# Variance of Interaction Effects of Sire and Herd for Yield Traits of Holsteins in California, New York, and Pennsylvania with an Animal Model[1]

**G. DIMOV,[2] L. G. ALBUQUERQUE,[3] and J. F. KEOWN**
Department of Animal Science
University of Nebraska
Lincoln 68583-0908

**L. D. VAN VLECK**
Roman L. Hruska US Meat Animal Research Center
ARS, USDA
A218 Animal Sciences
University of Nebraska
Lincoln 68583-0908

**H. D. NORMAN**
Animal Improvement Programs Laboratory
ARS, USDA
Beltsville, MD 20705

## ABSTRACT

An animal model with a REML algorithm was used to estimate variances of additive genetic effects and interaction effects of sire and herd. Milk and fat yields were analyzed for first, second, and third lactations of Holsteins from California, New York, and Pennsylvania. Twenty samples of data were used in the study: 10 from California, 4 from New York, and 6 from Pennsylvania. Mean number of lactations per sample was 36,820 from 18,189 cows in 156 herds. Mean fractions of phenotypic variance of interaction effects of sire and herd for milk and fat yields were .015 and .019 for first lactation and .019 and .021 for all (up to three) lactations rather than the .14 used for national genetic evaluations in the US. Mean heritability estimates for milk and fat yields were .26 and .24 for first lactation and .21 and .21 for all lactations in California and .34 and .35 for first lactations and .28 and .29 for all lactations in New York. Sums of variances of permanent environmental and interaction effects of sire and herd were similar to those used for national genetic evaluations in the US.

Analysis of another 10 samples from California and 10 samples from New York showed only slightly different fractions of phenotypic variance for milk yield for interaction effects of sire by herd, sire by herd by year, and sire by herd by year by season: .023, .027, and .037 for California and .023, .017, and .023 for New York, respectively.

(**Key words**: lactation yields, interaction of genotype and environment, restricted maximum likelihood)

**Abbreviation key**: $c^2$ = fraction of variance that was due to sire and herd interaction effects, **CA** = California records, **NYP** = New York and Pennsylvania records.

## INTRODUCTION

Interaction of sire and herd occurs when the differences among progeny groups are not the same in different environments. Similarity among progeny in the same environment may be due to management (22, 28). Then, the genetic correlations among expressions of the same genotype in different environments (11,

---

Received August 19, 1994.
Accepted November 14, 1994.

[1] Published as Paper Number 10,650 Journal Series, Nebraska Agricultural Research Division, University of Nebraska, Lincoln 68583-0908.

[2] Permanent address: Animal Science Institute, 2232 Kostinbrod, Bulgaria.

[3] Permanent address: Departamento de Melhoramento Genético Animal - FCAVJ-UNESP, 14870-000, Jaboticabal, Sao Paulo, Brazil.

15, 35, 47) are less than unity. Interaction variance also may be a consequence of heterogeneous variances within environmental groups (e.g., herds) and has been termed a pseudo interaction effect (11, 41). Meyer (19) concluded that interaction variance is mostly due to common environmental effects rather than to interaction of genotype and environment.

Ignoring interaction of sire and herd would inflate estimates of additive genetic variance (18, 19, 38, 41) and lead to an overestimation of accuracy of EBV (2, 19). The effect is more important for evaluation of cows and natural service bulls than for bulls used in AI service (3, 18, 19, 42). Dong and Mao (13) and Meyer (19) found that interaction effects were relatively higher for models with effects of herd-year-season than for models with effects of herd-year.

Variances due to interaction of sires and herds have been estimated by intraclass correlation (1, 37), Henderson's method 1 (18, 38, 44), Henderson's method 3 (3, 4, 8, 26, 27, 36), and single-trait REML with a sire model (19, 23, 25). Multiple-trait REML (9, 33) has been used to estimate genetic correlation between regions. For yield traits, REML estimates of variance of interaction of sire and herd with a sire model were between 1 and 4% of phenotypic variance (2, 19). A preliminary study of first lactation records with an animal model reported mean estimates of 1% of phenotypic variance (12).

