

Accounting for Heterogeneous Variances in Multitrait Evaluation of Jersey Type Traits

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ABSTRACT

The multitrait genetic evaluation system for type traits was modified to estimate adjustments for heterogeneous variance (HV) simultaneously with estimated breeding values (EBV) for final score and 14 linear traits. Each variance within herd, year, and parity was regressed toward a predicted variance, which was determined by fitting a model with fixed effects of the mean final score for herd, size of the contemporary group, appraisal month, and year-season and a random effect for herd-appraisal date. Herd-appraisal date was included as a random effect to regress the observed heterogeneity for a given herd-appraisal date toward the fixed effects. Method R was used to estimate variances for the heterogeneity model in each EBV iteration. To evaluate the effect of the adjustment, parent averages were calculated from evaluations with recent appraisals removed. The adjustment slightly improved correlations within birth year between those parent averages and EBV from current data on bulls for most traits, but did not improve correlations for final score, strength, dairy form, teat length, or foot angle. Annual trends for EBV were lower with HV adjustment than for unadjusted EBV for all traits except final score and rump angle for cows and rump width for bulls, which were essentially unchanged. Standard deviations of Mendelian sampling (evaluation minus mean of parent evaluations) declined less over time for HV-adjusted than for unadjusted evaluations. The slope at year 2000 of Mendelian-sampling standard deviations from HV-adjusted evaluations ranged from 10.0% for udder depth to 42.7% for teat length compared with the slope for unadjusted evaluations. This HV adjustment, which was implemented for USDA evaluations in May 2001 for Jerseys and in 2002 for other breeds, improves the

accuracy of evaluations, particularly comparisons over time, by accounting for the change in variation.

Key words: heterogeneous variance adjustment, type evaluation

INTRODUCTION

A multitrait animal model (Gengler et al., 1997a, 1997b, 1999) has been used to calculate type evaluations for the Jersey breed since February 1998. In that analysis, homogeneity of (co)variances is assumed. Weigel and Lawlor (1994) found that variance decreased as the average final score of a herd increased. This finding explained the results of Bell et al. (1982) that bull evaluations for type differed among groups stratified by herd average final score. Gengler et al. (2001) found that variances were heterogeneous for all type traits. This heterogeneity should be accounted for in routine genetic evaluations.

Data can be adjusted to stabilize variances by contemporary group before evaluation. This strategy is used for the Holstein final score. Weigel and Lawlor (1994) described a method of adjustment for heterogeneous variance (HV) that included predicting variance from the herd mean final score, registry status, and number of appraisals for the herd-classification date. Preadjustment of this type is independent of the evaluation model and therefore does not account for genetic or other (co)variances among observations. Simultaneous estimation of the HV adjustments allows updated estimates of genetic values to improve estimates of the variances. In addition, preadjustment requires a priori estimates of adjustment factors that may become outdated.

Meuwissen et al. (1996) developed a method for stabilizing of heterogeneous (co)variances simultaneously with the computation of the genetic evaluations. Gengler et al. (2000) applied this technique to Jersey type data. The objectives of this study were to describe its implementation for a Jersey type evaluation and assess its impact on predicting future progeny and the variance of Mendelian sampling.

Received December 28, 2005.

Accepted February 13, 2006.

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Table 1. Numbers of cows and bulls represented in the data by birth year group for animals born 1981 and later

Birth years	Cows	Appraisals/ cow	Bulls with ≥5 daughters
1981 to 1985	75,603	1.88	1,213
1986 to 1990	89,365	1.73	1,232
1991 to 1995	99,043	1.75	1,414
1996 to 2000	117,179	1.70	1,387
2001 to 2005 ¹	58,716	1.37	27
Total	439,906		5,273

¹Includes appraisals through June 2005.

MATERIALS AND METHODS

Data

The 14 linear type traits analyzed by USDA for the Jersey breed include stature, strength, dairy form, foot angle, rear legs (side view), rump angle, rump width, fore udder attachment, rear udder height, rear udder width, udder depth, udder cleft, front teat placement, and teat length. Scoring for most traits was begun in the early 1980s; however, scoring for teat length did not begin until the late 1980s. Therefore, many type records prior to 1990 are missing observations for that trait. Most linear type traits are scored from 1 to 50. However, stature may be scored as high as 80. The range was extended to accommodate crossbred cows. As data from crossbred cows accumulate, consideration of breed composition in both the mean and variance models could improve accuracy. Future research will address the impacts of crossbreeding on type evaluations. Final score is computed from linear type scores. Data were provided by the American Jersey Cattle Association and were the same data as used for the August 2005 USDA genetic evaluations. Table 1 reports the numbers of cows and bulls represented in the data by birth period. Only first and second parities were used for Jersey type evaluations.

Statistical Analyses

Type Trait Model. The genetic evaluation method with HV adjustments consisted of adjustments for age and lactation stage followed by 3 interdependent iterative systems: solution of regular mixed model equations, updates of canonical traits to account for missing original traits, and updates of adjustment factors for HV. Age and lactation stage were not included in the HV adjustment to avoid scaling their effects.

