

Estimation of (Co)Variance Components for Jersey Type Traits Using a Repeatability Model

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ABSTRACT

(Co)variance components for final score and 15 linear type traits of Jersey cows were estimated by multitrait REML using multiple diagonalization and a repeatability model with 34,999 records of 22,354 cows. Multiple diagonalization gave relative off-diagonals (ratio of squared off-diagonals to the product of diagonals) of <0.1%. Heritabilities and repeatabilities, respectively, were estimated as 0.29 and 0.48 for final score, 0.40 and 0.57 for stature, 0.26 and 0.39 for strength, 0.28 and 0.43 for dairy form, 0.13 and 0.25 for foot angle, 0.13 and 0.25 for rear legs (side view), 0.27 and 0.41 for body depth, 0.31 and 0.52 for rump angle, 0.22 and 0.33 for thurl width, 0.22 and 0.36 for fore udder attachment, 0.28 and 0.46 for rear udder height, 0.26 and 0.42 for rear udder width, 0.32 and 0.48 for udder depth, 0.20 and 0.36 for udder cleft, 0.29 and 0.46 for front teat placement, and 0.31 and 0.48 for teat length. Estimates of heritability generally were higher, and estimates of repeatability were lower, than values used previously for USDA genetic evaluations, which were based on data from the 1970s and early 1980s. Final score was highly correlated both genetically and phenotypically with dairy form and rear udder traits. These estimates of heritabilities and (co)variance components are necessary for multitrait genetic evaluation of linear type traits of US Jerseys.

(**Key words:** Jersey, type traits, (co)variance, repeatability model)

Abbreviation key: AJCA = American Jersey Cattle Association.

INTRODUCTION

All dairy breed associations and many AI organizations in the US have implemented linear type trait

programs that are similar to the program described by Wilson (19). The relationships of these traits to herd life and profitability (14), survival and workability (15, 17), udder health and somatic cell score (16), and genetic defects (4) have been investigated.

The American Jersey Cattle Association (AJCA) currently scores 15 linear type traits and assigns a calculated final score for all scored cattle. Breeders are also allowed to request that a final score be assigned by the classifier for all cows being scored in their herd. The linear traits are stature, strength, dairy form, foot angle, rear legs (side view), body depth, rump angle, thurl width, fore udder attachment, rear udder height, rear udder width, udder depth, udder cleft, front teat placement, and teat length.

Genetic evaluations for linear traits and for final score (appraiser assigned when available; otherwise, calculated) have used single-trait sire models (12). Use of a multitrait animal model improves accuracy of evaluations but requires estimates of (co)variance components from a model similar to the one proposed for evaluation. Because the linear scoring system used by AJCA allows for repeated scoring of cattle through second lactation (a 9-mo interval is recommended), a repeatability model that is similar to the one developed for Holsteins (9) is appropriate. The current evaluation system uses all scores in a repeatability model but gives a low weight (0.1) to scores after second lactation because they are optional. All first and second lactation cows in a herd are scored at each appraisal.

(Co)variance estimation for multitrait models with large numbers of traits can be simplified by use of a canonical transformation of original correlated traits to new, uncorrelated traits (5). This method requires that there be no missing values and that the same model apply to all traits. A canonical transformation exists for all simple models with two random effects (e.g., genetic and residual). For a repeatability model, an effect for permanent environment is required; therefore, a simple canonical transformation

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is not appropriate. When (co)variance matrices are linear functions of one another, diagonalization for more than two matrices is possible (6). An approximate multiple diagonalization of (co)variance matrices that are associated with more than two random effects can be achieved when matrices are approximate linear functions of one another. This method was used by Misztal et al. (10) for estimation of (co)variance components for Holstein linear type traits. The objective of this study was to use multiple diagonalization and a REML expectation-maximization algorithm with a repeatability model for estimation of (co)variance components for linear and final type scores of Jersey cows in the US.