The objective of this project was to estimate the component of variance for effects of interaction of sire and herd with an animal model similar to that used for the national genetic evaluation in the US. An objective added after completion of these analyses was to compare three models with interaction effects of sire and management assigned to 1) sire and herd, 2) sire and herd-year, and 3) sire and herd-year-season of freshening.

## MATERIALS AND METHODS

Records for first, second, and third lactations of Holstein cows for yields of 305-d, twice daily milking, mature equivalent milk and fat in California, New York, and Pennsylvania were from the Animal Improvement Programs Laboratory of the USDA. Years of calving were 1965 through 1991.

Twenty data sets were sampled randomly by herd code. Data sets 1 through 10 were from California (**CA**), 11 through 14 were from New York, and 15 through 20 were from Pennsylvania. Data from New York and Pennsylvania are designated as **NYP**.

Two edits were applied after the 20 data sets were selected. All lactations must have been more than 240 d, and a sire had to have progeny in at least two herds. Maximum size of a deleted sire progeny group was 70. These later edits decreased the data by about 22%. Corresponding numbers of lactations were 23,344 and 56,071. Table 1 summarizes the data structure for samples that were analyzed.

TABLE 1. Summary of data structure for 10 samples for California and 10 samples for New York and Pennsylvania.

| | California | | | New York and Pennsylvania | | |
|---|---|---|---|---|---|---|
| Number | Mean | Minimum | Maximum | Mean | Minimum | Maximum |
| Cows with records | 18,485 | 12,960 | 27,838 | 17,893 | 16,477 | 19,338 |
| Animals in relationship matrix | 25,070 | 16,407 | 37,510 | 26,978 | 25,283 | 28,685 |
| Lactations | 35,585 | 23,344 | 56,071 | 38,055 | 34,546 | 41,029 |
| Herds | 82 | 30 | 166 | 231 | 209 | 244 |
| Sires | 1266 | 846 | 1715 | 1264 | 1172 | 1369 |
| Sire-herds | 5083 | 2636 | 8323 | 7915 | 7414 | 8408 |
| Herd-years | | | | | | |
| First lactation | 662 | 204 | 1161 | 2489 | 2126 | 2833 |
| All lactations | 704 | 209 | 1248 | 2722 | 2306 | 3131 |
| Mixed model equations | | | | | | |
| First lactation | 30,813 | 19,248 | 46,988 | 37,382 | 34,885 | 39,800 |
| All lactations | 50,344 | 32,212 | 74,919 | 55,508 | 51,542 | 59,396 |

TABLE 2. Mean 305-d mature equivalent milk and fat yields and ranges in sample means for first and all lactations for 10 samples for California and 10 samples for New York and Pennsylvania.

| | Milk yield | | Fat yield | |
|---|---|---|---|---|
| | First | All | First | All |
| | (kg) | | | |
| California | | | | |
| All cows | | | | |
| Mean | 9225 | 9478 | 332 | 339 |
| Minimum | 2063 | 2063 | 77 | 77 |
| Maximum | 21,783 | 21,783 | 770 | 770 |
| Sample Mean | | | | |
| Minimum | 8894 | 9098 | 320 | 322 |
| Maximum | 9761 | 10,033 | 344 | 352 |
| New York and Pennsylvania | | | | |
| All cows | | | | |
| Mean | 7936 | 8060 | 289 | 294 |
| Minimum | 1731 | 1731 | 68 | 68 |
| Maximum | 18,438 | 18,622 | 726 | 870 |
| Sample mean | | | | |
| Minimum | 7828 | 7939 | 286 | 290 |
| Maximum | 8135 | 8290 | 294 | 299 |

For the 10 data sets from CA, mean milk and fat yields were 9225 and 332 kg for first lactation and 9478 and 339 kg for all lactations. Corresponding means for NYP were 7936 and 289 kg for first lactation and 8060 and 294 kg for all lactations. The means were similar for all samples (Table 2).