Mixed Model Equations. The following multitrait (single trait for final score) animal model (Gengler et al., 1999) was applied for all traits:

$$\mathbf{y} = \mathbf{Xh} + \mathbf{Ss} + \mathbf{Zp} + \mathbf{Z}^*\mathbf{u} + \mathbf{e} \quad [1]$$

where \mathbf{y} is the vector of type records; \mathbf{h} is the vector of fixed effects of the interaction of herd, date scored, and parity (first or later) group; \mathbf{s} is the vector of random effects of the interaction of herd and sire; \mathbf{p} is the vector of random effects of the permanent environment; \mathbf{u} is the vector of random additive genetic effects of animals and genetic groups ($\mathbf{u} = \mathbf{a} + \mathbf{Qg}$, where \mathbf{a} is the vector of random additive genetic effects of animals expressed as deviations from group means, \mathbf{g} is the vector of fixed effects of genetic groups, and \mathbf{Q} is the incidence matrix that links \mathbf{g} with \mathbf{u}); \mathbf{X} , \mathbf{S} , \mathbf{Z} , and \mathbf{Z}^* are incidence matrices that associate \mathbf{h} , \mathbf{s} , \mathbf{p} , and \mathbf{u} , respectively, with \mathbf{y} ; and \mathbf{e} is the vector of random residual effects.

For cows older than the highest age group within the parity, the parity was increased because birth dates were assumed to be more reliable than lactation numbers; even if a lactation number is correct, a very old first-lactation cow is best grouped with second-lactation cows. Additive corrections were applied for age and stage of lactation. These correction factors were obtained with a model that included age and stage effects in addition to those in Model 1; however, it was solved without correction for HV. These values were not updated each quarterly evaluation. Seventeen genetic groups were defined based on birth year (≤ 1966 , 1967 and 1968, ..., 1995 and 1996, ≥ 1997). The $\text{Var}(\mathbf{g}) = \mathbf{A}\sigma_g^2$. Inbreeding was accounted for in the construction of \mathbf{A}^{-1} .

The model for a particular trait t may be referred to as:

$$\mathbf{y}_t = \mathbf{Mm}_t + \mathbf{e}_t,$$

where \mathbf{M} is a design matrix grouping \mathbf{X} , \mathbf{H} , \mathbf{Z} , and \mathbf{Z}^* ; and \mathbf{m} is a vector of all the solutions. A canonical transformation based on multiple diagonalization (Miztal et al., 1995) of $\text{Var}(\mathbf{s})$, $\text{Var}(\mathbf{p})$, $\text{Var}(\mathbf{g})$, and $\text{Var}(\mathbf{e})$ was applied to transform the t observed traits for animal i in environment j (contemporary group) into t unrelated traits ($y_{Q_{ij}}$) with a residual variance of 1 using $\mathbf{y}_{Q_{ij}} = \mathbf{Qy}_{ij}$, where \mathbf{Q} is the transformation matrix and \mathbf{y}_{ij} is the vector of original traits. Where traits were missing, canonical observations were calculated from the observed original traits (y_{ij}^0) and the current solutions on the transformed canonical scales using the equation of Ducrocq and Besbes (1993):

$$\mathbf{y}_{Q_{ij}} = \mathbf{Q}_1\mathbf{y}_{ij}^0 + \mathbf{Q}_2\mathbf{M}_j\hat{\mathbf{m}}_{Q_{ij}},$$

where $\hat{\mathbf{m}}_{Q_{ij}}$ are the solutions on the transformed scale. The t mixed-model equation systems were then solved based on the general model:

$$\mathbf{y}_{Q_{ij}} = \mathbf{M}\mathbf{m}_{Q_{ij}} + \mathbf{e}_{Q_{ij}}, \quad [2]$$

with continuous updating for missing traits.

Integrated HV Adjustment. Using the HV model proposed by Meuwissen et al. (1996), Model 2 can be written on a canonical scale as:

$$\mathbf{y}_{Q_{ij}} = \Gamma_j(\mathbf{M}\mathbf{m}_{Q_{ij}}^a + \mathbf{e}_{Q_{ij}}^a),$$

where superscript a denotes adjusted and $\Gamma_j = \text{diag}[\exp(\gamma_{jt}/2)]$, which scales all effects for contemporary group j and canonical trait t by $\exp(\gamma_{jt}/2)$ and the associated variances by $\exp(\gamma_{jt})$. Because all associated variances were scaled identically, the transformation matrix \mathbf{Q} remained appropriate.

