curve and adjusted test day yields for those effects. The general linear models procedure of SAS (24) was used.

Step 2 estimated (co)variance components. Model effects that were specific to lactation stage (HYS, C, and a) were included. Because of selection, the number of observations decreased as lactation stage increased. Four data sets with progressively fewer records but more lactation stages were analyzed to determine the impact of selection. Pedigree information was included for animals born in 1980 or later. Pedigree data for animals born prior to 1980 were not included because of concern that the inclusion of the additional data in the analysis would slow convergence during iteration. Eight groups were defined for animals without known parents based on the birth year of the animal: 1980 and earlier, 1981 through 1982, . . ., 1991 through 1992, and 1993 and later. Variance components were estimated using the expectation-maximization REML algorithm of Misztal et al. (16, 17). Because no missing values are allowed with canonical transformation, only the fourth analysis that included records with observations for all lactation stages could provide estimates for all (co)variances.

Iterative Solution

To test the impact of solving of steps 1 and 2 iteratively, an additional analysis was conducted. Required variance components for solving step 2 were those from the fourth analysis that included records with observations for all lactation stages. Solutions for step 2 were obtained using data from all lactation stages for cows with records in analysis 1 and the method of Gengler et al. (6). Records then were adjusted for solutions from step 2, and the adjusted records

were used to compute solutions for step 1. The records were readjusted for new solutions from step 1, and solutions for step 2 were computed. Iteration continued until mean relative differences between animal solutions were <1%. This method simulated the procedure proposed for future genetic evaluation of yield traits in the US (34).

Heritabilities for Lactation

Lactation yield can be expressed as the sum of all test day yields, and, therefore, heritabilities for lactation yield can be derived from (co)variance components from test days. (Co)variance matrices for lactation were computed from weighted sums of the estimated (co)variances for test days: $\mathbf{G}_{\text{lactation}} = \mathbf{S}\mathbf{G}_{\text{test day}}\mathbf{S}'$, and $\mathbf{P}_{\text{lactation}} = \mathbf{S}\mathbf{P}_{\text{test day}}\mathbf{S}'$, where **G** = genetic (co)variance matrix, **P** = phenotypic (co)variance matrix, and **S** = summing matrix for test day yields by lactation stage within yield trait (milk, fat, and protein) :

$$\begin{bmatrix} 75 & 75 & 75 & 75 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 75 & 75 & 75 & 75 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 75 & 75 & 75 & 75 \end{bmatrix}.$$

The resulting heritabilities for the lactation based on test day information were compared with heritabilities that were estimated with the method of Van Tassell et al. (31) using USDA-DHIA data for 305-d lactations for cows with records in analysis 1. Heritability estimates also were computed from an approach that was similar to that of Van Tassell et al. (31) but that used multiple traits. To determine the effect of the summing of sampling errors from estimation of the test day (co)variance matrices, heritabilities also were computed from reconstructed lactation yield deviations using the same method as for test day yields.

RESULTS AND DISCUSSION

Descriptive Statistics

Means and standard deviations of milk, fat, and protein yields are presented in Table 1 for the progressive analyses of the four lactation stages. Elimination of records with missing observations resulted in a loss of 25% of the data. Means increased and standard deviations decreased with selection. The decrease of standard deviations indicated that selection eliminated animals with low yield without raising the mean substantially.

TABLE 1. Numbers of records and means and standard deviations for milk, fat, and protein yields for progressive analyses of four lactation stages.

Lactation stage[1]	Analysis[2]	Records	Milk		Fat		Protein	
		(no.)	(kg)		(g)			
			$\bar{x}$	SD	$\bar{x}$	SD	$\bar{x}$	SD
1	1	23,029	29.3	6.8	1056	283	862	193

	2	20,631	29.8	6.4	1067	273	875	181
	3	18,836	30.0	6.3	1073	270	880	176
	4	17,190	30.1	6.2	1075	269	883	177
2	2	20,631	30.0	6.4	1027	256	927	189
	3	18,836	30.3	6.2	1033	251	934	182
	4	17,190	30.4	6.1	1036	249	937	179
3	3	18,836	28.0	6.5	1002	251	902	200
	4	17,190	28.1	6.3	1005	245	906	193
4	4	17,190	24.7	6.7	937	256	828	210

[1]Lactation stage: 1 = test day nearest to 43 between 6 and 80 d, 2 = test day nearest to 118 between 81 and 155 d, 3 = test day nearest to 193 for 156 between 230 d, and 4 = test day nearest to 268 between 231 and 305 d.