MATERIALS AND METHODS

Data

Type data were provided by AJCA. Cows born after January 1, 1987 were chosen from 215 herds with 200 to 400 cows scored since 1990. Only scores assigned from January 1, 1990 through November 30, 1995 were retained to avoid missing values for traits that were added to the program during the late 1980s. Final scores that were calculated from the linear scores by AJCA were not included in the analysis, because this trait provides almost no new information beyond that available from the linear traits. Records without a final score assigned by the classifier were eliminated. A total of 34,999 records for 22,354 cows in first or second lactation were retained. At least one scoring during first lactation was required. Most animals were scored in both lactations (52%) and had more than one record (57%). A few cows (12%) were scored twice in their first lactation. Records were divided into 1334 groups by herd and date scored; groups included 3 to 142 animals, and the mean was 26. Data were adjusted for age and stage of lactation using the current multiplicative adjustment factors of USDA (J. R. Wright, 1991, unpublished research).

Pedigrees were extracted from the national USDA database of lactation records. Ancestors were traced back to 1978. Animals born before 1978 were considered to be the base population. After elimination of animals that did not have a type score and were not related to at least two other animals with type scores, 52,151 animals remained.

Model

The same model was applied to all traits for estimation of variance components:

$$\mathbf{y} = \mathbf{Xh} + \mathbf{Hc} + \mathbf{Zp} + \mathbf{Z}^*\mathbf{u} + \mathbf{e}$$

where \mathbf{y} is a vector of type records; \mathbf{h} is a vector of fixed effects of herd and date scored; \mathbf{c} is a vector of fixed effects of parity and age at classification; \mathbf{p} is a vector of random effects of permanent environment; \mathbf{u} is a vector of random additive genetic effects of animals and genetic groups ($\mathbf{u} = \mathbf{a} + \mathbf{Qg}$, where \mathbf{a} is a vector of random additive genetic effects of animals expressed as deviations from group means, \mathbf{g} is a vector of fixed effects of genetic groups, and \mathbf{Q} is an incidence matrix linking \mathbf{g} with \mathbf{u}); \mathbf{X} , \mathbf{H} , \mathbf{Z} , and \mathbf{Z}^* (\mathbf{Z} augmented with null columns for animals without records) are incidence matrices associating \mathbf{h} , \mathbf{c} , \mathbf{p} , and \mathbf{u} with \mathbf{y} ; and \mathbf{e} is a vector of random residual effects.

The effect of parity and age at classification (\mathbf{c}) was included in the model because of a concern in recent years about the accuracy of estimates of genetic trend (1) related to problems with adjustment of records for age at classification prior to analysis. Records were divided into six groups by parity (first or second lactation) and age within parity (<27 mo, 27 through 31 mo, and >31 mo for first lactation; <39 mo, 39 through 43 mo, and >43 mo for second lactation). Because maturity rate may change over time, effect of parity and age may need to be estimated within a time period. Because only records from January 1990 through November 1995 were included, the change in effect of parity and age over time was not accounted for in this study. An effect for lactation stage at classification was not included in the model because records were adjusted for lactation stage prior to analysis and because no problems were apparent because of adjustment for lactation stage.

To account for differences in mean genetic merit of unknown ancestors by birth year, genetic groups were included as proposed by Westell et al. (18). Nine genetic groups were defined based on birth year (<1979, 1979 and 1980, ..., 1991 and 1992, >1992).

Estimation of (Co)Variance Components

Estimates of (co)variance components were computed using the procedure developed by Misztal et al. (10) for Holstein type traits. The multitrait model for the 16 correlated traits was reduced to 16 single-trait models with multiple diagonalization using the F-G algorithm (2, 3). An expectation-maximization REML algorithm (7, 8) was used for estimation of (co)variance components on the transformed scales. Convergence was considered to be obtained when mean squared difference between (co)variance ma-

TABLE 1. Estimates of heritability and repeatability for final score and 15 linear type traits.