The influence of the mean on the HV adjustment system was addressed by expressing each original trait as a deviation from its overall mean. Because data were corrected for age and lactation stage before analysis, it was possible to define heterogeneity subclasses according to contemporary groups. For traits not missing on the original scale, a transformed record adjusted for HV, $\mathbf{y}_{Q_{ij}}^a$, was calculated as:

$$\mathbf{y}_{Q_{ij}}^a = \Gamma_j^{-1}\mathbf{Q}(\mathbf{y}_{ij}^0 - \bar{\mathbf{y}}^0).$$

Where traits were missing, an estimate of $\mathbf{y}_{Q_{ij}}^a$ was calculated as:

$$\mathbf{y}_{Q_{ij}}^a = \Gamma_j^{-1}[\mathbf{Q}_1(\mathbf{y}_{ij}^0 - \bar{\mathbf{y}}^0) + \mathbf{Q}_2\Gamma_j\mathbf{M}_j\hat{\mathbf{m}}_{Q_{ij}}^a].$$

Update of Heterogeneity Factors. Based on Meuwissen et al. (1996), a heterogeneity parameter z could be developed:

$$\mathbf{z}_{jt} = \left[(\mathbf{y}_{Q_{jt}}^a)' \mathbf{D}_{jt} \mathbf{e}_{Q_{jt}}^a - \sum_{k=1}^{n_j} \lambda_{jtk} \right] / 2,$$

where $\mathbf{D}_{jt} = \text{diag}(\lambda_{jtk})$, a diagonal matrix with element λ_{jtk} (weight associated with observation k in contemporary group j for trait t). The weight was assumed to be 1 if no original traits were missing and to be <1 if an original trait was missing. Computation of λ_{jtk} followed the methodology proposed in Gengler and Misztal (1996). The variance associated with the heterogeneity parameter was estimated as:

$$\text{Var}(\mathbf{z}_{jt}) = \left[(\hat{\mathbf{m}}_{Q_{jt}})' \mathbf{D}_{jt} \hat{\mathbf{m}}_{Q_{jt}} + 2 \sum_{k=1}^{n_j} \lambda_{jtk} \right] / 4.$$

A feature of the method of Meuwissen et al. (1996) is that the modeling of the heterogeneity parameter uses a weighted mixed model on constructed variates obtained by summing the current γ_{jt} with the remaining heterogeneity within contemporary group:

$$(\mathbf{S}'\mathbf{W}_t\mathbf{S} + \mathbf{A}_t^{-1})\beta_t = \mathbf{S}'\mathbf{W}_t[\Gamma_t + \mathbf{W}_t^{-1}\mathbf{z}_t]$$

where β_t is a vector of solutions; \mathbf{S} is the design matrix linking constructed variates and β_t ; $\mathbf{W}_t = \text{diag}[\text{Var}(\mathbf{z}_{jt})]$ diagonal matrix iterative weights; and $\mathbf{A}_t = \text{Var}(\beta_t)$.

In contrast to Meuwissen et al. (1996), γ_{jt} were scaled toward a common base, $\gamma_{jt} = \mathbf{S}\beta_t - \gamma_t^{\text{base}}$, because mean variances had to be retained for back solving. In addition, scaling toward a common base was conceptually similar to the approaches in other studies of type data (e.g., Koots et al., 1994; Weigel and Lawlor, 1994). Because the approach was similar to an additive base change before and after solving the mixed model equations, the definition of the base had no influence on the heterogeneity factor solutions.

Heterogeneity Model. Most studies of type traits have applied a structural model (e.g., Koots et al., 1994; Weigel and Lawlor, 1994). The heterogeneity model presented here contains fixed effects to pool information across contemporary groups and a random effect that regresses the observed heterogeneity for a given herd-appraisal date toward the fixed effects. The fixed effects are the size of the contemporary group by parity; the mean final score of the contemporary group by parity; the month of appraisal by parity; and the 6-mo season, year, and parity class. The ranges of contemporary group size and mean final score were separated into 10 groups of equal size within parity. Because the random effect was defined as herd-appraisal date (did not include parity), first- and second-parity classes were assumed to have the same variance except for systematic variance differences among parities that were modeled by the fixed effects. This is reasonable because first- and second-lactation scorings are mandatory in Jerseys. This heterogeneity model is a combination of the one used by Koots et al. (1994) for the random effect and the one by Weigel and Lawlor (1994) for fixed effects. The variance model provides a predicted value that pools a priori knowledge from fixed effects and directly observed heterogeneity. Therefore, it is conceptually close to the Bayesian approach used for the final score of US Holsteins (Weigel and Lawlor, 1994).

Ideally, the variance components necessary for the variance model should be estimated jointly (Meuwissen et al., 1996). To achieve this, the required repeatabilities of heterogeneity of variance were estimated using Method R (Reverter et al., 1994), because this method could be easily integrated into the algorithm.

Computational Aspects. The publicly available computer program MTJAAM (Gengler et al., 1999) was modified for this analysis. Estimation of adjustment factors was placed in a subroutine. To enhance convergence speed and stability, the relaxation factor used for the second-order Jacobi procedure was adjusted according to the value of the convergence criterion of the genetic effect. The relaxation factor was computed as $1 + 0.11[-\log_{10}(\text{convergence})]$ at every iteration, with a maximum of 1.9 where the convergence criterion was the squared relative differences between solutions of the genetic effect. Heterogeneity convergence was monitored, and heterogeneity adjustment updates were stopped if this convergence was below a threshold or did not improve for 5 rounds. A minimum of 5 heterogeneity rounds was imposed to avoid convergence problems.

Genetic Trend

Mean EBV were calculated by birth year. Genetic trend was calculated by regressing these means on birth year and birth year squared. The slope was evaluated at year 2000, the most recent year with complete data. Data were restricted to birth years 1981 through 2001 to eliminate years with few observations. Slope also was calculated using only birth years 1996 through 2000 to better determine the slope in the most recent data.

