COVARIANCES AMONG LACTATION YIELDS FOR MILK, FAT AND PROTEIN, USING AN ANIMAL MODEL.

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SUMMARY
A derivative-free restricted maximum likelihood algorithm to fit an animal model was used to estimate variances and covariances for milk, fat and protein yields among yields of the first three lactations, using 110,779 records of 54,634 Holstein cows from California. Heritability estimates for milk, fat and protein yields were, respectively, .34, .35 and .40 for first, .31, .33 and .39 for second and .27, .31 and .37 for third lactation. Estimates of genetic correlations among lactation yields, in general, were greater than .80. The phenotypic correlations varied from .52 to .66 and were similar for the three yield traits.

INTRODUCTION
Dairy sire evaluations have been estimated mainly from first lactation records or repeated records assuming correlation of unity among yields in different lactations (e.g., Swalve and Van Vleck, 1987). These two procedures assume that the first lactation can provide adequate information about later lactations or that the same genes influence first and later lactations. Estimates of correlations for yields across lactations obtained from sire models (Tong et al., 1979; Meyer, 1984) and animal models (Swalve and Van Vleck, 1987; Visscher and Thompson, 1992) are similar and above .80.

According to Ufford et al. (1979), the main benefit obtained by using later lactations for sire evaluation is the increase in accuracy of evaluation. A multi-trait analysis with different lactations as traits could be considered for sire evaluation, to account for bias in later lactations due to selection on early lactations. Previous estimates of genetic parameters using REML yields in the USA across lactations based on a multiple trait animal model were from small data sets with limited rounds of iteration. The objective of this study was to estimate genetic and phenotypic variances and covariances for production traits among lactations using an animal model and derivative-free REML.

MATERIAL AND METHODS
A total of 110,779 mature equivalent milk, fat and protein lactation yields of the first three lactations of 54,634 California Holstein cows, recorded from 1981 to 1990 were used. Yields in each of the three lactations were considered as different traits. Only records of cows first freshening from 1981 to 1988 were used so that each cow had the chance for a second and a third lactation. First lactation performance was required for all cows in the analyses. Lactations after the first were accepted only if the previous one was recorded.

The model included genetic effects of animal and residual effects as random and herd-year-seasons as fixed, with three seasons of four months each. The data were randomly assigned to 10 subsets with means described in Table 1. Number of cows with records in a subset varied from 4,611 to 5,940 with 7,080 to 10,438 animals in the A^{-1} matrix. Subsets averaged 16 herds. The number of mixed model equations ranged from 21,663 to 31,752 with an average of 28,070.

TABLE 1. Means for milk, fat and protein yields, average number of records and average number of herd-year-season (H-Y-S) levels for ten samples of records of California Holstein cows

Means	Lactation		
	1	2	3
Milk (kg)	10,198	10,923	10,796
Fat (kg)	368	388	382
Protein (kg)	313	338	340
No. of records	5,463	3,629	1,985
No. of H-Y-S	130	159	122

Analyses used derivative-free restricted maximum likelihood (Smith and Graser, 1986) with a multiple trait animal model utilizing an algorithm developed by Boldman et al. (1991, 1993). The convergence criterion was reached when the variance of the simplex was less than 1.e-9. Occurrence of local maxima was checked by restarting the analyses.

RESULTS

Averages for the 10 subsets of estimates of the genetic, environmental and phenotypic variances and covariances for milk, fat and protein yields are in Table 2. The largest estimate of genetic variance was for the second lactation consistently for the three yield traits, whereas estimates of environmental variances increased with order of lactation with the largest change from the first to second lactation. Similar results were described by Meyer (1984) and Visscher and Thompson (1992). Estimates of genetic and environmental covariances were consistently larger for the second and third lactations.