[2]Analysis 1 included records with a test day in lactation stage 1; analysis 2 included records with test days in lactation stages 1 and 2; analysis 3 included records with test days in lactation stages 1, 2, and 3; and analysis 4 included records with test days in all four lactation stages.

Mean yields for analyses within lactation stages 1 through 3 were remarkably similar; only lactation stage 4 had clearly lower means. Mean yields were highest in lactation stage 2 for milk and protein and in lactation stage 1 for fat. For the analysis of records without missing values (analysis 4), variability was highest at the end of lactation for milk and protein yields and at the beginning of lactation for fat yield.

Progressive Analyses

Genetic and residual variances from the four progressive analyses are in Table 2. Residual variances generally were largest from the analysis of early lactation (analysis 1) and smallest from the analysis with no missing observations (analysis 4). However, for protein yield, the residual variance from the end of lactation (analysis 4, lactation stage 4) was higher than the residual variance from analysis 1. Genetic variances did not exhibit a consistent pattern across analyses. In analysis 4, genetic variance increased with lactation stage except for lactation stages 1 and 2 for protein yield. Residual variance did not show a consistent pattern across lactation stages for analysis 4.

TABLE 2. Genetic and residual variances for milk, fat, and protein yields from four progressive across lactation stage and an iterative analysis using adjusted records .

		Analysis[2]									
		1		2		3		4		I	
Yield trait	Lactation stage[1]	Genetic	Residual	Genetic	Residual	Genetic	Residual	Genetic	Residual	Gene	

Milk, kg[2] × 100	1	420	2627	455	2276	419	2201	390	2156	3
	2	. . .	. . .	433	2229	429	2009	437	1933	4
	3	. . .	. . .	. . .	. . .	523	2079	509	1916	5
	4	. . .	. . .	. . .	. . .	. . .	. . .	585	2265	5
Fat, g[2]	1	6255	49,925	6155	45,263	6261	43,955	5220	43,979	53
	2	. . .	. . .	5188	40,796	6717	37,976	6364	37,712	64
	3	. . .	. . .	. . .	. . .	6762	36,106	6478	34,084	65
	4	. . .	. . .	. . .	. . .	. . .	. . .	7626	37,426	77
Protein, g[2]	1	3468	21,860	3587	18,939	3185	18,489	3017	18,091	30
	2	. . .	. . .	2882	20,409	2832	18,355	2934	17,678	29
	3	. . .	. . .	. . .	. . .	3999	20,372	3961	18,670	40
	4	. . .	. . .	. . .	. . .	. . .	. . .	4948	22,693	50

[1]Lactation stage: 1 = test day nearest to 43 between 6 and 80 d, 2 = test day nearest to 118 betw 155 d, 3 = test day nearest to 193 between 156 and 230 d, and 4 = test day nearest to 268 betwee 305 d.

[2]Analysis 1 included records with a test day in lactation stage 1; analysis 2 included records wi in lactation stages 1 and 2; analysis 3 included records with test days in lactation stages 1, 2, and analysis 4 included records with test days in all four lactation stages; and the iterative analysis in records from analysis 4 that had been adjusted using solutions obtained by fitting the full model.

Heritabilities, genetic correlations, and phenotypic correlations are in Tables 3 through 6 by progressive analysis. Effects of selection were limited; most heritability estimates changed only slightly (0.01 to 0.03), regardless of yield trait. All estimates were between 0.11 and 0.21, which agrees with results from other studies (15, 19, 23), although a few researchers (18, 28) reported slightly larger estimates. One recent study by Jamrozik et al. (10) found clearly higher estimates, but a change in the modeling of effects of permanent environment resulted in more similar estimates (26). Heritabilities estimated in this study usually were higher for milk yield than for protein and fat yields. Heritability estimates for all yield traits increased with lactation stage, which followed the patterns found for genetic and residual variances. Meyer et al. (15) reported lower estimates of heritability at the beginning and end of lactation. The increased heritabilities found with later lactation stages in this study may have resulted from differences between the US and Australian management systems (concentrate feeding vs. grazing) that allowed US dairy cows more opportunity to attain their genetic potential for yield. Mean heritabilities from analysis 4 were 0.19 for milk yield, 0.14 for fat yield, and 0.16 for protein yield.

