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Effect of Variance of Interaction Effects of Sire and Herd on Selection for Milk and Fat Yield¹

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ABSTRACT

The animal model for genetic evaluations of dairy cattle by the USDA currently includes a term for interaction effects of sire and herd. The relative magnitude of the variance of that effect was established in the 1960s as 14% of the total variance, but recent research has shown that the proportion is 2% or less. This report compared EBV using either the 14% or the actual estimate from 20 samples of records from herds in California, New York, and Pennsylvania. From 6 to 22% of bulls or cows selected for milk and fat yields based on evaluation with 14% of the total variance would not be selected using the sample estimates, depending on selection intensity, region, and whether only first or up to three lactations were used in the evaluations. Nevertheless, the average EBV of the bulls and cows selected based on 14% of the total variance were only slightly less than for those selected on 2%. This pilot research suggests that further study of the national data be done to establish the appropriate proportion of variance from interaction effects of sire and herd to use with national evaluations. Kinds of evaluations of bulls and ages of cows and bulls should be considered.

(**Key words:** selection, breeding values, variance of interaction)

Abbreviation key: c^2 = proportion of variance from interaction effects of sire and herd, **CA** = California herds, **NYP** = New York and Pennsylvania herds.

INTRODUCTION

Genetic evaluations of bulls by the USDA—beginning with implementation of the relative breed-

ing value (contemporary comparison) method during the 1960s, through the modified contemporary comparison method during the 1970s, and the current joint bull and cow evaluations with the animal model—have all used a factor, c^2 , to account for non-genetic likeness among records of paternal sisters. In most respects, the c^2 term, or environmental covariance between records of paternal sisters in the same herd or herd-year-season group, is equivalent to the interaction of sire and herd as used in the current USDA genetic evaluation. The equivalence was described by Henderson (6, 7), and Meyer (8) concluded that the effect was likely due to common environmental influences. The difference between c^2 and interaction of sire and herd is that, if sires are related, then interactions of genotype and environment such as interactions of sire and herd are correlated through the relationship matrix much as genetic values are (5, 17). Most applications have ignored these relationships, probably because the application has been to protect against similar treatment of paternal sisters in single or only a few herds. Estimates of c^2 range from the 14% used by the Animal Improvement Programs Laboratory of the USDA to nearly 0 (1, 2, 8, 12, 14, 15, 18, 19, 22, 23).

With an animal model, Dimov et al. (4) obtained estimates of proportion (c^2) of total variance from interaction effects of sire and herd for several samples; estimates were generally $\leq 2\%$ of phenotypic variance for milk and fat yields of herds of Holstein cows in California (**CA**) and herds in New York and Pennsylvania (**NYP**). These estimates agreed generally with estimates for sire models but were much less than the 14% used by USDA for national evaluations of dairy cattle (12, 16, 25). The value of 14% is used to adjust for the environmental correlation among records of daughters in the same herd, which may result in extreme deviations that are not genetic. Preferential treatment may be a reason for common environmental effects.

This pilot study examined the data analyzed by Dimov et al. (4) for assessment of the effect on genetic evaluations for milk and fat yields when vari-

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TABLE 1. Summary of data for means of 10 samples from California herds (CA) and 10 samples from New York-Pennsylvania herds (NYP).

	CA (n = 10)	NYP (n = 10)
Bulls, no.	1266	1264
Cows, no.	18,485	17,893
Registered cows, %	14	46
Lactations, no.	35,585	38,055
Herds, no.	82	231
Sire-herds, no.	5083	7915
Mean genetic SD, kg		
Milk		
First lactation	659	676
All lactations	639	639
Fat		
First lactation	23	24
All lactations	23	24
Mean yields, kg		
Milk		
First lactation	9225	7936
All lactations	9478	8060
Fat		
First lactation	332	289
All lactations	339	294

ance from interaction of sire and herd was assumed to be 14% of phenotypic variance compared with the effect when the interaction effect was estimated from the sample (usually ≤2% but indicated by 2% in the following text) in the calculation of EBV.

MATERIALS AND METHODS

Milk and fat yields (305-d, milked twice daily, mature equivalent) (9) for first, second, and third lactations of Holstein cows from CA and NYP were obtained from the Animal Improvement Programs Laboratory of the USDA. Years of calving were 1965 through 1991. Ten samples from CA and 10 from NYP were randomly chosen on the basis of herd code; samples were the same as those used previously to estimate the variance of interaction effects of sire and herd (4). Characteristics of the samples are in Table 1.

For the 10 samples from CA, mean yields of milk and fat were 9225 and 332 kg for first lactation and 9478 and 339 kg for all lactations. Corresponding yields for samples from NYP were 7936 and 289 kg for first lactation and 8060 kg and 294 kg for all lactations. The mean number of cows per sample was 18,485 for CA and 17,893 for NYP. More detail of the structure of the samples and the estimates of variances were described previously (4). Mean estimates of genetic standard deviations by state, trait, and model are also shown in Table 1.