Comparison of Evaluations With and Without HV Adjustment

To evaluate the benefit of the HV adjustment, evaluations also were calculated with and without HV adjustment from a truncated data set in which appraisals from August 2001 and later were removed. The truncation on appraisal date was imposed to enable calculation of parent averages of recent animals that did not include any data from their own appraisals or those of their progeny but still had evaluations that included their own information in the complete data. Correlations between parent averages from the truncated sets and EBV from the complete sets were calculated from both evaluations with and without HV adjustment. To remove the effect of genetic trend on correlations, birth-year means were subtracted from the EBV and parent averages before calculating the correlations. Mean differences between HV-adjusted and HV-unadjusted EBV and standard deviations of those differences also were calculated and stratified by reliability, year of birth, and mean daughter final score.

The International Bull Evaluation Service (Interbull, Uppsala, Sweden) requires new or changed evaluation systems to be validated by trend tests. Interbull Method

3 (Boichard et al., 1995; Fikse et al., 2003) involves calculating a test statistic based on a comparison of evaluations separated by 4 yr, and it considers the amount of new information added by year. This statistic was calculated for evaluations with and without the HV adjustment. Interbull Method 1 (Boichard et al., 1995) compares trends from evaluations using first records only with ones using all data. This test was applied to the HV-adjusted evaluations to determine whether they met Interbull requirements, not to determine the effect of HV adjustment.

Mendelian Sampling

Use of Mendelian-sampling (evaluation minus mean of parent evaluations) standard deviations as a test for the quality of model fit has been proposed recently (e.g., Miglior et al., 2002; Fikse et al., 2003). Mendelian-sampling standard deviations were studied for cows born in 1981 and later. Means, standard deviations, and the linear regression of the Mendelian-sampling standard deviations on birth year were calculated. Mendelian-sampling standard deviations should be stable over time, and the Mendelian-sampling mean should be zero and show no trend.

RESULTS

Comparison of Evaluations With and Without HV Adjustment

The evaluation with HV adjustment computation took approximately 17% longer per iteration (1.7 s total time per iteration on an IBM model 366 computer) than the evaluation without adjustment; however, more than double the number of iterations (168) were done. Problems with convergence can occur, and the starting values for the iteration can affect the outcome. Therefore, a run without HV adjustment was found to be useful to create adequate starting values to begin adjustment for HV from stable solutions. Also, experience showed that updating repeatabilities of the heterogeneity of variance using Method R on every run was not necessary; therefore, we used the same repeatabilities, which was analogous to using the same variance components.

The adjustment slightly improved correlations within birth year for 5,273 AI bulls born from 1981 to 2000 with ≥ 5 appraised daughters over all traits, but did not improve the correlations for final score, strength, dairy form, teat length, or foot angle. For bulls born from 1981 to 2001, correlations within birth year between HV-adjusted parent average and EBV (Table 2) ranged from 0.735 for thurl width to 0.908 for rear legs (side view). In contrast, correlations for HV-unadjusted parent average and EBV ranged from 0.732 for

Table 2. Correlations within birth year for bulls between parent average from truncated data and EBV from full data with and without heterogeneous variance (HV) adjustment

Trait name	HV adjustment		Difference ¹
	Yes	No	
Final score	0.786	0.793	-0.007
Stature	0.771	0.770	0.001
Strength	0.748	0.749	-0.001
Dairy form	0.826	0.829	-0.003
Foot angle	0.837	0.843	-0.006
Rear legs (side view)	0.908	0.907	0.001
Rump angle	0.828	0.818	0.010
Rump width	0.735	0.732	0.003
Fore udder attachment	0.833	0.830	0.003
Rear udder height	0.766	0.759	0.007
Rear udder width	0.796	0.794	0.002
Udder depth	0.832	0.827	0.005
Udder clef	0.798	0.791	0.007
Front teat placement	0.820	0.817	0.003
Teat length	0.800	0.811	-0.011

¹HV correlation – without-HV correlation.

thurl width to 0.907 for rear legs (side view). Correlations (results not shown) across birth year were higher for both HV-adjusted and HV-unadjusted evaluations because of genetic trend (HV-adjusted correlations ranged from 0.852 for strength to 0.966 for dairy form). The HV improvement also was greater, improving the correlation of parent average to future evaluation by a mean of 0.0039 over all traits; still, teat length and foot angle were not improved.

Genetic Trend

Estimates of genetic trend for cows with and without HV adjustment are given in Table 3 for 15 traits over

birth years from 1981 to 2000 and 1996 to 2000. The trend lines were largely linear, but quadratic coefficients did increase the adjusted R^2 for most traits with the application of HV adjustments. The adjusted R^2 was greater than 0.97 for 10 traits over all years and was not below 0.85 for any trait. The 5-yr trend was less stable than the 20-yr trend for both HV-adjusted and HV-unadjusted evaluations, but HV-adjusted trends were generally lower than those for the HV-unadjusted evaluations.