Model [1] was used for first lactation records only, and Model [2] was used for up to three lactations:

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

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

where

$y_{ijklm}$ = milk or fat yield;
$h_{ij}$ = fixed effect of year j in herd i;
$a_{kl}$ = random effect of cow l, daughter of sire k;
$c_{ik}$ = random environmental effect of sire k, associated with daughters in herd i;
$p_{kl}$ = random permanent environmental effect of cow kl; and
$e_{ijklm}$ = random environmental effect appropriate to the model.

For both models, variances of vectors of random effects were

$$V(\mathbf{a}) = \mathbf{A}\sigma_a^2$$

and

$$V(\mathbf{e}) = \mathbf{I}_N\sigma_e^2;$$

for Model [1],

$$V(\mathbf{c}) = \mathbf{I}_c\sigma_c^2,$$

and for Model [2]

$$V\begin{pmatrix}\mathbf{c}\\ \mathbf{p}\end{pmatrix} = \begin{pmatrix}\mathbf{I}_c\sigma_c^2 & 0\\ 0 & \mathbf{I}_p\sigma_p^2\end{pmatrix},$$

where **A** is the additive genetic relationship matrix with its inverse computed by the method of Quaas (29), and $\mathbf{I}_c$, $\mathbf{I}_p$, and $\mathbf{I}_N$ are identity matrices of order number of sire by herd levels, cows with records, and number of records.

Variance components were estimated by a derivative-free algorithm to obtain REML estimates (17, 32) using a Choleski decomposition algorithm (7). The minimization search was based on the Downhill simplex algorithm (6). The function minimized was –2 times the logarithm of the likelihood. The convergence criterion was the variance of the n + 1 functions in the simplex less than $10^{-9}$ where n is the number of variance components in the model. Convergence was achieved, on average, after 51 rounds for Model [1] and 82 rounds for Model [2]. At apparent convergence, analyses were restarted to check for possible local maxima. None were found.

Empirical standard errors of estimates of variance components and fractions of total variance were calculated from estimates from the 10 samples from CA and from the 10 samples from NYP.

## RESULTS AND DISCUSSION

Summaries of estimates of variance components and their empirical standard errors are represented in relative proportions of the total variance (Table 3) and in units of the traits (Table 4).

The mean ratios of variance of interaction of sire and herd to total variance ($c^2$) for milk yield were .015 ± .002 for first lactation and .019 ± .002 for all lactations for CA and .015 ± .002 and .018 ± .002 for NYP (Table 3). For fat yield, the corresponding ratios for CA and NYP were similar and averaged .019 ± .002 and .021 ± .002. Estimates from this study were smaller than for milk yield from first lactation of British Friesians, where $c^2$ estimated with a sire model was .031 for interaction effects of sire and herd and .036 for interaction effects of sire and herd-year-season (19). For REML analyses of milk yield, estimates of $c^2$ with a sire model increased from .018 for first lactation to .030 for third lactation (2). The same tendency was reported earlier from analyses with Henderson's method 1 of milk and fat yields (44). For both models, estimates of $c^2$ for fat exceeded those for milk yield, although, for an earlier study with Henderson's method 1 (38), the interaction component for milk was four times greater (.04 vs. .01) than that for fat yield.

All estimates of $c^2$ in this study were smaller than the .14 assumed in previous and current methods used by the USDA for evaluation of sires and dams (22, 23, 28, 39, 46). After a study of changes in evaluations of natural service sampled bulls brought into AI, Norman et al. (23, 24) indicated that the $c^2$ value of .14 currently used by the USDA may be too high. Misztal (20) also found that the variance of interaction effects of sire and herd was not significant for final type score. A value for $c^2$ that is too large may lead to underestimation of genetic merit of superior sires and dams. Research is in progress to study the effect of different values of $c^2$ on estimation of genetic merit.