Table 2. Averages of estimates from ten samples of genetic (g) and environmental (e) variances (σ^2) and covariances (σ) among lactations for milk ($kg^2 * 10^{-3}$), fat (kg^2) and protein (kg^2) yields in first (1), second (2) and third (3) lactations

Trait	σ^2_{g1}	σ^2_{g2}	σ^2_{g3}	σ_{g12}	σ_{g13}	σ_{g23}
Milk	655	727	613	596	478	629
Fat	856	1,071	1,052	851	784	1,020
Protein	625	786	774	635	574	750
Trait	σ^2_{e1}	σ^2_{e2}	σ^2_{e3}	σ_{e12}	σ_{e13}	σ_{e23}
Milk	1,293	1,594	1,617	652	603	799
Fat	1,601	2,233	2,307	804	713	1,035
Protein	927	1,224	1,305	430	361	587

Pooled heritability and correlation estimates are in Table 3. Heritability estimates decreased with order of lactation for the three yield traits, mainly as a result of the increase in environmental variances.

TABLE 3. Averages of estimates from ten samples (± empirical standard errors) of heritabilities (h^2) and genetic (r_g) and environmental (r_e) correlations among first (1), second (2) and third (3) lactations for yields of milk, fat, and protein

Parameters	Milk	Fat	Protein
h_1^2	.34 ± .03	.35 ± .03	.40 ± .04
h_2^2	.31 ± .04	.33 ± .02	.39 ± .04
h_3^2	.27 ± .02	.31 ± .02	.37 ± .03
r_{g12}	.86 ± .03	.89 ± .03	.90 ± .02
r_{g13}	.77 ± .02	.84 ± .03	.83 ± .02
r_{g23}	.96 ± .02	.97 ± .01	.97 ± .01
r_{e12}	.44 ± .03	.42 ± .02	.38 ± .05
r_{e13}	.42 ± .02	.37 ± .01	.32 ± .03
r_{e23}	.50 ± .02	.46 ± .01	.45 ± .04

The largest heritabilities were for protein yield, followed by fat and milk yields. The magnitude of these estimates varied widely from sample to sample, but on average they agree with other estimates obtained with animal models from smaller samples. All genetic correlations except between first and third lactation milk yields were greater than .80. These results agree with the estimates obtained by Swalve and Van Vleck (1987) in USA, using an animal model with small data sets and with those of Meyer (1984) and Visscher and Thompson (1992). Environmental correlations varied from .32 to .50 and were slightly larger for second and third lactations. Averages of phenotypic correlations between first and second, first and third and second and third lactations were, respectively, .59, .52 and .63 for milk, .58, .52 and .62 for fat and .60, .52 and .66 for protein yields with standard errors of .01.

DISCUSSION

The estimates of heritability for milk, fat and protein in the first three lactations were moderate to high and consistent with previous estimates obtained with animal models. Estimates of genetic correlations indicated that yields in all lactations are determined basically by the same genes. Thus, first lactation yields can be used as indicators of the later performance. Use of a repeatability model assuming genetic correlations among lactations to be one and a constant repeatability between yields of all pairs of lactations also seems acceptable.

REFERENCES

BOLDMAN, K.G., KRIESE, L.A., VAN VLECK, L.D., and KACHMAN, S.D.(1993) A Manual for Use of MTDFREML. USDA-ARS, Clay Center, NE.

BOLDMAN, K.G. and VAN VLECK, L.D. (1991) J. Dairy Sci., 74:4337-4343.

MEYER, K. (1984) Animal Production, 38:313-322.

SMITH, S.P. and GRASER, H.-U. (1986) J. Dairy Sci., 69:1156-1165.

SWALVE, H. and VAN VLECK, L.D. (1987) J. Dairy Sci., 70:842-849.

TONG, A.K.W., KENNEDY, B.W. and MOXLEY, J.E. (1979) J. Dairy Sci., 62:1784-1790.

UFFORD, G.R., HENDERSON, C.R., KEOWN, J.F. and VAN VLECK, L.D. (1979) J. Dairy Sci., 62:603-612.