Annual trends for bull EBV (Table 4) were generally lower than those for cows and the trend over 20 yr from the evaluation with HV adjustment was lower than the trend from HV-unadjusted evaluations for all traits except rump width, for which the trend was greater by 0.0004/yr. The greatest reduction in trend was for dairy form (0.0023 lower, or 22%). The trend over 5 yr showed a slightly higher trend with HV adjustment for a few traits.

As shown in Table 5, mean differences between HV-adjusted and HV-unadjusted EBV and standard deviations of those differences for most traits were highest for bulls with reliabilities below 81%. Evaluations for bulls with higher reliabilities were not regressed as strongly toward the parent average; therefore, the differences caused by the HV adjustment were expressed more in progeny information. Bulls with the highest reliabilities did not have great changes in EBV because with a large number of progeny, the effects of HV adjustments would tend to be averaged out. The HV-adjusted EBV for final score ranged from -8.74 to 5.77 after base adjustment, whereas HV-unadjusted EBV for final score ranged from -10.59 to 5.63 with a base ad-

Table 3. Trend in EBV for cows with and without heterogeneous variance (HV) adjustment from a quadratic regression on birth year evaluated at year 2000

Trait	1981 to 2000			1996 to 2000		
	HV adjustment			HV adjustment		
	Yes	No	Difference ¹	Yes	No	Difference
Final score	0.0015	0.0013	0.0003	0.0017	-0.0028	0.0045
Stature	0.0093	0.0104	-0.0011	0.0061	0.0083	-0.0022
Strength	0.0050	0.0055	-0.0005	0.0058	0.0074	-0.0016
Dairy form	-0.0027	-0.0030	0.0003	-0.0039	-0.0060	0.0021
Foot angle	0.0042	0.0051	-0.0010	0.0012	0.0013	0.0000
Rear legs (side view)	-0.0011	-0.0016	0.0005	-0.0117	-0.0135	0.0018
Rump angle	-0.0008	-0.0007	-0.0001	-0.0129	-0.0137	0.0008
Rump width	0.0024	0.0026	-0.0001	-0.0068	-0.0081	0.0013
Fore udder attachment	0.0056	0.0070	-0.0014	-0.0082	-0.0106	0.0024
Rear udder height	0.0023	0.0032	-0.0009	-0.0033	-0.0060	0.0027
Rear udder width	0.0014	0.0019	-0.0005	0.0006	-0.0005	0.0010
Udder depth	0.0068	0.0080	-0.0012	-0.0058	-0.0077	0.0018
Udder clef	0.0007	0.0011	-0.0004	0.0014	0.0014	-0.0001
Front teat placement	0.0046	0.0058	-0.0012	-0.0059	-0.0078	0.0020
Teat length	0.0034	0.0042	-0.0007	-0.0026	-0.0037	0.0010

¹HV EBV trend – without-HV EBV trend.

Table 4. Trend in EBV for AI bulls with ≥5 appraised daughters with and without heterogeneous variance (HV) adjustment from a quadratic regression on birth year evaluated at year 2000

Trait	1981 to 2000			1996 to 2000		
	HV adjustment		Difference ¹	HV adjustment		Difference
	Yes	No		Yes	No	
Final score	-0.0016	-0.0029	0.0013	0.0182	0.0156	0.0026
Stature	0.0083	0.0091	-0.0008	-0.0253	-0.0262	0.0009
Strength	0.0045	0.0048	-0.0003	-0.0096	-0.0113	0.0017
Dairy form	-0.0080	-0.0103	0.0023	0.0424	0.0436	-0.0012
Foot angle	0.0036	0.0043	-0.0007	0.0017	0.0039	-0.0022
Rear legs (side view)	-0.0028	-0.0036	0.0008	0.0090	0.0091	-0.0001
Rump angle	-0.0015	-0.0017	0.0002	-0.0120	-0.0127	0.0007
Rump width	0.0007	0.0004	0.0004	-0.0179	-0.0224	0.0045
Fore udder attachment	0.0058	0.0069	-0.0011	-0.0513	-0.0573	0.0060
Rear udder height	-0.0009	-0.0015	0.0006	0.0079	0.0069	0.0009
Rear udder width	-0.0026	-0.0037	0.0011	0.0336	0.0350	-0.0014
Udder depth	0.0081	0.0093	-0.0012	-0.0565	-0.0590	0.0025
Udder cleft	0.0022	0.0024	-0.0002	0.0087	0.0079	0.0008
Front teat placement	0.0056	0.0064	-0.0008	-0.0150	-0.0208	0.0057
Teat length	0.0035	0.0043	-0.0008	-0.0163	-0.0195	0.0032

¹HV EBV trend – without-HV EBV trend.

When stratified by birth year, the mean differences in EBV were generally highest for bulls born from 1981 to 1985 (Table 6). The evaluations of older bulls tended to increase and those of younger bulls decreased with HV adjustment, consistent with the reduction in estimated genetic trend. The standard deviations of differences were largest for most traits for bulls born from 1986 through 1990. As with the stratification by reliability, bulls born in the most recent years did not have large numbers of progeny, so they deviated less from their respective parent averages. Bulls born in the earliest years would have progeny well distributed over the

various HV levels, leaving the 2 middle groups as the ones with greatest potential for change. When stratified by base-adjusted final score EBV, mean differences between adjusted and unadjusted final scores decreased in magnitude as they approached the mean EBV, then increased as mean final scores increased (data not shown).

