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Genetic Parameters for Production Traits of Holsteins in California, New York, and Wisconsin

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ABSTRACT

Heritabilities and genetic correlations were estimated for milk and fat yields and fat percentage from 305-d, mature-equivalent records of registered and grade Holsteins in California, New York, and Wisconsin. Parameter estimates were obtained with daughter on dam regression within herd-year-season and sire of daughter. Data were pairs of first lactation records (38,115 in California, 171,555 in New York, and 136,031 in Wisconsin) from 1975 through 1984. California had higher means for milk (9046 kg) and fat (323 kg) than the other two states (approximately 7840 kg and 289 kg), but heritabilities of .36 and .34 were not greatly different from those for New York (.34 and .33) or Wisconsin (.38 and .35). Heritability of fat percentage, however, was smaller for California (.55 vs .66 for New York and .68 for Wisconsin). Logarithmic and square root transformations of the data resulted in little change in heritability estimates. For California, genetic correlation between milk and fat yields (.70) was larger than for New York (.55) or Wisconsin (.56), and correlation between fat yield and fat percentage was smaller (.31 vs .45 and .41). For each state, estimates of heritabilities were larger for registered than grade pairs.

INTRODUCTION

Much evidence in the literature (2, 3, 8, 14) suggests that heritability increases as level of milk production increases. Majjala and Hanna

(7) found this to be the general case, although there were exceptions (9, 12). If heritability increases with production, more dams for young sires should be chosen from geographic regions with higher production than from other regions because accuracy of evaluation would be greater. The implications from such a situation demand assurance of differences in heritability before such a policy is adopted.

The objective of this study was to estimate heritabilities of and genetic correlations among milk yield, fat yield, and fat percentage in California (CA), New York (NY), and Wisconsin (WI). Thus, the results should show whether 1) heritabilities differ across states and 2) genetic correlations have similar properties in each state. Any differences found in the correlations might give insight into differences (intended or otherwise) in the selection programs of each state.

MATERIALS AND METHODS

Data consisted of first lactation records for twice daily milking, 305-d, mature-equivalent milk and fat yields and fat percentage of Holstein cows from CA, NY, and WI. Both registered and grade cattle were represented. The study covered years of freshening from 1975 to 1984 inclusively. Two seasons were defined in each year (January through June and July through December).

Records of daughters and dams were matched and then edited for the usual anomalies. Because of a program limit on the number of different sires allowable, further edits were necessary. A single daughter of a sire had her record automatically discarded. Then sires with the fewest daughters were eliminated until the number of sires was reduced to 1000 or less. A summary of the data is in Table 1.

The procedure for estimating the residual

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covariance between daughter and dam for each trait, which is needed for calculation of heritability and genetic correlation, followed model 1 of DeVeer and Van Vleck (2). Their model 1 accounted for effect of herd-year-season (HYS) and sire of the daughter. The dam's model included the same HYS for all dams with daughters in the same HYS and also included the same sire effect, a dummy factor based on the assumption that daughter's sire was random with respect to dam's yield. Thus, with the same design matrices for daughter and dam records, both residual terms could be summed. The model in matrix notation is:

$$y = X\beta + Zu + e$$

where β and u are the HYS and sire effects, X and Z are the corresponding model matrices, and e is the vector of residuals. Then y can refer to the observations of daughter (D), parent (P), or sum of both (D + P). The following relationships hold among the estimates of β , u , and e :

$$\hat{\beta}_{D+P} = \hat{\beta}_D + \hat{\beta}_P, \hat{u}_{D+P} = \hat{u}_D + \hat{u}_P, \text{ and } \hat{e}_{D+P} = \hat{e}_D + \hat{e}_P.$$

Because the expectation of the variance of a sum can be expressed as:

$$E(\hat{\sigma}_{D+P}^2) = \sigma_D^2 + \sigma_P^2 + 2\sigma_{DP}$$

the residual covariances can be estimated as:

$$\hat{\sigma}_{e_{DP}} = (\hat{\sigma}_{e_{D+P}}^2 - \hat{\sigma}_{e_D}^2 - \hat{\sigma}_{e_P}^2) / 2.$$

Heritability can then be estimated in the usual way as:

$$h^2 = 2\hat{\sigma}_{e_{DP}} / \hat{\sigma}_{e_P}^2$$

and genetic correlation between traits A and B as:

$$r_{GAB} = .5[(\hat{\sigma}_{D_A P_B} + \hat{\sigma}_{D_B P_A}) / \sqrt{(\hat{\sigma}_{D_A P_A} \hat{\sigma}_{D_B P_B})}].$$

Estimates were obtained for each of the three states for each year of first freshening and for the complete 10-yr period.