The mean estimate of heritability (Table 3) for first lactation milk yield in CA (.26 ± .05) was similar to that from sire models (2, 10, 13, 30). The higher mean estimate for NYP (.34 ± .01) corresponds to results for a simple animal model in which estimates ranged from .18 to

TABLE 3. Estimates of fractions of total variance and standard errors for milk and fat yields for first and all lactation analyses for 10 samples from California and 10 samples from New York and Pennsylvania.

| | Heritability | | | | Sire by herd interaction | | | | Permanent environmental effect | |
|---|---|---|---|---|---|---|---|---|---|---|
| | Milk | | Fat | | Milk | | Fat | | | |
| Sample | First | All | First | All | First | All | First | All | Milk | Fat |
| California | | | | | | | | | | |
| Minimum | .198 | .160 | .218 | .167 | .008 | .012 | .010 | .012 | .259 | .242 |
| Maximum | .302 | .256 | .272 | .242 | .030 | .028 | .030 | .033 | .365 | .357 |
| Mean | .258 | .208 | .239 | .206 | .015 | .019 | .019 | .021 | .314 | .297 |
| SE | .012 | .009 | .007 | .008 | .002 | .002 | .002 | .002 | .011 | .011 |
| New York and Pennsylvania | | | | | | | | | | |
| Minimum | .299 | .248 | .293 | .259 | .003 | .013 | .000 | .010 | .196 | .188 |
| Maximum | .393 | .324 | .382 | .327 | .026 | .026 | .040 | .035 | .273 | .248 |
| Mean | .344 | .281 | .348 | .290 | .015 | .018 | .018 | .022 | .238 | .220 |
| SE | .010 | .009 | .009 | .007 | .002 | .002 | .004 | .003 | .008 | .006 |

.44 (5, 14, 21, 34, 43). The estimates for first lactation exceeded those for Model [2]: .21 ± .01 for CA and .28 ± .01 for NYP. These results agree with previous REML studies with sire (2, 10, 13, 30) and animal (45) models. The pattern was the same for estimates from regressions of daughters on dams (42). Larger estimates of heritabilities for New York data than for CA have been partially attributed (43) to a less complete identification in California herds.

Heritability estimates for fat yield (Table 3) were similar to those for milk yield. Differences between estimates for milk and fat yield in other studies (20, 28, 29, 31, 43) were only about .02, as in this study.

Variation in heritability estimates across the data sets was greater for milk yield from first lactation than from all records and was generally greater for milk than for fat yields (Table 3).

The proportions of permanent environmental variances for milk and fat yields were .31 ± .01 and .30 ± .01 for CA and .24 ± .01 and .22 ± .01 for NYP (Table 3). These estimates were somewhat smaller than those for British Friesians (45). For nearly all data sets, the estimates for milk yield exceeded those for fat yield. The estimates suggest that the variance of permanent environmental effects is larger than the 14% assumed for national evaluation of bulls and cows (23, 46). The sums of the proportions of total variance from permanent environmental effects and interaction effects of sire and herd from this study, however, are similar to that sum used in the national evaluation.

Estimates of phenotypic variances were larger for CA than for NYP and were smaller for first lactation than for all lactations.

