Estimation of (Co)variance Functions of Test Day Yields in First and Later Lactations of United States Holstein Cows

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Abstract

(Co)variance components for milk, fat, and protein yields during first and second, representing later, lactations 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 in each lactation, and the test day nearest the center of each interval was used. A total of 9110 observations were available for the final analysis of lactations with test days in all four lactation stages. Data were preadjusted for lactation curves within lactation stages using all available records. (Co)variance functions were used to describe the (co)variance structure within and across yield trait and parity. (Co)variance components of biological functions (305-d yields, persistency, defined as difference between yields on days 280 and 60, and maturity rate, defined as difference between second and first lactation yields) were developed from (co)variance functions. Results provide only a first indication of the (co)variance structure within and across lactations. Improved procedures are needed.

Introduction

While genetic parameters across 305-d yields for different lactations are well known, additional research is needed to determine the (co)variance structures among test days within and across lactations. Two methods are currently proposed: random regression models (e.g., Jamrozik et al., 1996) and multi-trait models (e.g., Gengler et al., 1999a). Random regressions have a problem correctly describing the tails of the lactation (e.g., Jamrozik and Schaeffer, 1997). Similar problems are expected when estimating (co)variance components across lactations. Therefore, the following study used the multi-trait method employing the simplified but robust approach described by Tijani et al. (1999) who used (co)variance functions to describe the (co)variance structure.

Materials and Methods

Data

First and second lactation records were obtained for 23,029 Holstein cows that calved between 1990 and 1996 in 37 herds in Pennsylvania and Wisconsin. Complete data were required to estimate the full set of genetic parameters. Therefore, first and second lactation records were used for the estimation of variance components from only the 9110 Holstein cows with test day data in all stages for both lactations. Four lactation stages of 75 d each were defined starting with d 6 for each lactation. 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.

Model

A model based on Gengler et al. (1999a) was used:

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

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 lactation-calving age and season (LAS) 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 $z_{2l} = \log(DIM_l)$; 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. The number of lactation specific effects HYS and C had to be doubled and separated into first and second lactation effects as the multiple-trait step using canonical transformation required the same model. Calving ages for major LAS classes were 20 to 23, 24 to 25, 26 to 27, 28 to 31, and 32 to 35 mo for the first lactation and 31 to 35, 36 to 38, 39 to 43, and 44 to 56 for the second lactation. Starting with January, six 2-mo calving seasons were defined for LAS and HYS effects.

(Co)variance Components

The model was analyzed in two steps as described by Tijani et al. (1999). Step 1 estimated effects that were not specific to lactation stage (HTF and LAS) for the shape of the lactation curve and adjusted test day yields for those effects. This was done using data from all 23,029 cows. Step 2 estimated (co)variance components. Model effects that were specific to lactation-lactation stage (HYS, C, and a) were included. Variance components were estimated using an expectation-maximization REML algorithm. Steps 1 and 2 were solved iteratively using current (co)variance components. Iteration continued until mean relative differences between animal solutions were <1%.

(Co)variance Functions

The method used to fit (co)variance functions was an adaptation of the one described by Tijani et al. (1999) to two lactations considering milk, fat, and protein yields in different stages in both lactations as different traits. Two different residual (time-independent) or measurement error (co)variance matrices among yields were fitted for first and second lactation assuming no measurement error correlations across lactations. Contrary to Tijani et al. (1999), the order for the genetic (co)variance functions were reduced to constant, linear, and quadratic Legendre polynomials: $I_0 = (1/2)^{0.5}$, $I_1 = (3/2)^{0.5}x$, and $I_2 = (5/8)^{0.5}(3x^2 - 1)$, where $x = -1 + 2[(DIM - 1)/(305 - 1)]$.

305-d Yields, Persistency, and Maturity Rate

(Co)variance functions allow easy definition of functions of yields at different test days. These functions can have more understandable biological meaning than regression coefficients. Three types of biological variates were defined: 305-d milk, fat, and protein yields as the average of the sums of test days yields between d 1 and 305 in first and second lactation; first and second lactation persistencies as the difference between test day yields at DIM 280 and DIM 60 (Jamrozik et al., 1997); and maturity rate as the difference between 305-d yields in second compared to first lactation.

Results and Discussion

(Co)variance Components

Estimates (not shown) were similar to previous results (Gengler et al., 1999a) for first lactation. Second lactation was slightly different from first lactation.