| Trait | Heritability | | | Repeatability | | |
|-----------------------|----------------------|-------|-------------------|----------------------|-------|------|
| | Cows scored per herd | | USDA ¹ | Cows scored per herd | | USDA |
| | 200 to 400 | ≥1000 | | 200 to 400 | ≥1000 | |
| Final score | 0.29 | 0.31 | 0.23 | 0.48 | 0.49 | 0.60 |
| Stature | 0.40 | 0.41 | 0.40 | 0.57 | 0.60 | 0.60 |
| Strength | 0.26 | 0.28 | 0.24 | 0.39 | 0.43 | 0.40 |
| Dairy form | 0.28 | 0.26 | 0.16 | 0.43 | 0.41 | 0.45 |
| Foot angle | 0.13 | 0.13 | 0.12 | 0.25 | 0.23 | 0.29 |
| Rear legs (side view) | 0.13 | 0.14 | 0.12 | 0.25 | 0.25 | 0.29 |
| Body depth | 0.27 | 0.29 | 0.34 | 0.41 | 0.45 | 0.45 |
| Rump angle | 0.31 | 0.35 | 0.27 | 0.52 | 0.54 | 0.65 |
| Thurl width | 0.22 | 0.23 | 0.24 | 0.33 | 0.35 | 0.40 |
| Fore udder attachment | 0.22 | 0.24 | 0.18 | 0.36 | 0.38 | 0.51 |
| Rear udder height | 0.28 | 0.33 | 0.17 | 0.46 | 0.51 | 0.40 |
| Rear udder width | 0.26 | 0.27 | 0.17 | 0.42 | 0.42 | 0.40 |
| Udder depth | 0.32 | 0.33 | 0.27 | 0.48 | 0.50 | 0.65 |
| Udder cleft | 0.20 | 0.23 | 0.16 | 0.36 | 0.39 | 0.45 |
| Front teat placement | 0.29 | 0.29 | 0.18 | 0.46 | 0.47 | 0.51 |
| Teat length | 0.31 | 0.30 | 0.26 | 0.48 | 0.46 | 0.40 |

¹Current heritabilities used by USDA for calculating genetic evaluations with a sire model.

trices in consecutive rounds was $<10^{-6}$. (Co)variance components were obtained through backtransformation to the original scale.

Relative off-diagonals (ratio of squared off-diagonals to the product of diagonals) of transformed (co)variance matrices were computed to check the degree of diagonalization; those values provided an indication of the loss from the application of the approximate transformation by the F-G algorithm (10).

Preliminary Study

Similar data for 40 herds with ≥ 1000 cows scored from 1990 through 1995 also were analyzed in a preliminary study using the same model to estimate (co)variance components. These herds were chosen because their large contemporary groups were expected to provide more accurate estimates of contemporary group effects. However, because such large herds might not be representative of the national population, the current study was limited to herds with 200 to 400 cows scored. Results from the preliminary and current studies were compared to determine the effect of herd size on estimation of (co)variance components.

RESULTS AND DISCUSSION

At convergence, mean squared differences between (co)variance matrices in consecutive rounds were 0.72×10^{-6} for permanent environment effects, $0.33 \times$

10^{-6} for genetic effects, and 0.59×10^{-8} for residual effects. The exact numbers of rounds of iteration needed to obtain convergence were not available because starting values from preliminary analysis were used; theoretically, with starting covariances of 0 and a value of 2.0 assumed for the ratio of error variance to other variances, >50 rounds of iteration would have been required for an equivalent level of convergence. One round of iteration took approximately 8 h of central processing unit time (DECstation 5000-240; Digital Equipment Corporation, Marlboro, MA) with 64 MB of memory. After diagonalization, relative off-diagonals were low [0.032% for permanent environment and 0.017% for genetic (co)variance matrices].