The HV-adjusted mean differences for EBV averaged higher for most traits for bulls with daughters with the lowest mean final scores (Table 7). Standard deviations of the differences were also largest for those bulls. Weigel and Lawlor (1994) showed that for type data,

Table 5. Differences between bull EBV calculated with and without heterogeneous variance (HV) adjustment, and their SD by reliability of final score

Trait	Reliability of final score							
	≤70%		71 to 80%		81 to 90%		>90%	
	Difference ¹	SD	Difference	SD	Difference	SD	Difference	SD
Final score	0.026	0.034	0.023	0.039	0.019	0.036	0.012	0.029
Stature	0.007	0.043	0.011	0.048	0.010	0.043	0.006	0.039
Strength	0.004	0.030	0.007	0.035	0.005	0.031	0.005	0.029
Dairy form	0.045	0.061	0.035	0.061	0.027	0.056	0.009	0.041
Foot angle	0.005	0.027	0.009	0.031	0.007	0.031	0.003	0.029
Rear legs (side view)	0.003	0.023	-0.002	0.026	-0.002	0.029	-0.002	0.028
Rump angle	0.005	0.035	0.003	0.042	0.002	0.044	0.006	0.041
Rump width	0.008	0.026	0.011	0.030	0.009	0.028	0.007	0.027
Fore udder attachment	0.002	0.035	0.009	0.040	0.011	0.043	0.006	0.041
Rear udder height	0.037	0.051	0.033	0.054	0.030	0.052	0.016	0.045
Rear udder width	0.040	0.050	0.033	0.052	0.030	0.048	0.015	0.040
Udder depth	-0.005	0.044	0.001	0.051	0.004	0.057	0.002	0.047
Udder cleft	0.015	0.028	0.013	0.033	0.014	0.032	0.006	0.030
Front teat placement	0.013	0.037	0.015	0.043	0.016	0.043	0.007	0.041
Teat length	0.002	0.034	0.002	0.040	0.002	0.043	0.002	0.038
Number of bulls	3,325		1,112		542		285	

¹HV EBV – without-HV EBV.

Table 6. Means and SD of differences between bull EBV calculated with and without heterogeneous variance (HV) adjustment by birth-year group

Trait	Birth years							
	1981 to 1985		1986 to 1990		1991 to 1995		1996 to 2000	
	Difference ¹	SD	Difference	SD	Difference	SD	Difference	SD
Final score	0.054	0.033	0.031	0.035	0.011	0.029	0.003	0.018
Stature	0.015	0.047	0.019	0.050	0.004	0.033	-0.005	0.042
Strength	0.009	0.036	0.009	0.037	0.003	0.024	-0.001	0.026
Dairy form	0.108	0.044	0.056	0.055	0.008	0.037	-0.003	0.029
Foot angle	0.015	0.029	0.009	0.034	0.007	0.026	-0.005	0.019
Rear legs (side view)	0.009	0.030	0.001	0.029	-0.003	0.022	-0.001	0.015
Rump angle	0.014	0.040	0.009	0.051	-0.001	0.034	-0.002	0.022
Rump width	0.019	0.030	0.012	0.032	0.005	0.021	0.002	0.023
Fore udder attachment	0.010	0.040	0.012	0.043	0.007	0.034	-0.008	0.030
Rear udder height	0.083	0.039	0.051	0.048	0.014	0.037	-0.003	0.033
Rear udder width	0.088	0.036	0.053	0.047	0.014	0.034	-0.001	0.027
Udder depth	-0.005	0.049	-0.001	0.060	0.005	0.042	-0.008	0.035
Udder cleft	0.029	0.031	0.021	0.030	0.009	0.025	0.000	0.023
Front teat placement	0.027	0.041	0.026	0.043	0.011	0.034	-0.006	0.028
Teat length	-0.001	0.049	0.007	0.040	0.001	0.027	0.003	0.026
Number of bulls	1,210		1,232		1,412		1383	

¹HV EBV – without-HV EBV.**Table 7.** Differences between bull EBV calculated with and without heterogeneous variance (HV) adjustment and their SD by mean daughter final score