TABLE 3. Heritabilities (on diagonal and bold), genetic correlations (above diagonal), and phenotypic correlations (below diagonal) for milk, fat, and protein yields from analysis of records with test days in the beginning of lactation (lactation stage 1, analysis 1).[1]

Yield trait	Milk	Fat	Protein
Milk	**0.14**	0.56	0.83
Fat	0.69	**0.11**	0.71
Protein	0.92	0.68	**0.14**

[1]Lactation stage 1 = test day nearest to 43 between 6 and 80 d; analysis 1 included records with a test day in lactation stage 1.

TABLE 4. Heritabilities (on diagonal and bold), genetic correlations (above diagonal), and phenotypic correlations (below diagonal) for milk, fat, and protein yields from progressive analysis of records with test days in the first two lactation stages (analysis 2).

		Lactation stage					
		Milk		Fat		Protein	
Yield trait	Lactation stage[1]	1	2	1	2	1	2
Milk	1	**0.17**	0.93	0.53	0.32	0.84	0.80
	2	0.57	**0.16**	0.38	0.23	0.70	0.74
Fat	1	0.66	0.36	**0.12**	0.92	0.68	0.62
	2	0.31	0.60	0.40	**0.12**	0.41	0.35
Protein	1	0.91	0.47	0.66	0.29	**0.16**	0.96
	2	0.49	0.91	0.35	0.61	0.48	**0.12**

[1]Lactation stage: 1 = test day nearest to 43 between 6 and 80 d, and 2 = test day nearest to 118 between 81 and 155 d.

TABLE 5. Heritabilities (on diagonal and bold), genetic correlations (above diagonal), and phenotypic correlations (below diagonal) for milk, fat, and protein yields from progressive analysis of records with test days in the first three lactation stages (analysis 3).

		Lactation stage								
		Milk			Fat			Protein		
Yield trait	Lactation stage[1]	1	2	3	1	2	3	1	2	3
Milk	1	**0.16**	0.90	0.83	0.54	0.33	0.34	0.81	0.75	0.75
	2	0.56	**0.18**	0.98	0.37	0.28	0.32	0.64	0.72	0.77

	3	0.47	0.64	**0.20**	0.34	0.30	0.36	0.57	0.71	0.79
Fat	1	0.65	0.34	0.29	**0.13**	0.90	0.86	0.67	0.63	0.64
	2	0.29	0.58	0.33	0.39	**0.15**	0.98	0.40	0.43	0.49
	3	0.27	0.37	0.64	0.34	0.47	**0.16**	0.40	0.48	0.57
Protein	1	0.91	0.45	0.37	0.65	0.27	0.24	**0.15**	0.92	0.83
	2	0.48	0.90	0.53	0.34	0.59	0.37	0.47	**0.13**	0.97
	3	0.42	0.55	0.92	0.31	0.35	0.67	0.40	0.56	**0.16**

[1]Lactation stage: 1 = test day nearest to 43 between 6 and 80 d, 2 = test day nearest to 118 between 81 and 155 d, and 3 = test day nearest to 193 between 156 and 230 d.

TABLE 6. Heritabilities (on diagonal and bold), genetic correlations (above diagonal), and phenotypic correlations (below diagonal) for milk, fat, and protein yields from progressive analysis of records with test days in all four lactation stages (analysis 4).

