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Estimates Using an Animal Model of (Co)variances for Yields of Milk, Fat, and Protein for the First Lactation of Holstein Cows in California and New York¹

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ABSTRACT

First lactation yields of milk, fat, and protein from Holstein cows in New York and California were used to obtain REML estimates of (co)variances for yield traits using a multitrait animal model. Data from each state were split randomly into 10 samples, averaging 5504 cows per sample from California and 5078 from New York. Mean heritability estimates for milk, fat, and protein yields were $.30 \pm .02$, $.31 \pm .01$, and $.29 \pm .01$ for California data and $.33 \pm .01$, $.35 \pm .01$, and $.30 \pm .01$ for New York data. Averages of genetic correlation estimates for California and New York were $.63 \pm .01$ and $.52 \pm .02$ between milk and fat, $.84 \pm .01$ and $.83 \pm .01$ between milk and protein, and $.73 \pm .01$ and $.68 \pm .01$ between fat and protein. Estimates of environmental correlations were larger than estimates of genetic correlations. Mean estimates of phenotypic correlations for California and New

York were $.75 \pm .01$ and $.72 \pm .01$ between milk and fat, $.92 \pm .01$ and $.91 \pm .01$ between milk and protein, and $.81 \pm .01$ and $.79 \pm .01$ between fat and protein yields. On average, these estimates agree with those obtained from animal models with limited rounds of iteration for small data files.

(Key words: genetic parameters, yield traits, Holsteins)

Abbreviation key: CA = California, NY = New York.

INTRODUCTION

Estimates of genetic parameters for yield traits of dairy cows obtained with sire models are frequently in the literature, but mostly for yields of milk and fat; estimates of correlations with protein yield are relatively rare (3, 5, 11, 14, 15). Genetic variances might be underestimated if selection intensity is larger for males than for females because analyses with sire models accounted only for genetic variance of sires (16, 22). Animal models take into account differential selection of males and females and might provide more accurate estimates of parameters than do sire models.

Since the late 1980s, genetic parameters for yield traits have been estimated using animal models, but most estimates have been obtained with small data files and with convergence assumed after relatively few rounds of iteration. Swalve and Van Vleck (18) used records of 4000 cows to estimate genetic parameters for milk yields of first, second, and third lactations with an animal model. Only 18 rounds of iteration were allowed, and iterative REML

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and relationships across herds were not considered. Van Vleck and Dong (20), with a similar strategy, estimated genetic parameters for yields of milk, fat, and protein for the first lactation using a total of 8044 records. Van Vleck et al. (21) analyzed yields of milk and fat with two samples of 4000 cows from New York (NY), California (CA), and Wisconsin. In those two studies (20, 21), the relationships across herds also were assumed to be zero, and the analyses were stopped after 300 rounds of iteration. Dong and Van Vleck (8) used two samples, each with about 3000 cows, to estimate genetic parameters for milk yield, calving interval, and survival for first lactation. In that study (8), relationships across herds were ignored as were daughter-dam relationships. The number of iterations allowed was 20 and 23, respectively, for each sample. Using two samples with 4000 cows, Dong et al. (9) studied the effect of using different relationships on variance component estimates for milk and fat yields. Misztal et al. (16) used a relatively larger data file (20,836 registered Holstein cows) to estimate genetic parameters for three yield traits and 15 type traits with a multitrait animal model. The convergence criterion was not described.

Parameter estimates from a sample of data may vary, depending on the kind of analyses used (single-trait or multitrait) and also on which traits are included in a multitrait analysis (12). Yields of milk, fat, and protein seem to be the main traits considered for dairy cattle selection, but estimates of genetic parameters for these traits obtained with an animal model and REML and using a large data file, have not been available.

The objective of this study was to obtain REML estimates of genetic and phenotypic

variances and covariances for yields of milk, fat, and protein for first lactation, using a multitrait animal model and data files that were much larger than those previously reported to determine the validity of the earlier estimates and to obtain empirical standard errors of the estimates. Another objective was to determine whether the genetic correlations among the yield traits were the same for herds in NY and CA.

MATERIALS AND METHODS

Yields of milk, fat, and protein from first lactation, standardized to basis of twice daily milking and a mature equivalent 305-d lactation, for Holstein cows from CA and NY, were used. Cows without measurements on yields of milk, fat, or protein or with records from <240 d of lactation were deleted. All herds had to have cows freshening in at least 3 yr. The minimum herd size was 100 cows for CA and 50 cows for NY. Herds in each state were assigned randomly to 10 samples, according to the herd code. The structures of the samples of data are summarized in Table 1. Mean yields for milk, fat, and protein were larger for CA than for NY. Records were analyzed from a total of 55,043 cows from CA and 50,780 cows from NY, calving from 1986 to 1990 and from 1981 to 1990, respectively.