Trait		Mean daughter final score							
		<75	75	76	77	78	79	80	≥81
Final score	Difference ¹	0.063	0.035	0.025	0.012	0.005	0.003	0.005	0.009
	SD	0.036	0.027	0.027	0.027	0.024	0.021	0.020	0.020
Stature	Difference	0.030	0.019	0.007	0.007	0.000	-0.002	-0.008	-0.015
	SD	0.051	0.049	0.042	0.039	0.038	0.031	0.038	0.039
Strength	Difference	0.018	0.010	0.004	0.003	0.000	-0.001	-0.002	-0.005
	SD	0.040	0.035	0.031	0.029	0.025	0.021	0.024	0.026
Dairy form	Difference	0.099	0.064	0.046	0.027	0.011	0.005	0.001	0.003
	SD	0.055	0.052	0.053	0.052	0.044	0.041	0.040	0.036
Foot angle	Difference	0.019	0.014	0.010	0.007	0.000	-0.003	-0.005	-0.009
	SD	0.033	0.032	0.029	0.027	0.022	0.020	0.020	0.018
Rear legs (side view)	Difference	0.003	0.001	0.001	-0.001	0.000	0.001	0.002	0.004
	SD	0.031	0.030	0.027	0.025	0.020	0.018	0.018	0.016
Rump angle	Difference	0.010	0.012	0.006	0.003	0.003	0.001	-0.001	-0.001
	SD	0.049	0.046	0.041	0.038	0.032	0.027	0.024	0.024
Rump width	Difference	0.026	0.015	0.008	0.006	0.003	0.001	-0.001	-0.005
	SD	0.033	0.029	0.025	0.024	0.021	0.018	0.021	0.022
Fore udder attachment	Difference	0.025	0.015	0.011	0.005	0.000	-0.007	-0.013	-0.021
	SD	0.046	0.039	0.036	0.033	0.028	0.026	0.026	0.027
Rear udder height	Difference	0.087	0.056	0.044	0.026	0.012	0.002	-0.005	-0.007
	SD	0.045	0.039	0.039	0.040	0.038	0.036	0.035	0.033
Rear udder width	Difference	0.090	0.058	0.044	0.026	0.011	0.005	0.000	0.000
	SD	0.042	0.039	0.040	0.040	0.036	0.033	0.033	0.031
Udder depth	Difference	0.004	0.003	0.003	0.002	-0.002	-0.008	-0.013	-0.020
	SD	0.064	0.053	0.051	0.045	0.035	0.032	0.029	0.030
Udder cleft	Difference	0.036	0.023	0.019	0.011	0.004	0.001	0.000	0.000
	SD	0.032	0.027	0.026	0.026	0.022	0.023	0.022	0.020
Front teat placement	Difference	0.044	0.026	0.019	0.010	0.001	-0.004	-0.007	-0.013
	SD	0.044	0.038	0.036	0.031	0.028	0.027	0.027	0.025
Teat length	Difference	0.007	0.003	0.002	0.000	0.000	0.000	0.001	0.002
	SD	0.046	0.043	0.040	0.034	0.031	0.026	0.026	0.023
Number of bulls		1,091	503	593	626	649	700	410	433

¹HV EBV – without-HV EBV.

Table 8. Trend in standard deviations of Mendelian sampling for cow EBV calculated with and without heterogeneous variance (HV) adjustment and EBV slope ratio by birth-year group

Trait	1981 to 2000			1996 to 2000		
	HV adjustment		HV slope/ (no HV slope) × 100%	HV adjustment		HV slope/ (no HV slope) × 100%
	Yes	No		Yes	No	
Final score	0.0000	-0.0018	16.8	0.0016	0.0139	14.8
Stature	0.0001	-0.0020	27.1	-0.0042	0.0194	-20.6
Strength	0.0000	-0.0016	32.7	0.0034	0.0175	30.9
Dairy form	-0.0002	-0.0030	29.5	-0.0066	0.0027	-29.0
Foot angle	-0.0003	-0.0013	28.1	0.0059	0.0158	46.6
Rear legs (side view)	-0.0001	-0.0009	35.5	-0.0001	0.0048	11.3
Rump angle	-0.0005	-0.0033	31.7	0.0039	0.0229	22.2
Rump width	-0.0001	-0.0015	34.4	0.0046	0.0164	39.1
Fore udder attachment	-0.0004	-0.0028	23.3	0.0002	0.0154	12.6
Rear udder height	0.0000	-0.0029	10.4	-0.0119	0.0050	-51.1
Rear udder width	-0.0004	-0.0031	23.4	-0.0033	0.0085	24.1
Udder depth	-0.0008	-0.0043	10.0	-0.0027	0.0142	-44.3
Udder cleft	0.0002	-0.0014	23.6	0.0068	0.0172	52.4
Front teat placement	0.0000	-0.0024	29.5	0.0037	0.0160	45.7
Teat length	-0.0016	-0.0031	42.7	0.0133	0.0265	51.5

herds with the highest final scores had the lowest variance. In this stratification on the mean final score, the bulls with daughters in the most extreme groups showed greater change than those with daughters in less extreme groups, as expected.

Mendelian sampling was calculated for cows born from 1981 through 2000 (Table 8). With HV adjustment, Mendelian-sampling standard deviations declined less over time than for unadjusted evaluations for all traits except rump width. The slope at year 2000 of Mendelian-sampling standard deviations from HV-adjusted evaluations ranged from 10.0% for udder depth to 42.7% for teat length of the slope for unadjusted evaluations. Ideally, the Mendelian-sampling variance should be stable over time. The reduced slope of the Mendelian-sampling standard deviations from the HV-adjusted analysis for most traits is an indication that the adjustment more correctly models the data.

The Interbull trend validation was performed for stature and udder support. Evaluations with the HV adjustment passed both the Method 1 and Method 3 tests, indicating that the large changes in trend did not cause inconsistency in the trend either between first and all appraisals or over time within sire. The HV adjustment performed better for the Interbull Method 3 test for the 2 required traits. Both tests were performed to ensure Interbull compliance following adjustment.