		Lactation stage											
		Milk				Fat				Protein			
Yield trait	Lactation stage[1]	1	2	3	4	1	2	3	4	1	2	3	4
Milk	1	**0.15**	0.90	0.83	0.75	0.49	0.30	0.30	0.38	0.79	0.75	0.74	0.72
	2	0.56	**0.18**	0.98	0.92	0.35	0.26	0.29	0.40	0.62	0.73	0.76	0.78
	3	0.47	0.63	**0.21**	0.97	0.31	0.26	0.32	0.45	0.55	0.72	0.78	0.82
	4	0.38	0.51	0.62	**0.21**	0.30	0.28	0.36	0.53	0.50	0.68	0.75	0.84
Fat	1	0.64	0.33	0.28	0.21	**0.11**	0.91	0.89	0.82	0.63	0.62	0.64	0.61
	2	0.28	0.57	0.32	0.27	0.38	**0.14**	0.96	0.90	0.37	0.39	0.44	0.47
	3	0.26	0.35	0.62	0.36	0.34	0.47	**0.16**	0.97	0.37	0.46	0.53	0.58
	4	0.24	0.32	0.41	0.72	0.27	0.39	0.49	**0.17**	0.38	0.49	0.58	0.68
Protein	1	0.91	0.45	0.37	0.28	0.64	0.26	0.24	0.21	**0.14**	0.92	0.83	0.75
	2	0.47	0.90	0.52	0.42	0.33	0.58	0.35	0.32	0.47	**0.14**	0.97	0.92
	3	0.42	0.54	0.91	0.54	0.30	0.34	0.65	0.43	0.39	0.55	**0.18**	0.97
	4	0.35	0.45	0.56	0.93	0.24	0.30	0.39	0.76	0.31	0.45	0.58	**0.18**

[1]Lactation stage: 1 = test day nearest to 43 between 6 and 80 d, 2 = test day nearest to 118 between 81 and 155 d, 3 = test day nearest to 193 between 156 and 230 d, and 4 = test day nearest to 268 between 231 and 305 d.

Genetic and phenotypic correlations from analysis 4 were all positive and ranged from 0.21 to 0.98. Correlations between milk and protein yields were higher (0.28 to 0.91) than those between milk and fat yields (0.21 to 0.72). The genetic correlation declined from 0.90 for adjacent

lactation stages to 0.75 for milk and protein yields and 0.82 for fat yield between lactation stages 1 and 4. Within lactation stage, genetic correlations averaged 0.40 between milk and fat yields, 0.78 between milk and protein yields, and 0.56 between fat and protein yields. Mean phenotypic correlations within lactation stage were 0.64 between milk and fat yields, 0.91 between milk and protein yields, and 0.66 between fat and protein yields. The genetic and phenotypic correlations from this study correspond to those reported by most authors (e.g., 23).

Iterative Analysis

Genetic variances from the iterative analysis were slightly higher, and residual variances were slightly lower, than corresponding variances from analysis 4 (Table 2). The iterative analysis had slightly higher heritability estimates (Table 7) than did those from analysis 4 (Table 6), especially at the beginning of the lactation, which was expected given the differences for genetic and residual variances. The adjustment of records using solutions obtained by fitting the full model may improve estimation of heritabilities; estimates from analysis 4 should be considered to be the lower bounds for heritabilities.

TABLE 7. Heritabilities (on diagonal and bold), genetic correlations (above diagonal), and phenotypic correlations (below diagonal) for milk, fat, and protein yields from iterative analysis of records with test days in all four lactation stages that had been adjusted using solutions obtained by fitting the full model.