(Co)variance Functions

Tables 1 to 4 show the heritabilities and correlations among milk, fat and protein yields at the beginning (DIM 5) and the end of the lactation (DIM 305), and at the day of peak milk production (DIM 65) that were estimated from covariance functions. Heritabilities were at the lower limit of what might be expected. This could be a consequence of the preadjustments. Genetic and phenotypic correlations in first and second lactation were similar to what was expected with a tendency to show low correlation between fat and the other traits. Across lactation this tendency was even stronger showing very low genetic correlation between milk in first and fat yield in second lactation.

305-d Yields, Persistency, and Maturity Rate

Table 5 gives the heritabilities, genetic and phenotypic correlations among the three types of biological functions (305-d yields, persistency, and maturity rate). Heritabilities for mean 305-d yields were at a low end of the expected range. Persistency was defined separately for first and second lactation. Heritabilities were different with clearly lower values in the first and higher for the second lactation. Maturity rate defined as the difference between second and first lactation showed rather low heritabilities. Genetic and phenotypic correlations among all traits were positive. Genetic correlations among 305-d yield traits were remarkably low, phenotypic correlations were closer to the expected values. Persistency and maturity rates were all correlated moderately to 305-d yields. Corresponding phenotypic correlations were similar. The results showed that the definition of persistency used by Jamrozik et al. (1997) is not phenotypically independent from 305-d yield. A

major concern recently has been very low correlation between first and later lactation persistencies as reported by Swalve and Gengler (1999). The present results confirm this for phenotypic correlations, but showed clearly higher genetic correlations with values around 0.70. It appears that persistencies in first and second lactation are phenotypically rather different traits but with high genetic correlations between them.

Conclusions

A major problem in test day model development is the estimation of useful and correct genetic parameters needed for genetic evaluations. This already arduous task in multi-trait multi-lactation test day models is even more difficult due to the structure of the data and the complexity of the models. This study used an indirect approach to get initial, preliminary, findings. The results showed some similarities with those obtained from an earlier study using the same methodology but for first lactation only records of the same cows. The results also showed the relative weakness of the proposed methodology that must preadjust test day yields within lactation stages. Alternative strategies should be considered for future studies. Recent advances were reported concerning different solving algorithms for test day models (e.g., Gengler et al, 1999b). Future research should determine if alternative (co)variance estimation strategies could be based on this or similar approaches.

Acknowledgments

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Table 1. Heritabilities (on diagonal and bold), genetic correlations (above), and phenotypic correlations (below) for milk, fat, and protein yields for first lactation.

Yield trait	DIM	Milk			Fat			Protein		
		5	65	305	5	65	305	5	65	305
Milk	5	**0.10**	0.81	0.53	0.46	0.17	0.42	0.72	0.60	0.47
	65	0.64	**0.14**	0.64	0.35	0.26	0.40	0.52	0.68	0.58
	305	0.32	0.34	**0.15**	0.19	0.13	0.58	0.22	0.24	0.80
Fat	5	0.56	0.36	0.17	**0.08**	0.83	0.69	0.58	0.65	0.51
	65	0.37	0.65	0.19	0.60	**0.12**	0.76	0.28	0.49	0.48
	305	0.20	0.22	0.66	0.37	0.25	**0.12**	0.22	0.30	0.73
Protein	5	0.88	0.51	0.25	0.59	0.36	0.21	**0.10**	0.84	0.38
	65	0.57	0.91	0.26	0.39	0.65	0.20	0.58	**0.15**	0.53
	305	0.30	0.30	0.92	0.25	0.22	0.73	0.31	0.28	**0.11**

Table 2. Heritabilities (on diagonal and bold), genetic correlations (above), and phenotypic correlations (below) for milk, fat, and protein yields for second lactation.

Yield trait	DIM	Milk			Fat			Protein		
		5	65	305	5	65	305	5	65	305
Milk	5	**0.08**	0.81	0.52	0.40	0.30	0.58	0.80	0.70	0.51
	65	0.66	**0.11**	0.45	0.13	0.13	0.34	0.51	0.69	0.39
	305	0.27	0.25	**0.25**	0.06	0.10	0.90	0.48	0.35	0.96
Fat	5	0.48	0.29	0.11	**0.12**	0.89	0.40	0.53	0.41	0.13
	65	0.34	0.60	0.16	0.67	**0.15**	0.39	0.39	0.35	0.20
	305	0.18	0.19	0.74	0.34	0.23	**0.22**	0.59	0.40	0.92
Protein	5	0.88	0.53	0.25	0.48	0.33	0.20	**0.10**	0.85	0.55
	65	0.58	0.90	0.21	0.30	0.60	0.18	0.61	**0.13**	0.43
	305	0.25	0.23	0.96	0.14	0.18	0.79	0.28	0.22	**0.23**

Table 3. Genetic correlations among milk, fat, and protein yields for first and second lactation.