The EBV of bulls and cows for milk and fat yields were obtained (3) for two models that were similar to the model used for national genetic evaluations (16, 25). Model [1] was used for yield records of first lactation only, and Model [2] was used for yield of all (up to three) lactations of cows:

$$Y_{ijklm} = h_{ij} + c_{ik} + a_{kl} + e_{ijklm} \quad [1]$$

$$Y_{ijklm} = h_{ij} + c_{ik} + p_{kl} + a_{kl} + e_{ijklm} \quad [2]$$

where h_{ij} is a fixed effect of year j in herd i , a_{kl} is additive genetic value of cow l , a daughter of sire k , c_{ik} is random effect of interaction of sire and herd, p_{kl} is a random permanent environmental effect associated with all records of cow kl , and e_{ijklm} is a random environmental effect. Numerator relationships were accounted for as described by Quaas (13). For each sample, two genetic evaluations of bulls and cows were obtained. The first evaluation used the sample estimate of c^2 (which, as a proportion of phenotypic variance, was about 2% for most samples). The second evaluation used c^2 of 14% as is used in the national genetic evaluation (16, 25).

To calculate genetic evaluations for a sample, additive genetic and total variances were kept constant. The assumptions, for the first lactation (Model [1]), were that the sum of interaction of sire and herd and residual variances was constant and, for the all lactations (Model [2]), that the sum of interaction of sire and herd and permanent environmental variances were constant; that is, if variance of interaction of sire and herd increased, then residual variance decreased correspondingly for Model [1] and the variance of permanent environmental effects decreased correspondingly for Model [2]. This approach kept heritability and repeatability constant for evaluations with c^2 from a sample and with c^2 of 14%. According to selection index theory, if a bull had only one daughter per herd, the sire evaluation with c^2 of 2 and 14% would be the same [e.g., (20, 21)]. Application of the same principles shows that evaluation of bulls with more than one daughter per herd would be regressed more with c^2 of 14% than with c^2 of 2%. With a constant repeatability, the evaluations of a cow unrelated to any other animal would be the same whether c^2 was 2% or 14%. Thus, any effect on cow evaluation would likely be due to the effect on evaluations of related bulls.

To compare the evaluations with c^2 of 2 and 14%, differences were computed between the mean EBV of the animals selected on the basis of c^2 estimated from the sample and average EBV when the selected group was chosen from evaluations based on c^2 of 14% (10,

TABLE 2. Means of EBV as fractions of sample genetic standard deviations for proportions selected with sample estimates of variance of interaction of sire and herd used in calculation of EBV.

State, ¹ trait, and model	Cows selected ²			Bulls selected ³		
	1%	2%	10%	5%	10%	20%
CA (n = 10)						
Milk						
First lactation	2.00	1.81	1.32	1.30	1.06	0.81
All lactations	2.04	1.84	1.34	1.28	1.04	0.80
Fat						
First lactation	2.07	1.86	1.32	1.32	1.06	0.80
All lactations	2.10	1.88	1.34	1.29	1.05	0.79
NYP (n = 10)						
Milk						
First lactation	1.91	1.71	1.21	1.24	1.02	0.78
All lactations	2.00	1.79	1.26	1.25	1.02	0.78
Fat						
First lactation	1.98	1.75	1.22	1.27	1.03	0.78
All lactations	2.12	1.78	1.30	1.26	1.03	0.79

¹Herds in California (CA) or New York and Pennsylvania (NYP).

²Empirical standard errors for selection of cows ranged from 0.020 to 0.103.

³Empirical standard errors for selection of bulls ranged from 0.008 to 0.032.

24). The mean EBV of selected animals was calculated for evaluations that used c^2 estimated from the sample (11). Differences were computed for the proportions of selected bulls and registered cows in each sample. Proportions selected for cows were 1, 2, and 10%, and proportions for bulls were 5, 10, and 20%.

Differences in mean EBV were expressed as fractions of the corresponding genetic standard deviations estimated from the samples. For each sample, the percentages were calculated of cows or bulls that had been dropped from the group selected from evaluations based on c^2 of 2% when selection was based on evaluation with c^2 of 14%.

RESULTS AND DISCUSSION

Table 2 lists the means over 10 samples of EBV by trait, model, and region for different percentages of cows and bulls selected on genetic evaluations based on c^2 of 2%. These means are expressed as fractions of sample genetic standard deviations. Table 3 reports the reduction in mean EBV when selection was based on evaluations using c^2 of 14%. The reductions in average merit, calculated from evaluations assuming c^2 of 2% to be correct, were generally <2% of the mean EBV of the selected group for cows and <4% for bulls for all 48 combinations shown in Table 3. The reduction was greater for CA than for NYP, for the all lactation model than for the first lactation model, and

for more intense selection than for less intense selection.

Mean reduction in EBV in units of genetic standard deviation for cows exceeded that for bulls, corresponding to proportions dropped from selected groups of 14.2 and 11.0%, respectively, for cows and bulls. With increasing proportions selected, mean reduction decreased from 0.029 to 0.019 genetic standard deviations for cows and from 0.026 to 0.012 for bulls; proportions of animals dropped from selected groups decreased from 16.7 to 11.4% for cows and from 14.0 to 8.0% for bulls.