Estimates of heritabilities and repeatabilities (Table 1) were compared with the values currently being used by USDA for genetic evaluation; the current USDA values were based on data from the 1970s and early 1980s and on the weighted means of heritability estimates from several studies (11, 13). For herds with 200 to 400 cows scored, heritability estimates were higher (mean increase of 0.04) than current USDA estimates for all traits except stature (same heritability) and body depth and thurl width (lower estimates). Increases were largest for dairy form (from 0.16 to 0.28) and some udder traits (from 0.18 to 0.29 for front teat placement, from 0.17 to 0.28 for rear udder height, and from 0.17 to 0.26 for rear udder width). Misztal et al. (10) found a similar increase for rear udder height of Holsteins. For Australian Jerseys, Visscher and Goddard (17) found

similar estimates for height (comparable with stature), rear legs, fore udder attachment, and front teat placement; higher estimates for overall type (final score), dairy character (dairy form), and medial suspensory ligament (udder cleft); and lower estimates for rear attachment height (rear udder height). For capacity, a trait related to strength and body depth, Visscher and Goddard (17) reported a heritability estimate (0.17) that was lower than for either of the US traits (0.26 for strength and 0.27 for body depth).

Repeatabilities (Table 1) for herds with 200 to 400 cows scored were lower (mean decrease of 0.05) for all traits except rear udder height, rear udder width, and teat length compared with current USDA estimates. The largest decrease was for udder depth (0.65 to 0.48), and the largest increase was for teat length (0.40 to 0.48). Variances for permanent environment, expressed as repeatability minus heritability, were lower than corresponding differences between current USDA repeatabilities and heritabilities for all traits except body depth and teat length (increase of 0.03); the greatest decrease was 0.22 (from 0.38 to 0.16) for udder depth.

For herds with ≥ 1000 cows scored (Table 1), heritability and repeatability estimates generally were similar or slightly higher than for herds with 200 to 400 cows scored. However, these differences may be the result of sampling error as well as herd size.

Estimates for heritability and repeatability generally were similar to those reported by Misztal et al. (10) for Holsteins. The largest negative differences were for body depth (0.10 for heritability, 0.17 for repeatability), rear legs (0.08 for heritability, 0.09 for repeatability), and fore udder attachment (0.07 for heritability, 0.13 for repeatability); the largest positive differences were for udder depth, rear udder height, and front teat placement (0.03 to 0.04 for heritability and repeatability). Variances of permanent environment, expressed as repeatability minus heritability, were similar or slightly less; the largest negative difference (0.07) was for body depth. Although the same statistical methodology was used for both studies, differences could result from differences in trait definitions and scales as well as in genetic parameters for breeds.

Correlations for permanent environment and residuals among final score and the 15 linear type traits are in Table 2 for herds with 200 to 400 cows scored; corresponding correlations for herds with ≥ 1000 cows scored were similar and are not shown. These correlations reflect the (co)variance matrices for \mathbf{p} and \mathbf{e} , which are required for calculation of multitrait genetic evaluations.

Genetic and phenotypic correlations among the 16 traits are in Table 3 for herds with 200 to 400 cows scored; corresponding correlations for herds with ≥ 1000 cows scored were similar and are not shown. Highest genetic correlations with final score were 0.86 for rear udder width, 0.81 for rear udder height, and 0.75 for dairy form. Genetic correlations also were high for strength with thurl width (0.96) and body depth (0.86), thurl width and body depth (0.82), rear udder width with rear udder height (0.83) and dairy form (0.79), and fore udder attachment and udder depth (0.75). In general, final score and linear type traits were correlated similarly or less correlated for permanent environment effects than for genetic effects; for residual effects and, therefore, phenotypic effects, type traits were even less correlated than for genetic effects.

In general, genetic correlations were similar for linear type traits of Jerseys and Holsteins (10), but several differences between breeds were found. Stature was less linked to strength and body depth for Jerseys than for Holsteins, which indicates that taller Jerseys are not necessarily as strong and deep-bodied as taller Holsteins; strength and body depth were more correlated genetically to thurl width for Jerseys than for Holsteins. Dairy form was more related to rear udder traits for Jerseys than for Holsteins; perhaps dairyness is more independent from rear udder traits for Holsteins. Correlation of foot angle and rear legs was similarly negative for both breeds. For Jerseys, a moderately negative genetic relationship was found between body depth and udder depth; however, this negative correlation was small for Holsteins. Mammary traits generally were more closely linked for Holsteins than for Jerseys. Teat length of Jerseys was moderately correlated (0.28 to 0.33) with stature, strength, body depth, and thurl width and had a genetic correlation of 0.21 with udder cleft. These differences between Jerseys and Holsteins could be reflections of differences in classification programs as well as true breed differences.