		Second lactation DIM								
Yield trait	First lactation DIM	Milk			Fat			Protein		
		5	65	305	5	65	305	5	65	305
Milk	5	0.64	0.63	0.29	0.10	0.06	0.25	0.33	0.39	0.24
	65	0.71	0.82	0.32	0.13	0.02	0.24	0.38	0.46	0.24
	305	0.48	0.61	0.77	0.00	0.02	0.58	0.26	0.25	0.64
Fat	5	0.48	0.23	0.20	0.77	0.62	0.46	0.57	0.55	0.26
	65	0.50	0.22	0.24	0.87	0.83	0.54	0.61	0.49	0.33
	305	0.58	0.39	0.64	0.62	0.66	0.83	0.49	0.39	0.67
Protein	5	0.47	0.38	0.12	0.31	0.19	0.16	0.59	0.62	0.15
	65	0.66	0.57	0.20	0.42	0.22	0.26	0.76	0.80	0.25
	305	0.60	0.63	0.76	0.26	0.29	0.70	0.62	0.67	0.77

Table 4. Phenotypic correlations among milk, fat, and protein yields for first and second lactation.

		Second lactation DIM								
Yield trait	First lactation DIM	Milk			Fat			Protein		
		5	65	305	5	65	305	5	65	305
Milk	5	0.23	0.23	0.13	0.07	0.08	0.09	0.19	0.21	0.11
	65	0.26	0.33	0.17	0.08	0.11	0.10	0.21	0.28	0.15
	305	0.18	0.24	0.30	0.03	0.09	0.20	0.17	0.21	0.27
Fat	5	0.12	0.12	0.12	0.10	0.13	0.14	0.13	0.15	0.13
	65	0.14	0.15	0.13	0.17	0.25	0.18	0.16	0.19	0.16
	305	0.11	0.14	0.23	0.08	0.17	0.24	0.13	0.17	0.24
Protein	5	0.18	0.18	0.09	0.08	0.09	0.07	0.20	0.22	0.09
	65	0.23	0.28	0.13	0.11	0.14	0.10	0.25	0.32	0.14
	305	0.18	0.23	0.27	0.08	0.14	0.21	0.19	0.26	0.27

Table 5. Estimates of heritabilities (bold on diagonal), genetic (above), and phenotypic correlations (below) among 305-d yields, persistency in first and second lactation, and maturity rate.

					Persistency[2]								
		305-d yield[1]			First lactation			Second lactation			Maturity rate[3]		
Trait		Milk	Fat	Protein	Milk	Fat	Protein	Milk	Fat	Protein	Milk	Fat	Protein
305-d yield[1]	Milk	**0.21**	0.30	0.72	0.27	0.50	0.41	0.32	0.50	0.40	0.32	0.11	0.31
	Fat	0.66	**0.23**	0.51	0.20	0.35	0.38	0.35	0.13	0.39	0.29	0.58	0.39
	Protein	0.91	0.70	**0.21**	0.06	0.15	0.23	0.29	0.39	0.28	0.42	0.23	0.47
First lactation	Milk	0.27	0.24	0.26	**0.05**	0.60	0.81	0.77	0.53	0.68	0.41	0.36	0.44
	Fat	0.23	0.26	0.20	0.73	**0.03**	0.73	0.63	0.68	0.77	0.45	0.51	0.53
	Protein	0.31	0.26	0.31	0.94	0.67	**0.05**	0.65	0.54	0.70	0.44	0.35	0.55
Second lactation	Milk	0.30	0.36	0.31	0.10	0.06	0.09	**0.11**	0.84	0.95	0.55	0.49	0.59
	Fat	0.33	0.27	0.31	0.07	0.06	0.07	0.77	**0.11**	0.85	0.54	0.23	0.56
	Protein	0.35	0.37	0.35	0.09	0.06	0.09	0.95	0.73	**0.11**	0.56	0.53	0.61
Maturity rate[3]	Milk	0.53	0.47	0.53	0.40	0.30	0.36	0.44	0.41	0.48	**0.06**	0.72	0.96
	Fat	0.42	0.60	0.40	0.33	0.40	0.26	0.43	0.36	0.43	0.80	**0.05**	0.77
	Protein	0.52	0.46	0.56	0.39	0.26	0.39	0.47	0.40	0.51	0.96	0.75	**0.07**

[1] 305-d yields defined as average of 305-d yields in first and second lactation.
[2] Persistency of yields defined as difference between test day yields at day 280 and day 60.
[3] Maturity rate defined as difference between 305-d yields in second and first lactation.