### Comparison of Three Models for Interaction Effects of Sire and Management

At the suggestion of a reviewer, 10 additional data sets were analyzed from California and New York for milk yield with three differ-

TABLE 4. Estimates of variances[1] and standard errors for milk and fat yield for first lactation and all lactation analyses for 10 samples from California and 10 samples from New York and Pennsylvania.

| | First lactation | | | | All lactations | | | | |
|---|---|---|---|---|---|---|---|---|---|
| | A[1] | SH | E | Total | A | SH | PE | E | Total |
| | Milk yield (kg$^2$/100) | | | | | | | | |
| California | | | | | | | | | |
| Minimum | 3335 | 132 | 11,567 | 16,811 | 2900 | 243 | 4945 | 8348 | 18,071 |
| Maximum | 5285 | 524 | 14,224 | 18,760 | 4885 | 563 | 7206 | 9706 | 20,962 |
| Mean | 4561 | 265 | 12,837 | 17,663 | 4113 | 382 | 6193 | 9019 | 19,707 |
| SE | 236 | 34 | 279 | | 207 | 34 | 215 | 140 | |
| New York and Pennsylvania | | | | | | | | | |
| Minimum | 4058 | 38 | 7894 | 12,812 | 3555 | 176 | 2838 | 6497 | 14,124 |
| Maximum | 5191 | 355 | 9322 | 13,605 | 4695 | 382 | 3992 | 6942 | 15,068 |
| Mean | 4587 | 193 | 8556 | 13,336 | 4088 | 266 | 3469 | 6733 | 14,556 |
| SE | 127 | 31 | 164 | | 133 | 23 | 122 | 47 | |
| | Fat yield (kg$^2$) | | | | | | | | |
| California | | | | | | | | | |
| Minimum | 481 | 22 | 1454 | 2031 | 407 | 28 | 594 | 1119 | 2434 |
| Maximum | 617 | 67 | 1767 | 2381 | 629 | 80 | 921 | 1305 | 2792 |
| Mean | 513 | 40 | 1600 | 2153 | 524 | 56 | 765 | 1219 | 2564 |
| SE | 18 | 3 | 31 | | 22 | 5 | 32 | 23 | |
| New York and Pennsylvania | | | | | | | | | |
| Minimum | 503 | 0 | 1035 | 1636 | 504 | 19 | 369 | 895 | 1936 |
| Maximum | 663 | 69 | 1178 | 1769 | 660 | 71 | 493 | 960 | 2029 |
| Mean | 596 | 32 | 1087 | 1715 | 569 | 44 | 438 | 930 | 1981 |
| SE | 16 | 6 | 16 | | 15 | 6 | 12 | 7 | |

[1] A = Additive genetic variance, SH = variance from interaction of sire by herd, PE = variance from permanent environmental effects, and E = variance from residual effects.

TABLE 5. Summary of the data structure for 10 California and 10 New York samples used to compare models with interaction effects of sire by herd (S × H), sire by herd by year (S × H × Y), and sire by herd by year by season (S × H × Y × Se) for milk yield.

| | California | | | New York | | |
|---|---|---|---|---|---|---|
| Number | Mean | Minimum | Maximum | Mean | Minimum | Maximum |
| Cows with records | 11,922 | 11,063 | 12,826 | 10,788 | 10,531 | 11,034 |
| Animals in relationship matrix | 18,944 | 16,390 | 21,306 | 17,332 | 16,746 | 18,098 |
| Lactations | 20,029 | 18,431 | 21,749 | 21,372 | 21,202 | 21,595 |
| Herd-year-seasons | 327 | 282 | 317 | 1962 | 1752 | 2127 |
| Model | | | | | | |
| S × H | 3211 | 2853 | 3742 | 4654 | 4534 | 4861 |
| S × H × Y | 6818 | 6088 | 7925 | 11,830 | 11,389 | 12,252 |
| S × H × Y × Se | 9948 | 9069 | 11,426 | 15,392 | 14,914 | 15,754 |
| Mixed model equations | | | | | | |
| S × H | 34,405 | 30,940 | 38,268 | 34,736 | 33,960 | 36,040 |
| S × H × Y | 38,011 | 34,340 | 42,434 | 42,912 | 41,175 | 43,304 |
| S × H × Y × Se | 41,141 | 37,147 | 45,880 | 45,474 | 44,824 | 46,702 |

ent models. The basic model is described in Model [2]. The three models included the interaction effects of sire by herd, or sire by herd by year, or sire by herd by year by season of freshening. Data included in the additional analyses are summarized in Table 5.