The model included herd-year-seasons of calving as fixed effects and animal genetic and residual effects as random effects. Three seasons of freshening were defined for CA data (January to April, May to August, and September to December) and four for NY (January to March, April to June, July to September, and October to December).

TABLE 1. Summary of the data structure of 10 samples from California and 10 samples from New York.

	California			New York		
	\bar{X}	Minimum	Maximum	\bar{X}	Minimum	Maximum
Records, no.	5504	5134	5927	5078	4719	5761
Herd-year-seasons, no.	142	91	188	1040	975	1124
Animals in relationship matrix, no.	8861	8049	9650	8341	7720	9219
Mixed model equations, no.	27,009	24,582	29,352	28,343	26,169	30,840
Yield, kg						
Milk	10,294	9839	10,702	8712	8484	9015
Fat	367	349	384	317	310	327
Protein	318	304	332	276	268	287

Mean samples of data from CA and NY had 8861 and 8341 animals represented in the numerator relationship matrices; of those, 5504 and 5078 had records resulting in mixed model equations of average order 27,009 and 28,343, respectively. The mean number of herd-year-seasons was much larger for NY, 1040, than for CA, 142, because of differences in herd sizes, number of years, and one more season per year.

The data were analyzed by derivative-free REML (10, 17) with a multiple-trait animal model, using an algorithm developed by Boldman et al. (1) and Boldman and Van Vleck (2). Convergence was assumed when the variance of the log-likelihood values in the simplex reached $<10^{-9}$. Occurrence of local maxima was checked by repeatedly restarting the analyses until the log-likelihood did not change beyond the first decimal.

Estimates of variances and covariances were pooled by calculating the arithmetic average of the 10 samples of data from each state from which empirical standard errors were calculated.

RESULTS AND DISCUSSION

Phenotypic, genetic, and environmental correlations were largest between milk and

protein, followed by correlations for fat and protein (Table 2). This same trend was observed for both states and was consistent with the patterns described previously for sire models (3, 4, 5, 11) and animal models (9, 16, 21, 23).

Estimates of genetic correlations between milk and protein yields were almost the same for CA and NY data, but, between milk and fat yields and between fat and protein yields, the estimates were significantly larger for CA than for NY. Van Vleck et al. (21), using small data files, also found smaller estimates of genetic correlation between yields of milk and fat for NY data, .54, than for CA data, .70. Estimates of genetic correlations obtained in the present study were smaller than those obtained from other studies with animal models, except for between yields of milk and protein. Mean estimates of genetic correlation between yields of milk and fat for NY were similar, but between yields of milk and protein were much higher, than those obtained by Lawlor (11) with a sire model and NY data of .51 and .65, respectively. Van Vleck et al. (21), using NY data and an animal model, found a similar genetic correlation, .54, between milk and fat yields. The mean estimates of genetic correlations and heritabilities were significantly lower than those reported by Misztal et al. (16) from a

TABLE 2. Means and empirical standard errors of estimates of heritabilities and genetic, environmental, and phenotypic correlations for yields of milk, fat, and protein of first lactation cows from 10 samples from California and 10 from New York.

Yield traits	California				New York			
	\bar{X}	SE	Minimum	Maximum	\bar{X}	SE	Minimum	Maximum
Heritabilities								
Milk (M)	.30	.02	.22	.39	.33	.01	.26	.37
Fat (F)	.31	.01	.23	.37	.35	.01	.29	.42
Protein (P)	.29	.01	.23	.37	.30	.01	.25	.39
Genetic correlations								
M \times F	.63	.03	.47	.83	.52	.02	.40	.60
M \times P	.84	.01	.78	.91	.83	.01	.76	.87
F \times P	.73	.02	.66	.87	.68	.01	.61	.71
Environmental correlations								
M \times F	.80	.01	.77	.82	.81	.01	.79	.83
M \times P	.94	.01	.93	.96	.96	.01	.95	.96
F \times P	.84	.01	.81	.86	.84	.01	.80	.86
Phenotypic correlations								
M \times F	.75	.01	.72	.80	.72	.01	.70	.73
M \times P	.92	.01	.90	.93	.91	.01	.91	.92
F \times P	.81	.01	.78	.83	.79	.01	.78	.80

TABLE 3. Mean estimates of genetic and phenotypic (co)variances and empirical standard errors (SE) for milk, fat, and protein yields (kg) for first lactation for 10 samples from California and 10 from New York.