Table 4 shows the mean percentages of cows and bulls that were dropped from the selected groups when ranked by evaluations using c^2 of 14%. Mean percentages of animals that were dropped from the selected groups when 14% was used rather than when the sample estimate was used ranged from 9 to 22% for CA and 6 to 18% for NYP and from 6 to 22% for evaluations from first lactations and 6 to 19% for evaluations from all lactations. The percentages of misranked animals increased as selection intensity increased. Table 4 shows that 8 to 22% of cows and 6 to 19% of bulls would be incorrectly included in the selected group, depending mostly on selection intensity. Empirical observation, in agreement with the small reduction in mean EBV of selected animals, was that animals dropping out of the selected groups were ranked in the next proportion selected; for example, those that dropped from ranking in the first 1% were often ranked in the next 1%.

TABLE 3. Means as fractions of sample genetic standard deviations (kilograms) of differences in EBV between animals ranked on EBV using the sample estimates of the variance of interaction effects of sire and herd and ranked using an estimate corresponding to 14% of phenotypic variance for different proportions of cows and bulls selected (percentage).

State, ¹ trait, and model	Cows selected ²			Bulls selected ³		
	1%	2%	10%	5%	10%	20%
CA (n = 10)						
Milk						
First lactation	0.036	0.030	0.024	0.036	0.026	0.015
All lactations	0.046	0.038	0.031	0.048	0.029	0.019
Fat						
First lactation	0.031	0.028	0.020	0.028	0.023	0.016
All lactations	0.030	0.026	0.024	0.039	0.027	0.019
NYP (n = 10)						
Milk						
First lactation	0.013	0.015	0.009	0.013	0.011	0.006
All lactations	0.027	0.024	0.016	0.018	0.011	0.008
Fat						
First lactation	0.017	0.014	0.010	0.013	0.007	0.005
All lactations	0.029	0.023	0.015	0.015	0.011	0.006

¹Herds from California (CA) or New York and Pennsylvania (NYP).

²Empirical standard errors for selection of cows ranged from 0.001 to 0.018.

³Empirical standard errors for selection of bulls ranged from 0.001 to 0.006.

CONCLUSIONS

As expected, evaluations with c^2 that were large (14% of total variance) and evaluations using estimates of c^2 from data ($\leq 2\%$ of total variance) resulted in different ranking on EBV. Nevertheless, mean EBV of selected groups of cows and bulls changed little when those groups were selected on the basis of

the evaluation with c^2 of 14% rather than the evaluations with c^2 of about 2%. Many other factors, such as heterogeneous variances, inappropriate age adjustments, extended contemporary groups, adjustments for times milked per day, month of freshening, and initial test day, may have more effect on the rate of genetic improvement. From 12 to 22% of cows ranked in the top 1% with sample estimates of c^2 were not in

TABLE 4. Means of percentages of cows and bulls dropping out of the selected group for different percentages selected when ranked using variance of interaction effects of sire and herd corresponding to 14% of phenotypic variance rather than sample estimate.

State, ¹ trait, and model	Cows selected ²			Bulls selected ³		
	1%	2%	10%	5%	10%	20%
CA (n = 10)						
Milk						
First lactation	22	15	14	16	13	10
All lactations	19	19	15	19	14	10
Fat						
First lactation	16	15	12	15	13	9
All lactations	17	16	13	17	14	11
NYP (n = 10)						
Milk						
First lactation	12	12	8	11	9	6
All lactations	17	14	10	12	8	6
Fat						
First lactation	13	11	9	10	7	6
All lactations	18	14	10	12	9	6

¹Herds from California (CA) or New York and Pennsylvania (NYP).

²Empirical standard errors from 10 samples for selection of cows ranged from 0.2 to 4.1.

³Empirical standard errors for selection of bulls ranged from 0.2 to 1.7.

the top 1% when ranked using c^2 of 14%. Although the drop in rank may not be great, those cows might be removed from lists of potential bull-dams. Changing c^2 does not change the need for sire analysts to identify cows with potentially biased genetic evaluations from preferential treatment even though the purpose of the large c^2 is to lessen the impact of deliberate preferential treatment.

Although types of bulls were not available in this study, the effect of c^2 of 2% would be to increase evaluations of bulls with daughters in few herds having above average deviations from contemporaries compared with using c^2 of 14%. This result would raise the rank of bulls that were not stud sampled, but this change in rank might not be desirable. High c^2 tends to reduce the range of evaluations under extremes in sampling systems: a truly random evaluation from AI versus sampled in only a few herds.

The effect on genetic gain appeared to be small in this study of 20 samples of about 18,000 cows in each. The question then becomes one of fairness. Is the gain from partial protection against occasional fraudulent records by using a large c^2 sufficient to offset the inequity of more numerous cases of qualified cows being excluded from consideration as bull-dams? The negative impact on genetic progress seems to be slight for limited protection against fraud. The use may be warranted of different c^2 for different sires, based on the sampling method for the bull and distribution of daughters per herd. To examine more completely changes in evaluations that might occur with c^2 of 2% compared with 14%, the national evaluations should be calculated with both values and the effects on various classes and ages of bulls and cows documented.

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