Estimates of fractions of total variance and empirical standard errors for milk yield for the 10 New York and 10 California samples for the three models are in Table 6. The mean fraction of variance from interaction effects of sire and herd is the same for both states, .023. The corresponding fraction of variance from interaction effects of sire by herd by year is larger for California, .027, than for New York, .017. The same trend is evident in the fraction of variance due to interaction effects of sire by herd by year by season: .037 for California and .023 for New York. Regardless of the model used, no important interaction is evident among effects for sire, herd, year, or season for milk yield in either California or New York. If

TABLE 6. Mean estimates for fractions of total variance and empirical standard errors for milk yield for 10 samples from California and 10 from New York for three models for sire by management interaction.

| | California | | | | New York | | | |
|---|---|---|---|---|---|---|---|---|
| Effect | Mean | SE | Minimum | Maximum | Mean | SE | Minimum | Maximum |
| | Model [1], sire by herd | | | | | | | |
| Genetic | .227 | .009 | .178 | .282 | .274 | .005 | .237 | .295 |
| Sire by herd | .023 | .003 | .011 | .041 | .023 | .002 | .015 | .033 |
| Permanent environmental | .298 | .009 | .253 | .336 | .258 | .007 | .230 | .301 |
| Residual | .453 | .005 | .428 | .475 | .445 | .004 | .424 | .464 |
| | Model [2], sire by herd by year | | | | | | | |
| Genetic | .239 | .008 | .200 | .283 | .283 | .006 | .243 | .302 |
| Sire by herd by year | .027 | .001 | .022 | .033 | .017 | .002 | .009 | .025 |
| Permanent environmental | .304 | .009 | .264 | .342 | .269 | .007 | .239 | .312 |
| Residual | .430 | .005 | .409 | .454 | .432 | .004 | .411 | .452 |
| | Model [3], sire by herd by year by season | | | | | | | |
| Genetic | .246 | .007 | .211 | .287 | .284 | .006 | .243 | .303 |
| Sire by herd by year by season | .037 | .002 | .029 | .045 | .023 | .004 | .009 | .041 |
| Permanent environmental | .298 | .009 | .262 | .337 | .269 | .007 | .238 | .312 |
| Residual | .419 | .006 | .395 | .444 | .425 | .005 | .395 | .451 |

the interaction of sire and herd represents true interaction of genotype and environment, these estimates are probably slightly smaller than if relationships among sires had been considered in estimating the component of variance for interaction of sire and herd (16, 40).

## CONCLUSIONS

The mean estimates of variance of interaction effects of sire and herd relative to phenotypic variance for yield traits of Holsteins from CA and NYP were .015 to .022. These estimates are markedly smaller than the .14 currently used for national genetic evaluations in the US. The effects on ranking of bulls and cows caused by use of a value of .14 rather than .01 to .02 should be considered. Estimates of heritabilities for first lactation were somewhat larger than for all lactations. For yield traits, these heritabilities were smaller than for most similar studies with animal models but were similar to those used for the national evaluation program. The estimates of repeatability in the data are similar to those used nationally.

The effect on selection response of using the smaller fractions of interaction variance of sire and herd found here or of using interaction variance of sire and herd equivalent to .14 of phenotypic variance is being studied on the original data sets from CA and NYP.

A more definitive study would be to use the national sire and cow evaluations updated over a number of years. The question of whether to use .14 or some smaller value for the fraction of variance for interaction of sire and herd is a policy as well as a scientific issue. One factor to consider is whether to incorporate different fractions for the three classes of sires (multiple herd sampling, standard sampling, or other sampling) identified by USDA in genetic evaluations. Such a modification of national genetic evaluation would not be difficult. Further research to estimate interaction variance of sire and herd for those three classes of sires would seem warranted to aid in making a decision on how to account for possibility of preferential treatment.