	Genetic		Phenotypic	
	\bar{X}	SE	\bar{X}	SE
California				
Variances, kg ²				
Milk (M)	586,526	37,857	1,984,076	24,351
Fat (F)	773	36	2502	54
Protein (P)	462	26	1562	17
Covariances, kg ²				
M \times F	13,494	1192	52,889	1211
M \times P	14,018	948	50,890	682
F \times P	441	31	1593	29
New York				
Variances, kg ²				
M	502,928	91,963	1,510,883	32,557
F	682	84	1966	30
P	380	69	1249	25
Covariances, kg ²				
M \times F	9754	2057	38,952	744
M \times P	11,484	2374	39,697	849
F \times P	347	63	1243	21

canonical analysis of 18 traits and 100 rounds of REML involving records of 20,836 registered US Holsteins.

Estimates of environmental correlations were larger than the genetic correlations and within 1% of those reported by Misztal et al. (16). Estimates of phenotypic correlations were similar for records from both states and consistent with most of the estimates described in the literature for sire and animal models.

Mean estimates of genetic and phenotypic (co)variances for yields of milk, fat, and protein were higher for CA data than for NY data (Table 3), probably because of higher yield of CA cows. However, genetic variances for milk and fat as proportions of the phenotypic variances were smaller for CA than for NY. Consequently, for milk and fat yields, mean heritability estimates were higher for NY than for CA, .33 and .30 for milk yields and .35 and .31 for fat yields, respectively. Heritability estimates for protein yields were almost the same for both states, .30 for NY and .29 for CA. Previous reports (6, 7, 13, 19, 21) indicated that heritability estimates may increase as yield increases. Although mean yield was higher for CA than for NY (Table 1), heritability estimates were somewhat lower. This result may be due to more complete relationship matrices

for data from NY than from CA. Van Vleck et al. (21) and Dong et al. (9) found smaller fractions of nonzero off-diagonal elements in the inverse of relationship matrix and of daughter and dam pairs for data from CA than from NY. Those authors (9, 21) suggested that this result could be due to misidentification or purchase of replacements from other herds. In a study that compared parameter estimates obtained using different relationship matrices, Dong et al. (9) observed that heritability estimates were smaller if complete relationship matrices were not used.

In general, heritability estimates obtained in the present study are higher than those obtained with sire models (5, 11, 13, 14). However, Cue et al. (4), using a sire model with Canadian data, reported heritability estimates of .36 for milk and fat yields and .25 for protein yield.

Heritability estimates obtained with animal models vary, but most are higher than those obtained with sire models. Van Vleck and Dong (20), using data from NY, reported heritability estimates of .36 for milk yield, .35 for fat yield, and .33 for protein yield. However, lower estimates were obtained by Van Vleck et al. (21) for the period from 1978 to 1985 of .26 and .28 for milk yield and .29 and

.27 for fat yield for CA and NY, respectively. Depending on the relationship matrix utilized, Dong et al. (9) obtained heritability estimates varying from .25 to .33 for milk yield, .26 to .36 for fat yield, and from .22 to .34 for protein yield. With a model including milk yield from first lactation, calving interval, and survival, Dong and Van Vleck (8) estimated heritability for milk yield to be .33 and .28 for two small data files. Misztal et al. (16) obtained much higher heritability estimates than those in the present study of .44, .42, and .40, respectively, for yields of milk, fat, and protein. The high estimates were thought to have been due to use of only registered cows or inclusion of genetic levels of unknown parents in the analysis. Visscher and Thompson (23), with British cows, also reported higher heritability estimates for yields of milk and fat of .39 and .36, respectively.

CONCLUSIONS

Genetic correlations between yields of milk and fat and between yields of fat and protein were higher for CA data than for NY data, which confirms the results for yields of milk and fat that were reported previously for small samples from CA and NY. Reasons for a difference in genetic correlations between NY and CA are not apparent but may be associated with yield or with management systems. Estimates of environmental and phenotypic correlations were similar for CA and NY. Heritability estimates for yields of milk, fat, and protein were moderate and slightly higher for NY than for CA. These estimates were similar to previous estimates obtained using an animal model with smaller data files and fewer rounds of iteration than in the present study.