		Lactation stage											
		Milk				Fat				Protein			
Yield trait	Lactation stage[1]	1	2	3	4	1	2	3	4	1	2	3	4
Milk	1	**0.16**	0.90	0.83	0.75	0.49	0.30	0.30	0.38	0.79	0.75	0.74	0.72
	2	0.56	**0.19**	0.98	0.92	0.34	0.26	0.28	0.39	0.62	0.72	0.76	0.78
	3	0.48	0.63	**0.22**	0.97	0.31	0.25	0.31	0.44	0.55	0.71	0.77	0.82
	4	0.38	0.52	0.62	**0.21**	0.29	0.27	0.35	0.52	0.49	0.68	0.75	0.84
Fat	1	0.64	0.33	0.28	0.21	**0.11**	0.91	0.89	0.82	0.63	0.62	0.64	0.61
	2	0.28	0.57	0.32	0.27	0.38	**0.15**	0.96	0.90	0.37	0.39	0.43	0.46
	3	0.26	0.35	0.62	0.36	0.34	0.47	**0.16**	0.97	0.38	0.45	0.53	0.58
	4	0.24	0.32	0.41	0.72	0.27	0.39	0.49	**0.17**	0.38	0.48	0.58	0.67
Protein	1	0.91	0.45	0.37	0.28	0.64	0.26	0.24	0.21	**0.15**	0.92	0.83	0.75
	2	0.48	0.90	0.52	0.42	0.33	0.58	0.35	0.32	0.47	**0.15**	0.97	0.92
	3	0.42	0.54	0.91	0.54	0.30	0.34	0.65	0.43	0.40	0.56	**0.18**	0.97
	4	0.35	0.46	0.56	0.93	0.25	0.30	0.39	0.76	0.32	0.45	0.58	**0.18**

[1]Lactation stage: 1 = test day nearest to 43 between 6 and 80 d, 2 = test day nearest to 118 between 81 and 155 d, 3 = test day nearest to 193 between 156 and 230 d, and 4 = test day

nearest to 268 between 231 and 305 d.

Genetic and phenotypic correlations from the iterative analysis (Table 7) were almost identical to those from analysis 4 (Table 6).

Lactation Heritabilities

Heritability estimates for lactation that were derived from test day (co)variance components were 0.27, 0.25, and 0.25 for milk, fat, and protein yields, respectively. Lactation heritabilities that were estimated from lactation yield deviations were slightly higher (0.28, 0.26, and 0.26 for milk, fat, and protein yields, respectively). The lower estimates for the heritabilities derived from the test day (co)variance components reflect the accumulation across the entire lactation of sampling errors from estimation of those (co)variance components. Heritability estimates from both methods were lower than the heritabilities of 0.29, 0.30, and 0.27 that were estimated by the single-trait method of Van Tassell et al. (31) using USDA-DHIA data for 305-d lactations for cows with records in analysis 1. To allow comparison with the multivariate heritabilities estimated from this study, a bivariate analysis was performed using a method similar to that of Van Tassell et al. (31); mean estimates for heritability were 0.30, 0.30, and 0.27. A possible cause for the lower estimates of heritability for lactation based on test day information is the contribution of more lactation and test day records to the analysis of 305-d records, which did not require the presence of a test day for each of the four lactation stages and included all test days rather than just one for each lactation stage.

Genetic and phenotypic correlations, computed from lactation (co)variance matrices, were 0.38 and 0.65 between milk and fat yields, 0.79 and 0.91 between milk and protein yields, and 0.56 and 0.70 between fat and protein yields, respectively. Although the correlations were lower than those reported by Misztal et al. (16), the correlations were confirmed using reconstructed lactation yield deviations and the original 305-d records.

CONCLUSIONS

The estimation of (co)variance components is crucial for implementation of genetic evaluation systems that use test day yields. This study used a simple approach based on canonical transformation to construct (co)variance matrices. Selection was found to have only a small effect on correlations and heritabilities. Schaeffer (25) has shown that genetic evaluations are insensitive to small changes in parameters. The results obtained provide initial estimates for genetic and residual (co)variance across four lactation stages and three yield traits.

Milk and protein yields were more highly correlated than were milk and fat yields. As expected, genetic correlations between lactation stages were high for each yield trait. Genetic correlations were lower between milk and fat yields and between fat and protein yields than between milk and protein yields; phenotypic correlations showed a similar pattern.

Because this study was limited to four lactation stages, the results are only the initial step in estimating the (co)variance components needed for computation of test day evaluations. Appropriate methods are required to obtain results that avoid selection bias across test days and to extend the (co)variance structure among milk, fat, and protein yields to all days of lactation.

(Co)variance functions that were proposed by Kirkpatrick et al. (13) may provide a method of extending estimates to the entire range of the lactation.

In the test day model proposed for genetic evaluation of yield traits in the US (34), lactation stages are shorter (30 d). Therefore, the herd-year-season effect within lactation stage, which is solved in step 2, aids in accounting for differences among lactation curves. A possible improvement could be to define lactation stages by variable rather than by fixed intervals with shorter stages for the beginning of lactation and longer intervals for the end.