## ACKNOWLEDGMENTS

The authors thank the Holstein Association of America, Brattleboro, Vermont for support of the senior author and the National Association of Animal Breeders, Columbia, Missouri for support of this project.

## REFERENCES

1 Arora, K. K., and A. E. Freeman. 1971. Environmental correlations between paternal half-sisters for milk and fat production. J. Dairy Sci. 54:880.

2 Banos, G., and G. E. Shook. 1990. Genotype by environment interaction and genetic correlations among parities for somatic cell count. J. Dairy Sci. 73:2563.

3 Bertrand, J. K., P. J. Berger, and R. L. Willham. 1985. Sire × environment interactions in beef cattle weaning weight field data. J. Anim. Sci. 60:1396.

4 Bertrand, J. K., J. D. Hough, and L. L. Benyshek. 1987. Sire by environment interaction and genetic correlations of sire progeny performance across regions in dam-adjusted field data. J. Anim. Sci. 64:77.

5 Boldman, K. G., and A. E. Freeman. 1990. Adjustment for heterogeneity of variances by herd production level in dairy cow and sire evaluation. J. Dairy Sci. 73:503.

6 Boldman, K. G., L. A. Kreise, L. D. Van Vleck, and S. D. Kachman. 1993. A Manual for Use of MTDFREML. USDA-ARS, Clay Center, NE.

7 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.

8 Buchanan, D. S., and M. K. Nielsen. 1979. Sire by environment interactions in beef cattle field data. J. Anim. Sci. 48:307.

9 Carabaño, M. J., K. M. Wade, and L. D. Van Vleck. 1990. Genotype by environmental interaction for milk and fat production across regions of the United States. J. Dairy Sci. 73:173.

10 Chauhan, V.P.S., and J. F. Hayes. 1991. Genetic parameters for first lactation milk production and composition traits for Holsteins using multivariate REML. J. Dairy Sci. 74:603.

11 Dickerson, G. E. 1962. Implications in genetic-environmental interaction in animal breeding. Anim. Prod. 4:47.

12 Dimov, G. J., J. F. Keown, L. D. Van Vleck, and H. D. Norman. 1993. Sire by herd interaction for milk and fat yield in California Holsteins. J. Dairy Sci. 76(Suppl. 1):294.(Abstr.)

13 Dong, M. C., and I. L. Mao. 1990. Heterogeneity of (co)variance and heritability in different levels of intraherd milk production variance and of herd average. J. Dairy Sci. 73:1990.

14 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.

15 Falconer, D. S. 1952. The problem of environment and selection. Am. Nat. 86:293.

16 Foulley, J. L., and C. R. Henderson. 1989. A simple model to deal with sire by treatment interactions when sires are related. J. Dairy Sci. 72:167.

17 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.

18 Legates, J. E., F. J. Verlinden, and J. F. Kendrick. 1956. Sire by herd interaction in production traits in dairy cattle. J. Dairy Sci. 39:1055.

19 Meyer, K. 1987. Estimates of variances due to sire × herd interactions and environmental covariances between paternal half-sibs for first lactation dairy production. Livest. Prod. Sci. 17:95.

20 Misztal, I. 1990. Restricted maximum likelihood estimation of variance components in animal model using sparse matrix inversion and a supercomputer. J. Dairy Sci. 73:163.

21 Misztal, I., T. Lawlor, T. Short, and P. M. VanRaden. 1992. Multiple trait estimation of variance components of yield and type traits using an animal model. J. Dairy Sci. 75:544.

22 Norman, H. D. 1974. Factors that should be considered in a national sire summary model. J. Dairy Sci. 57:955.

23 Norman, H. D., R. L. Powell, and G. R. Wiggans. 1991. Comparison of genetic evaluations from animal model and modified contemporary comparison. J. Dairy Sci. 74:2309.