Correlations in Table 3 were also compared with those reported by Visscher and Goddard (17) for Australian Jerseys. Phenotypic correlations of overall type, the Australian equivalent of final score, with linear type traits were similar to those for US Jerseys. Genetic correlations of final score with linear traits varied more between the two populations, especially for stature (height) (0.08 for Australian Jerseys vs. 0.43 for US Jerseys). This lower genetic correlation for final score and stature for Australian Jerseys may result from differences between the two Jersey populations. Most relationships between the reported traits were similar for the two populations

TABLE 2. Correlations for permanent environmental (above diagonal) and residual (below diagonal) effects among final score and 15 linear type traits of Jerseys.

| Trait | Fore | | | | | | | | | | | | | | | Front | |
|-----------------------|-------------|---------|----------|------------|------------|-----------|------------|------------|-------------|-------------|------------------|-------------------|------------------|-------------|-------------|-------------|-------------|
| | Final score | Stature | Strength | Dairy form | Foot angle | Rear legs | Body depth | Rump angle | Thurl width | Thurl width | Udder attachment | Rear udder height | Rear udder width | Udder depth | Udder cleft | Udder depth | Udder cleft |
| Final score | ... | 0.29 | 0.32 | 0.73 | 0.33 | -0.13 | 0.38 | -0.08 | 0.41 | 0.42 | 0.77 | 0.81 | 0.16 | 0.52 | 0.53 | 0.07 | 0.07 |
| Stature | 0.14 | ... | 0.64 | 0.29 | 0.21 | -0.06 | 0.52 | 0.12 | 0.61 | 0.09 | 0.14 | 0.24 | 0.05 | 0.07 | 0.05 | 0.17 | 0.17 |
| Strength | 0.21 | 0.37 | ... | 0.23 | 0.23 | -0.17 | 0.82 | 0.08 | 0.94 | 0.12 | 0.11 | 0.37 | -0.15 | 0.12 | 0.16 | 0.21 | 0.21 |
| Dairy form | 0.61 | 0.14 | 0.15 | ... | 0.11 | 0.06 | 0.43 | 0.08 | 0.32 | 0.02 | 0.59 | 0.76 | -0.30 | 0.30 | 0.24 | 0.08 | 0.08 |
| Foot angle | 0.17 | 0.07 | 0.12 | 0.07 | ... | -0.42 | 0.12 | -0.04 | 0.22 | 0.13 | 0.13 | 0.16 | 0.10 | 0.12 | 0.09 | 0.05 | 0.05 |
| Rear legs | -0.05 | -0.03 | -0.08 | 0.01 | -0.20 | ... | 0.06 | 0.06 | -0.17 | -0.07 | -0.05 | -0.11 | -0.10 | -0.02 | 0.02 | -0.07 | -0.07 |
| Body depth | 0.21 | 0.30 | 0.55 | 0.22 | 0.09 | -0.01 | ... | 0.08 | 0.78 | 0.08 | 0.19 | 0.43 | -0.29 | 0.18 | 0.16 | 0.18 | 0.18 |
| Rump angle | 0.04 | 0.08 | 0.07 | 0.11 | 0.02 | 0.03 | 0.06 | ... | 0.01 | -0.20 | -0.09 | -0.05 | -0.17 | -0.01 | -0.03 | 0.04 | 0.04 |
| Thurl width | 0.26 | 0.29 | 0.56 | 0.19 | 0.14 | -0.06 | 0.43 | 0.07 | ... | 0.19 | 0.22 | 0.48 | -0.09 | 0.16 | 0.18 | 0.17 | 0.17 |
| Fore udder attachment | 0.27 | 0.06 | 0.14 | 0.06 | 0.10 | -0.05 | 0.09 | -0.06 | 0.13 | 0.26 | 0.48 | 0.36 | 0.67 | 0.17 | 0.42 | 0.00 | 0.00 |
| Rear udder height | 0.56 | 0.09 | 0.12 | 0.42 | 0.08 | -0.03 | 0.14 | 0.06 | 0.17 | 0.19 | 0.61 | 0.84 | 0.22 | 0.42 | 0.37 | 0.07 | 0.07 |
| Rear udder width | 0.57 | 0.14 | 0.24 | 0.46 | 0.11 | -0.03 | 0.23 | 0.07 | 0.30 | 0.31 | 0.08 | 0.02 | 0.20 | 0.38 | 0.40 | 0.09 | 0.09 |
| Udder depth | 0.18 | 0.07 | 0.02 | -0.06 | 0.03 | 0.00 | 0.02 | -0.16 | 0.02 | 0.17 | 0.29 | 0.28 | 0.20 | 0.08 | 0.24 | -0.15 | -0.15 |
| Udder cleft | 0.43 | 0.05 | 0.07 | 0.20 | 0.05 | 0.03 | 0.08 | 0.01 | 0.09 | 0.24 | 0.19 | 0.19 | 0.26 | 0.31 | 0.39 | 0.11 | 0.11 |
| Front test placement | 0.34 | 0.05 | 0.08 | 0.10 | 0.06 | 0.01 | 0.09 | -0.03 | 0.09 | 0.03 | 0.07 | 0.11 | 0.26 | 0.31 | 0.39 | 0.11 | 0.11 |
| Test length | 0.10 | 0.07 | 0.08 | 0.09 | 0.03 | 0.01 | 0.09 | 0.01 | 0.10 | 0.03 | 0.07 | 0.11 | -0.02 | 0.09 | 0.03 | 0.03 | 0.03 |