RESULTS

Despite differences in yields among CA, NY, and WI (Table 1), no real differences were found among states for estimates of heritability of either milk or fat yield, either in trends during the 10-yr period or for the period as a whole. However, heritability estimate for fat percentage in CA was smaller relative to the other two states. Standard errors were of the order of .011 for CA, .005 for NY, and .006 for WI.

Transformations of the records also were analyzed to determine if some of the heterogeneity of variance among states might be reduced and thus increase estimates of heritability. Transformations were logarithm of milk yield (log milk), square root of milk yield (root milk), and square root of fat percentage (root percent). The transformations yielded little change in estimates, with root milk falling between log milk and actual milk as found in other studies (4, 14). The overall estimates of heritability for production traits and transformed traits are in Table 2, and the trends with time are in Figures 1 through 3.

Genetic correlations are in Table 3 for the 10-yr period as a whole. In general, estimates for CA differed from the other two states except for correlation between milk yield and fat percentage. Data from CA yielded a larger cor-

TABLE 1. Summary of data.

	California	New York	Wisconsin
Numbers			
Records	579,006	671,436	633,586
Pairs ¹	78,913	241,574	219,739
Pairs ²	38,115	171,555	136,031
Milk yield, kg			
Mean	9046	7874	7805
SD	1361	1228	1180
Fat yield, kg			
Mean	323	287	291
SD	46	42	41
Fat percentage			
Mean	3.60	3.66	3.76
SD	.32	.35	.37

¹Number of daughter-dam matches.

²Number of daughter-dam matches used in analyses after editing for sires.

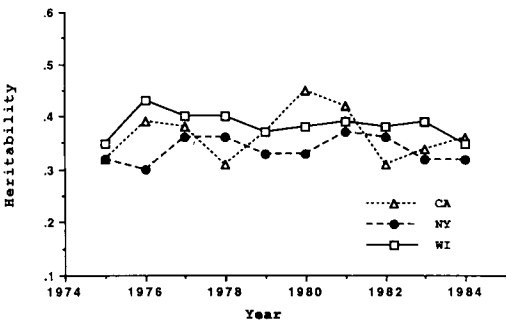


Figure 1. Estimates of heritability for milk yield from 1975 through 1984 for California, New York, and Wisconsin.

relation between milk and fat yields than either NY or WI records and a smaller correlation between fat yield and fat percentage. When yearly estimates were examined, the differences seemed to be associated with a trend in time. For milk and fat yields, correlations were almost equal in all three states at the beginning of the period. However, NY and WI estimates decreased with time while CA estimates remained consistent over the 10-yr period (Figure 4). Trends in correlation between milk yield and fat percentage (Figure 5) and between fat yield and fat percentage (Figure 6) were similar for NY and WI but different from the trend for CA.

Some patterns also were evident for estimates obtained separately from registered and

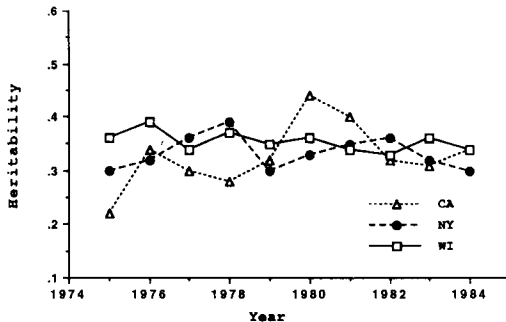


Figure 2. Estimates of heritability for fat yield from 1975 through 1984 for California, New York, and Wisconsin.

TABLE 2. Estimates of heritability for production traits and selected transformed production traits for records from California, New York, and Wisconsin from 1975 through 1984.