CONCLUSIONS

Evaluations with HV adjustment were highly correlated with the evaluations without the adjustment, but differed in expected ways. The bulls with the greatest

changes were generally those with the lowest mean daughter final scores. Records on daughters of these bulls received the most adjustment. Some reduction over time in Mendelian-sampling standard deviations is expected if older animals have higher reliability and lower inbreeding; however, those factors are unlikely to explain the higher slopes for EBV trend found in the evaluations without HV adjustment. Therefore, the lower slopes from the HV adjustment also indicate the superiority of the HV-adjusted evaluations. The reduction in estimates of genetic trend also indicates that the HV adjustment affected comparisons across time. These reductions in trend are likely due to changes in the variance of Mendelian sampling. The additional computations required are manageable. The starting values for the iteration may determine whether convergence is achieved. A run without HV adjustment may be useful to create adequate starting values. The HV-adjusted evaluations were adopted as official for the Jersey breed for the May 2001 evaluation and for the other breeds for which USDA calculates evaluations for the February 2002 evaluation. This enhancement improved the accuracy of selection decisions based on type traits, particularly over time.

ACKNOWLEDGMENTS

N. Gengler, Chercheur Qualifié of the National Fund for Scientific Research (Brussels, Belgium), and T. Druet, Chargé de Recherches of the National Fund for Scientific Research (Brussels, Belgium), currently at the Institut National de la Recherche Agronomique (Jouy-en-Josas, France), acknowledge the financial support of their organizations. Partial funding provided

by the American Jersey Cattle Association (Reynoldsburg, OH) and manuscript review by Kent Weigel (University of Wisconsin, Madison) are also acknowledged.

REFERENCES

- Bell, B. R., W. E. Vinson, J. M. White, H. D. Norman, and R. H. Kliewer. 1982. Effects of genetic merit of herdmates on sire summaries for type in Holstein cattle. *J. Dairy Sci.* 65:126–135.
- Boichard, D., B. Bonaiti, A. Barbat, and S. Mattalia. 1995. Three methods to validate the estimation of genetic trend for dairy cattle. *J. Dairy Sci.* 78:431–437.
- Ducrocq, V., and B. Besbes. 1993. Solution of multiple trait models with missing data on some traits. *J. Anim. Breed. Genet.* 110:81–92.
- Fikse, W. F., L. Klei, Z. Liu, and P. G. Sullivan. 2003. Procedure for validation of trends in genetic variance. *Interbull Bull.* 31:30–36.
- Gengler, N., T. Dusseldorf, G. R. Wiggans, J. R. Wright, and T. Druet. 2000. Multitrait genetic evaluation of Jersey type with integrated accounting for heterogeneous (co)variances. *Interbull Bull.* 25:108–122.
- Gengler, N., T. Dusseldorf, G. R. Wiggans, J. R. Wright, and T. Druet. 2001. Heterogeneity of (co)variance components for Jersey type traits. *J. Dairy Sci.* 84:1772. Online. Available: <http://jds.fass.org/>
- Gengler, N., and I. Misztal. 1996. Approximation of reliability for multiple-trait animal models with missing data by canonical transformation. *J. Dairy Sci.* 79:317–328.
- Gengler, N., G. R. Wiggans, and J. R. Wright. 1999. Animal model genetic evaluation of type traits for five dairy cattle breeds. *J. Dairy Sci.* 82:1350. Online. Available: <http://jds.fass.org/>
- Gengler, N., G. R. Wiggans, J. R. Wright, H. D. Norman, and C. W. Wolfe. 1997a. Application of canonical transformation with missing values to multitrait evaluation of Jersey type. *J. Dairy Sci.* 80:2563–2571.
- Gengler, N., G. R. Wiggans, J. R. Wright, H. D. Norman, and C. W. Wolfe. 1997b. Estimation of (co)variance components for Jersey type traits using a repeatability model. *J. Dairy Sci.* 80:1801–1806.
- Koots, K. R., K. M. Wade, B. W. Kennedy, J. C. M. Dekkers, G. C. Smith, and E. B. Burnside. 1994. Method and effect of adjustment for heterogeneous variance of Holstein conformation traits. *J. Dairy Sci.* 77:294–302.
- Meuwissen, T. H. E., G. de Jong, and B. Engel. 1996. Joint estimation of breeding values and heterogeneous variances of large data files. *J. Dairy Sci.* 79:310–316.
- Miglior, F., P. G. Sullivan, and B. J. Van Doormaal. 2002. Preliminary analysis of Mendelian sampling terms for genetic evaluation validation. *Interbull Bull.* 27:183–187.
- Misztal, I., K. Weigel, and T. J. Lawlor. 1995. Approximation of estimates of (co)variance components with multiple trait restricted maximum likelihood by multiple diagonalization for more than one random effect. *J. Dairy Sci.* 78:1862–1872.
- Reverter, A., B. L. Golden, and R. M. Bourdon. 1994. Method R variance components procedure: Application on the simple breeding value model. *J. Anim. Sci.* 72:2247–2253.
- Weigel, K. A., and T. J. Lawlor. 1994. Adjustment of heterogeneous variance in genetic evaluations for conformation of United States Holsteins. *J. Dairy Sci.* 77:1691–1701.