TABLE 3. Genetic (above diagonal) and phenotypic (below diagonal) correlations among final score and 15 linear type traits of Jerseys.

| Trait | Fore | | | | | | | | | | | | | | | Front | |
|-----------------------|-------------|---------|----------|------------|------------|-----------|------------|------------|-------------|-------------|------------------|-------------------|------------------|-------------|-------------|-------------|-------------|
| | Final score | Stature | Strength | Dairy form | Foot angle | Rear legs | Body depth | Rump angle | Thurl width | Thurl width | Udder attachment | Rear udder height | Rear udder width | Udder depth | Udder cleft | Udder depth | Udder cleft |
| Final score | ... | 0.43 | 0.44 | 0.75 | 0.39 | 0.12 | 0.48 | 0.01 | 0.51 | 0.38 | 0.81 | 0.86 | 0.04 | 0.59 | 0.51 | 0.17 | 0.17 |
| Stature | 0.27 | ... | 0.69 | 0.37 | 0.39 | -0.12 | 0.58 | 0.18 | 0.67 | 0.12 | 0.22 | 0.33 | 0.04 | 0.11 | 0.05 | 0.33 | 0.33 |
| Strength | 0.29 | 0.51 | ... | 0.33 | 0.38 | -0.23 | 0.86 | 0.14 | 0.96 | 0.12 | 0.17 | 0.47 | -0.21 | 0.23 | 0.16 | 0.32 | 0.32 |
| Dairy form | 0.67 | 0.24 | 0.21 | ... | 0.13 | 0.14 | 0.52 | 0.09 | 0.39 | -0.15 | 0.60 | 0.79 | -0.46 | 0.41 | 0.21 | 0.16 | 0.16 |
| Foot angle | 0.23 | 0.16 | 0.18 | 0.08 | ... | -0.39 | 0.23 | -0.01 | 0.38 | 0.23 | 0.21 | 0.24 | 0.16 | 0.20 | 0.12 | 0.15 | 0.15 |
| Rear legs | -0.08 | -0.06 | -0.12 | 0.04 | -0.25 | ... | -0.12 | 0.06 | -0.21 | -0.23 | -0.10 | -0.06 | -0.21 | -0.04 | 0.04 | -0.10 | -0.10 |
| Body depth | 0.31 | 0.42 | 0.67 | 0.33 | 0.12 | -0.02 | ... | 0.13 | 0.82 | -0.01 | 0.24 | 0.53 | -0.40 | 0.28 | 0.15 | 0.28 | 0.28 |
| Rump angle | 0.00 | 0.12 | 0.09 | 0.09 | 0.00 | 0.04 | 0.08 | ... | 0.08 | -0.17 | -0.03 | 0.02 | -0.13 | 0.02 | -0.01 | 0.05 | 0.05 |
| Thurl width | 0.34 | 0.44 | 0.70 | 0.26 | 0.19 | -0.10 | 0.57 | 0.06 | ... | 0.18 | 0.27 | 0.56 | -0.16 | 0.25 | 0.16 | 0.28 | 0.28 |
| Fore udder attachment | 0.32 | 0.08 | 0.13 | 0.00 | 0.12 | -0.08 | 0.07 | -0.11 | 0.15 | ... | 0.48 | 0.26 | 0.75 | 0.09 | 0.36 | -0.01 | -0.01 |
| Rear udder height | 0.67 | 0.14 | 0.14 | 0.50 | 0.11 | -0.04 | 0.18 | 0.01 | 0.20 | 0.35 | ... | 0.83 | 0.19 | 0.45 | 0.30 | 0.11 | 0.11 |