	California	New York	Wisconsin
Milk yield	.36	.34	.38
Fat yield	.34	.33	.35
Fat percentage	.55	.66	.68
Log milk ¹	.33	.31	.36
Root milk ²	.35	.33	.37
Root percent ³	.54	.65	.68

¹Logarithm of milk yield.

²Square root of milk yield.

³Square root of fat percentage.

grade animals. Table 4 shows estimates of heritability for and genetic correlations among traits for registered and grade Holsteins in each of the three states. Degrees of freedom and percentage of population on a within-state basis also are reported in Table 4 for registered and grade cows.

Registered cows had higher production and larger residual variances than grade cows in each state, and heritability estimates for registered were higher for each trait than for grade cows. Registered data yielded larger estimates of genetic correlation between milk and fat yields and smaller negative correlation between milk and fat percentage in all states compared with results from grade data. There may be a trend showing a lower genetic correlation between fat yield and fat percentage in registered versus grade, but CA did not support this, showing the opposite trend. There were, however, fewer pairs available for analysis in CA relative to NY or WI.

TABLE 3. Estimates of genetic correlations among milk yield, fat yield, and fat percentage for records from California, New York, and Wisconsin from 1975 through 1984.

	California	New York	Wisconsin
Milk yield, fat yield	.70	.55	.56
Milk yield, fat percentage	-.45	-.49	-.52
Fat yield, fat percentage	.31	.45	.41

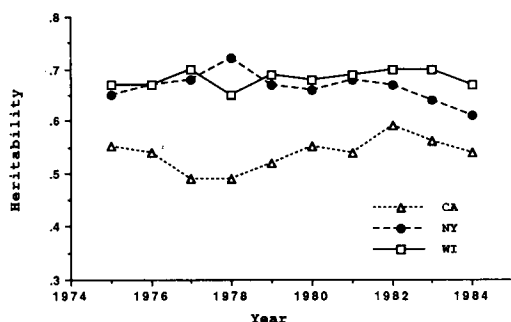


Figure 3. Estimates of heritability for fat percentage from 1975 through 1984 for California, New York, and Wisconsin.

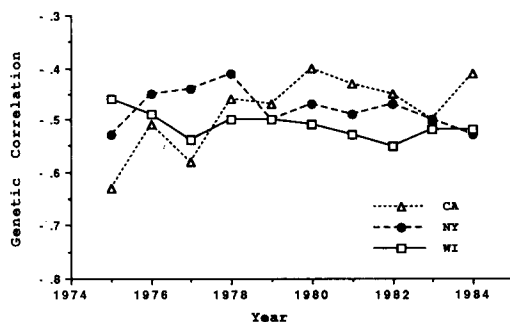


Figure 5. Estimates of genetic correlation between milk yield and fat percentage from 1975 through 1984 for California, New York, and Wisconsin.

DISCUSSION

Although higher yields and residual variances gave rise to higher heritabilities within each state, this trend was not evident across states. Heritabilities were equal from state to state for all practical purposes. In fact, WI, with the lowest milk yield, had the highest estimate of heritability. The method of estimation used may explain these apparent anomalies; Van Vleck and Bradford (12), using both parental half-sib correlation (PHS) and daughter on dam regression (DD) methods, found that heritability estimates increased as production increased only in the case of the PHS method. They also found that, in general, PHS estimates were smaller than those from DD (12, 13). However, other studies using DD regression (10, 14)

found the trend of higher heritabilities with higher production. The DD regression method was chosen for this study because the resulting estimates are unaffected by selection of dams (5).

Potentially important is that fewer pairs were found in CA than in NY or WI. This may be true or due in part to some misidentification, which is likely for a state with large herd sizes such as CA. Van Vleck (11) concluded that "misidentification of sires of cows in paternal half-sib analyses of variances biases the estimate of heritability downward." He also showed that heritability estimates obtained from DD regression would be reduced to a fraction, p , of the actual heritability, where p is the fraction of dams correctly identified (11).