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REFERENCES

1 Cornell Cooperative Extension. 1997. AI Bull Census, Test-Day Model, July 1997. Dep. Anim. Sci., Cornell Univ., Ithaca, NY.

2 Ducrocq, V., and B. Besbes. 1993. Solution of multiple trait animal models with missing data on some traits. J. Anim. Breed. Genet. 110:81-92.

3 Everett, R. W., F. Schmitz, and L. H. Wadell. 1994. A test-day model for monitoring management and genetics in dairy cattle. J. Dairy Sci. 77(Suppl. 1):267.(Abstr.)

4 García-Cortés, L. A., C. Moreno, L. Varona, M. Rico, and J. Altarriba. 1995. (Co)variance component estimation of yield traits between different lactations using an animal model. Livest. Prod. Sci. 43:111-117.

5 Gengler, N. 1996. Persistency of lactation yields: a review. Proc. Int. Workshop Genet. Improvement Functional Traits in Cattle, Gembloux, Belgium, January 21-23, 1996. Int. Bull Eval. Serv. Bull. No. 12:87-96. Dep. Anim. Breed. Genet., SLU, Uppsala, Sweden.

6 Gengler, N., G. R. Wiggans, J. R. Wright, H. D. Norman, and C. W. Wolfe. 1997. Application of canonical transformation with missing values to multitrait evaluation of Jersey type. J. Dairy Sci. 80:2563-2571.

7 Guo, Z., and H. H. Swalve. 1995. Modelling of the lactation curve as a sub-model in the evaluation of test day records. Proc. Open Session INTERBULL Annu. Mtg., Prague, Czech Republic, Sept. 7-8, 1995. Int. Bull Eval. Serv. Bull. No. 11. Dep. Anim. Breed. Genet., SLU, Uppsala, Sweden.

8 Jamrozik, J., and L. R. Schaeffer. 1997. Estimates of genetic parameters for a test day model with random regression for yield traits of first lactation Holsteins. J. Dairy Sci. 80:762-770.

9 Jamrozik, J., L. R. Schaeffer, and J.C.M. Dekkers. 1996. Random regression models for production traits in Canadian Holsteins. Proc. Open Session INTERBULL Annu. Mtg., Veldhoven, The Netherlands, June 23-24, 1996. Int. Bull Eval. Serv. Bull. No. 14:124-134. Dep. Anim. Breed. Genet., SLU, Uppsala, Sweden.

10 Jamrozik, J., L. R. Schaeffer, and J.C.M. Dekkers. 1997. Genetic evaluation of dairy cattle using test day yields and random regression model. J. Dairy Sci. 80:1217-1226.

11 Johnson, D. L. 1996. Estimation of lactation yield from repeated measures of test day yields. Proc. N.Z. Soc. Anim. Prod. 56:16-18.

12 Jones, L. P., and M. E. Goddard. 1990. Five years experience with the animal model for dairy evaluations in Australia. Proc. 4th World Congr. Genet. Appl. Livest. Prod., Edinburgh, Scotland, XIII:382-385.

13 Kirkpatrick, M., W. G. Hill, and R. Thompson. 1994. Estimating the covariance structure of traits during growth and ageing, illustrated with lactation in dairy cattle. Genet. Res. Camb. 64:57-69.

14 Lin, C. Y., and S. P. Smith. 1990. Transformation of multitrait to unitrait mixed model analysis of data with multiple random effects. J. Dairy Sci. 73:2494-2502.

15 Meyer, K., H.-U. Graser, and K. Hammond. 1989. Estimates of genetic parameters for first lactation test day production of Australian Black and White cows. Livest. Prod. Sci. 21:177-199.

16 Misztal, I., T. J. Lawlor, T. H. Short, and P. M. VanRaden. 1992. Multiple-trait estimation of variance components of yield and type traits using an animal model. J. Dairy Sci. 75:544-551.

17 Misztal, I., K. Weigel, and T. J. Lawlor. 1995. Approximation of estimates of (co)variance components with multiple-trait restricted maximum likelihood by multiple diagonalization for more than one random effect. J. Dairy Sci. 78:1862-1872.