| Rear udder width | 0.69 | 0.22 | 0.32 | 0.59 | 0.14 | -0.05 | 0.34 | 0.04 | 0.38 | 0.23 | 0.70 | ... | -0.17 | 0.48 | 0.35 | 0.15 | 0.15 |
| Udder depth | 0.13 | 0.06 | -0.07 | -0.22 | 0.07 | -0.06 | -0.15 | -0.15 | -0.04 | 0.48 | 0.14 | -0.04 | ... | -0.09 | 0.16 | -0.16 | -0.16 |
| Udder cleft | 0.48 | 0.07 | 0.11 | 0.26 | 0.09 | 0.01 | 0.14 | 0.01 | 0.13 | 0.16 | 0.35 | 0.34 | 0.10 | ... | 0.43 | 0.21 | 0.21 |
| Front test placement | 0.42 | 0.05 | 0.11 | 0.16 | 0.07 | 0.01 | 0.12 | -0.02 | 0.12 | 0.30 | 0.25 | 0.27 | 0.22 | 0.35 | ... | -0.10 | -0.10 |
| Test length | 0.12 | 0.18 | 0.17 | 0.11 | 0.06 | -0.03 | 0.16 | 0.03 | 0.16 | 0.01 | 0.08 | 0.12 | -0.08 | 0.12 | -0.04 | ... | ... |

except that dairy form (dairy character) and rear legs (rear legs set) of Australian Jerseys tended to be more closely linked to individual udder traits. However, different trait definitions for the two populations make direct comparisons difficult.

CONCLUSIONS

(Co)variance components were estimated for type traits of US Jersey cattle. Because there were repeated records, approximate multiple diagonalization was used to allow for three random effects (permanent environment, genetic, and residual) in the model. Through this method, 16 related traits were transformed to 16 uncorrelated traits. After diagonalization, relative off-diagonals, a measure of the success of the approximation, were extremely small (<0.1%). Heritabilities and repeatabilities generally were different from those currently used for USDA genetic evaluations. Heritabilities often were higher, and repeatabilities often were lower, which reflected smaller permanent environmental variances. Heritabilities and repeatabilities were similar to those reported for Holsteins by Misztal et al. (10), who also used multiple diagonalization. Correlations, however, showed specific differences between Holsteins and Jerseys. Such differences also existed between Jersey populations in the US and Australia. Genetic parameters, especially correlations, should be estimated for every breed and country to avoid biasing genetic evaluations as a result of inappropriate (co)variance components.

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