24 Norman, H. D., R. L. Powell, and J. R. Wright. 1985. Changes of evaluation for natural-service sampled bulls brought into artificial insemination. J. Dairy Sci. 68:1513.

25 Notter, D. R., B. Tier, and K. Meyer. 1992. Sire by herd interaction for weaning weight in beef cattle. J. Anim. Sci. 70:2359.

26 Nunn, T. R., D. D. Kress, P. J. Burfening, and D. Vaniman. 1978. Region by sire interaction for reproduction traits in beef cattle. J. Anim. Sci. 46:957.

27 Petersen, P. H. 1975. Genotype-environment interaction in milk production under Danish and Bulgarian-Czechoslovakian conditions. Anim. Prod. 21:101.

28 Plowman, R. D., and B. T. McDaniel. 1968. Changes in USDA sire summary procedures. J. Dairy Sci. 51:306.

29 Quaas, R. L. 1976. Computing the diagonal elements and inverse of a large numerator relationship matrix. Biometrics 32:949.

30 Robinson, J.A.B. 1988. Multiple lactation variance components estimation using restricted maximum likelihood. Diss. Abstr. Int. B. 49 (6):2007; Anim. Breeding Abstr. 58(11):7198.

31 Short, T. H., R. W. Blake, R. L. Quaas, and L. D. Van Vleck. 1990. Heterogeneous within-herd variance. 1. Genetic parameters for first and second lactation milk yield of grade Holstein cows. J. Dairy Sci. 73:3312.

32 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.

33 Stanton, T. S., R. W. Blake, R. L. Quaas, L. D. Van Vleck, M. J. Carabaño. 1991. Genotype by environment interaction for Holstein milk yield in Colombia, Mexico, and Puerto Rico. J. Dairy Sci. 74:1700.

34 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.

35 Syrstad, O. 1976. Interaction between genotype and nutrition in dairy production—a review. World Anim. Rev. 2:33.

36 Tess, M. W., D. D. Kress, P. J. Burfening, and R. L. Fredrich. 1979. Sire by environment interactions in Simmental-sired calves. J. Anim. Sci. 49:964.

37 Thomson, G. M., and A. E. Freeman. 1970. Environmental correlations in pedigree estimates of breeding value. J. Dairy Sci. 53:1259.

38 Tong, A.K.W., B. W. Kennedy, and J. E. Moxley. 1977. Sire by herd interactions for milk yield and composition traits. Can. J. Anim. Sci. 57:383.

39 VanRaden, P. M., and G. R. Wiggans. 1991. Derivation, calculation and use of national animal model information. J. Dairy Sci. 74:2737.

40 Van Tassell, C. P., and P. J. Berger. 1994. Consideration of sire relationships for estimation of variance components with interaction of herd and sire. J. Dairy Sci. 77:313.

41 Van Vleck, L. D. 1963. Genotype and environment in sire evaluation. J. Dairy Sci. 46:983.

42 Van Vleck, L. D., and G. E. Bradford. 1966. Genetic and maternal influence on the first three lactations of Holstein cows. J. Dairy Sci. 49:45.

43 Van Vleck, L. D., M. C. Dong, and G. R. Wiggans. 1988. Genetic (co)variances for milk, fat and protein yield in Holsteins using animal model. J. Dairy Sci. 71:3053.

44 Van Vleck, L. D., L. H. Wadell, and C. R. Henderson. 1961. Components of variance associated with milk and fat records of artificially sired Holstein daughters. J. Anim. Sci. 20:812.

45 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.

46 Wiggans, G. R., I. Misztal, and L. D. Van Vleck. 1988. Implementation of an animal model for genetic evaluation of dairy cattle in the United States. J. Dairy Sci. 71(Suppl. 2):54.

47 Yamada, Y. 1962. Genotype by environment interaction and genetic correlation of the same trait under different environments. Jpn. J. Genet. 37:498.