18 Pander, B. L., W. G. Hill, and R. Thompson. 1992. Genetic parameters of test day records of British Holstein-Friesian heifers. Anim. Prod. 55:11-21.

19 Pösö, J., E. A. Mäntysaari, and A. Kettunen. 1996. Estimation of genetic parameters of test day production in Finnish Ayrshire cows. Proc. Open Session INTERBULL Annu. Mtg., Veldhoven, The Netherlands, June 23-24, 1996. Int. Bull Eval. Serv. Bull. No. 14:45-48. Dep. Anim. Breed. Genet., SLU, Uppsala, Sweden.

20 Ptak, E., and L. R. Schaeffer. 1993. Use of test day yields for genetic evaluation of dairy sires and cows. Livest. Prod. Sci. 34:23-34.

21 Reents, R., J.C.M. Dekkers, and L. R. Schaeffer. 1995. Genetic evaluation for somatic cell score with a test day model for multiple lactations. J. Dairy Sci. 78:2858-2870.

22 Reents, R., and L. Dopp. 1996. Genetic evaluation for dairy production traits with a test day model for multiple lactations. Proc. Open Session INTERBULL Annu. Mtg., Veldhoven, The Netherlands, June 23-24, 1996. Int. Bull Eval. Serv. Bull. No. 14:113-117. Dep. Anim. Breed. Genet., SLU, Uppsala, Sweden.

23 Rekaya, R., F. Béjar, M. J. Carabaño, and R. Alenda. 1995. Genetic parameters for test day measurements in Spanish Holstein-Friesian. Proc. Open Session INTERBULL Annu. Mtg., Prague, Czech Republic, Sept. 7-8, 1995. Int. Bull Eval. Serv. Bull. No. 11. Dep. Anim. Breed. Genet., SLU, Uppsala, Sweden.

24 SAS/STAT® User's Guide. Version 6, Fourth Edition, Vol. 2. 1994. SAS Inst. Inc., Cary,

NC.

25 Schaeffer, L. R. 1984. Sire and cow evaluation under multiple trait models. J. Dairy Sci. 67:1567-1580.

26 Schaeffer, L. R. 1997. Subject: random regressions. http://chuck.agsci.colostate.edu/wais/logs/agdg869258263.html. Accessed Nov. 18, 1997.

27 Schaeffer, L. R., and B. P. Sullivan. 1994. Genetic evaluation of dairy goats using test day yields. Proc. 5th World Congr. Genet. Appl. Livest. Prod. 18:182-185.

28 Swalve, H. H. 1995. The effect of test day models on the estimation of genetic parameters and breeding values for dairy yield traits. J. Dairy Sci. 78:929-938.

29 Swalve, H. H. 1995. Test day models in the analysis of dairy production data-a review. Arch. Tierz. 38:591-612.

30 Van Tassell, C. P., R. L. Quaas, and R. W. Everett. 1992. Parameter estimates for 305-day ME records and 305-day test-day residual records. J. Dairy Sci. 75(Suppl. 1):251.(Abstr.)

31 Van Tassell, C. P., G. R. Wiggans, H. D. Norman, and R. L. Powell. 1997. Estimation of heritability for yield of U.S. dairy cattle. Proc. Open Session INTERBULL Annu. Mtg., Vienna, Austria, August 28-29, 1997. Int. Bull Eval. Serv. Bull. No. 16:104-107. Dep. Anim. Breed. Genet., SLU, Uppsala, Sweden.

32 Veerkamp, R. F., and M. E. Goddard. 1998. Covariance functions across herd production levels for test day records on milk, fat, and protein yields. J. Dairy Sci.81:1690-1701.

33 Wiggans, G. R. 1985. Procedures for calculating lactation records. Natl. Coop. Dairy Herd Impr. Progr. Handbook. Fact Sheet G-1. Ext. Serv., USDA, Washington, DC.

34 Wiggans, G. R., and M. E. Goddard. 1997. A computationally feasible test day model for genetic evaluation of yield traits in the United States. J. Dairy Sci. 80:1795-1800.