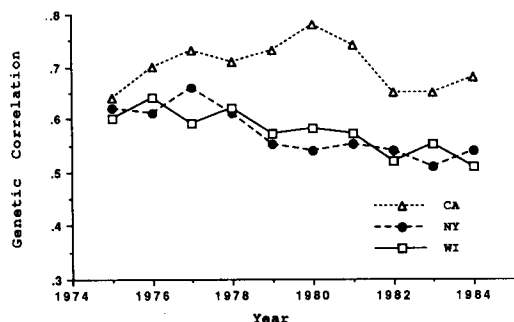


Figure 4. Estimates of genetic correlation between milk yield and fat yield from 1975 through 1984 for California, New York, and Wisconsin.

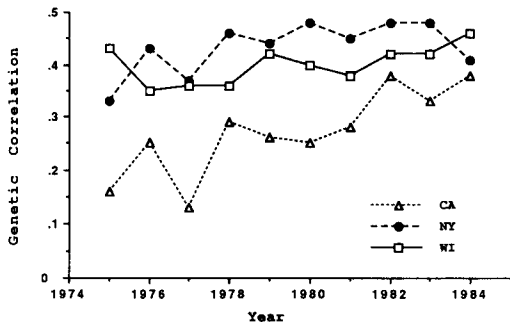


Figure 6. Estimates of genetic correlation between fat yield and fat percentage from 1975 through 1984 for California, New York, and Wisconsin.

TABLE 4. Estimates of heritability for and genetic correlations among production traits of registered (R) and grade (G) Holsteins for records from California, New York, and Wisconsin from 1975 through 1984.

	California		New York		Wisconsin	
	R	G	R	G	R	G
Heritability						
Milk yield	.37	.34	.37	.29	.40	.34
Fat yield	.38	.29	.35	.29	.37	.29
Fat percentage	.56	.53	.68	.63	.69	.67
Correlation						
Milk yield, fat yield	.71	.68	.57	.52	.58	.49
Milk yield, fat percentage	-.41	-.50	-.48	-.50	-.51	-.56
Fat yield, fat percentage	.34	.30	.43	.48	.40	.44
df	11,246	17,979	72,751	43,489	63,255	22,919
% ¹	38	62	63	37	73	27

¹Percentage of state population.

This same study also suggested that misidentification is more likely among grade than registered cows. In this study CA had the largest percentage of grade cows (Table 4), and downward effects on the estimates of heritability are not unreasonable if misidentification was present.

Despite the seeming simplicity of the model used in this study, attempts to account further for HYS of dam using modifications of model 1 resulted in only slightly higher estimates of heritabilities (2). Therefore, model 1 was determined to be adequate for the purposes of this study, and estimates were not biased upward, although estimates of heritability might be slightly larger if the HYS effects on records of the dam were accounted for more precisely (2).

Cue et al. (1) in a recent study of Canadian Holsteins with mean lactation yields below those reported in this study found a heritability of .36 for milk, the same as found in this study for American Holsteins in the three states. The method of estimation was a sire model with a multivariate REML algorithm that ignored relationships. These estimates are, however, higher than expected from such a method (7).

In a parallel study (15) to that presented here, genetic (co)variances were estimated using small samples of the same data with an animal model using REML and all relationships among animals within a herd. Results obtained were remarkably similar to those reported here, even though the method used necessitated

smaller data sets.

The genetic correlation between milk and fat for CA found in this study agreed with those of other studies (1, 7, 8, 15, 16). Estimates for NY and WI in this study were smaller than previously reported (7), but Lawlor (6) obtained generally smaller estimates for Northeast data. The decrease in this correlation with time for NY and WI records seems difficult to explain but may be because of selection or an interaction between genetic expression and production level. Correlations with fat percentage were larger than for previous studies (1, 7, 8, 15, 16).

CONCLUSIONS

Higher heritabilities for registered cows than for grade cows in each state may indicate a positive association between higher production and higher heritabilities within states. However, differences in heritabilities are small across states at least for milk and fat yield. New York and WI tend to have similar genetic correlations, which are different from those of CA. Therefore, selecting bull dams from the higher producing herds within any one region still seems reasonable. However, this study provided no evidence to suggest that choosing all dams from the highest producing region would be beneficial. Although heritabilities generally did not change across regions, variance estimates did, a fact currently being ignored in genetic evaluation models.

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