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REFERENCES

- 1 Boldman, K. G., L. A. Kriese, L. D. Van Vleck, and S. D. Kachman. 1993. Page 1 in A manual for use of MTDFREML. USDA-ARS, Clay Center, NE.
- 2 Boldman, K. G., and L. D. Van Vleck. 1991. Derivative-free restricted maximum likelihood estimation in animal models with a sparse matrix solver. *J. Dairy Sci.* 74:4337.
- 3 Chauhan, V.P.S., and J. F. Hayes. 1991. Genetic parameters for first lactation milk production and composition traits for Holsteins using multivariate restricted maximum likelihood. *J. Dairy Sci.* 74:603.
- 4 Cue, R. I., H. G. Monardes, and J. F. Hayes. 1987. Correlations between production traits in first lactation Holstein cows. *J. Dairy Sci.* 70:2132.
- 5 deJager, D., and B. W. Kennedy. 1991. Genetic parameters of milk yield and composition and their relationship with alternative breeding goal. *J. Dairy Sci.* 70:1258.
- 6 DeVeer, J. C., and L. D. Van Vleck. 1986. Comparison of heritability estimates from daughter on dam regression with three models to account for production level of dam. *J. Dairy Sci.* 69:2890.
- 7 DeVeer, J. C., and L. D. Van Vleck. 1987. Genetic parameters for first lactation milk yields at three levels of herd production. *J. Dairy Sci.* 70:1434.
- 8 Dong, M. C., and L. D. Van Vleck. 1989. Estimates of genetic and environmental (co)variances for first lactation milk yield, survival, and calving interval. *J. Dairy Sci.* 72:678.
- 9 Dong, M. C., L. D. Van Vleck, and G. R. Wiggans. 1988. Effect of relationships on estimation of variance components with an animal model and restricted maximum likelihood. *J. Dairy Sci.* 71:3047.
- 10 Graser, H.-U., S. P. Smith, and B. Tier. 1987. A derivative-free approach for estimating variance components in animal model by restricted maximum likelihood. *J. Anim. Sci.* 64:1362.
- 11 Lawlor, T. J., Jr. 1984. Estimation of genetic and phenotypic parameters of milk, fat and protein yields of Holstein cattle under selection. Ph.D. Diss., Cornell Univ., Ithaca, NY.
- 12 Lin, C. Y., and A. J. Lee. 1986. Sequential estimation of genetic and phenotypic parameters in multitrait mixed model analysis. *J. Dairy Sci.* 69:2696.
- 13 Majjala, K., and M. Hanna. 1974. Reliable phenotypic and genetic parameters in dairy cattle. *Proc. 1st World Congr. Genet. Appl. Livest. Prod., Madrid, Spain I:* 541.
- 14 Manfredi, E. J., R. W. Everett, and S. R. Searle. 1984. Phenotypic and genetic statistics of components of milk and two measures of somatic cell concentration. *J. Dairy Sci.* 76:2028.
- 15 Meyer, K. 1985. Genetic parameters for dairy production of Australian Black and White cows. *Livest. Prod. Sci.* 12:205.
- 16 Misztal, I., T. J. Lawlor, T. H. Short, and P. M. Van Raden. 1992. Multiple-trait estimation of variance components of yield and type traits using an animal model. *J. Dairy Sci.* 75:544.
- 17 Smith, S. P., and H. U. Graser. 1986. Estimating variance components in a class of mixed models by restricted maximum likelihood. *J. Dairy Sci.* 69:1156.
- 18 Swalve, H., and L. D. Van Vleck. 1987. Estimation of genetic (co)variances for milk yield in first three lactations using an animal model and restricted maximum likelihood. *J. Dairy Sci.* 70:842.
- 19 Van Vleck, L. D., L. R. Cox, and S. L. Mirande. 1985. Heritability estimates of milk production from daugh-

- ter on dam regression by year and management level. *J. Dairy Sci.* 68:2964.
- 20 Van Vleck, L. D., and M. C. Dong. 1988. Genetic (co)variances for milk, fat, and protein yield in Holsteins using an animal model. *J. Dairy Sci.* 71:3040.
- 21 Van Vleck, L. D., M. C. Dong, and G. R. Wiggans. 1988. Genetic (co)variances for milk and fat yield in California, New York, and Wisconsin for an animal model by restricted maximum likelihood. *J. Dairy Sci.* 71:3053.
- 22 Visscher, P. M., and R. Thompson. 1990. REML estimates of parameters for fat yield in pedigree herds in the U.K. using an individual animal model; male and female heritability estimates. *Proc. 4th World Congr. Genet. Appl. Livest. Prod., Edinburgh, Scotland XIV*:233.
- 23 Visscher, P. M., and R. Thompson. 1992. Univariate and multivariate parameter estimates for milk production traits using an animal model. I. Description and results of REML analyses. *Genet. Sel. Evol.* 24:415.