

Application of Canonical Transformation with Missing Values to Multitrait Evaluation of Jersey Type

N. GENGLER,* G. R. WIGGANS,^{†,1} J. R. WRIGHT,[†]
H. D. NORMAN,[†] and C. W. WOLFE[‡]

*Fonds National Belge de la Recherche Scientifique, Unité de Zootechnie, Faculté Universitaire des Sciences Agronomiques, B-5030 Gembloux, Belgium

[†]Animal Improvement Programs Laboratory, Agricultural Research Service, USDA, Beltsville, MD 20705-2350

[‡]American Jersey Cattle Association, Reynoldsburg, OH 43068-2362

ABSTRACT

A multitrait animal model was used to calculate predicted transmitting ability and reliabilities for final score and 15 linear type traits of 225,632 US Jersey cows. Records were adjusted for age and stage of lactation before analysis. The model contained effects for interactions of herd and date scored; year scored, parity, and age; and herd and sire; effects of permanent environment and additive genetics were also included. Of the 381,511 records included, some observations were missing for final score (8%), body depth (43%), and teat length (33%). The evaluation system used a canonical transformation, included several random effects, and estimated missing values with each iteration. Inbreeding was considered in the computations. Convergence was achieved in approximately 50 rounds of iteration. Correlations between animal and sire model predicted transmitting ability ranged from 0.56 to 0.95 and generally were higher for bulls than for cows and for more recent birth years. Genetic trend was strongly positive for dairy form, final score, and rear udder traits (height and width) and negative for udder depth. For other traits, genetic trend was small. This methodology should improve the accuracy of genetic evaluations for type traits of US Jerseys.

(**Key words:** Jersey, type traits, genetic evaluation, canonical transformation)

Abbreviation key: AJCA = American Jersey Cattle Association.

INTRODUCTION

The American Jersey Cattle Association (AJCA) scores 15 linear type traits: 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. A final score is calculated for all scored cattle, but breeders can request that an appraiser also assign final scores for all scored cows. Genetic evaluations for type traits have used single-trait sire models (13). Because the linear scoring system used by AJCA allows for repeated scoring of cattle, a repeatability model has been used. The current evaluation system uses all scores but gives a low weight (0.1) to scores after second lactation because those are optional. The PTA for cows are derived from the sire model using the approach described by Weller et al. (17).

Recent advances in genetic evaluations for type have included multitrait analysis and use of animal models (10). Computational requirements can be greatly reduced with canonical transformation, the most common approach for simultaneous genetic evaluation of more than one trait (6). This method transforms the initial, correlated traits to uncorrelated, canonical traits. Recent enhancements in this transformation method have been multiple diagonalization (generalization of canonical transformation to several random effects rather than only additive genetic effects) (3, 7, 11) and an expectation-maximization algorithm that permits the use of this approach even if observations for some traits are missing for some cows (2). Inbreeding coefficients now can be calculated and used in genetic evaluations for large populations (16, 20). The objective of this study was to use these advanced methods to evaluate US Jersey cows for genetic merit of type traits.

MATERIALS AND METHODS

Data

Scores for type traits were provided by AJCA. Linear type scoring began on January 1, 1980, and only data since then were included. Final score as-

Received December 26, 1996.

Accepted April 9, 1997.

¹Reprint requests.

TABLE 1. Distribution of type records of US Jersey cows by scoring year and trait.

Scoring year	Total records	Records with trait		
		Final score	Body depth	Teat length
		(no.)		
1980	7965	7965	0	0
1981	7808	7808	0	0
1982	11,153	11,153	0	0
1983	11,553	11,553	0	0
1984	23,353	23,353	0	0
1985	26,545	26,545	0	0
1986	24,289	24,289	0	0
1987	27,615	27,611	0	13,330
1988	25,624	25,065	33	25,620
1989	30,341	23,624	30,341	30,341
1990	31,945	26,239	31,945	31,945
1991	28,492	24,046	28,492	28,492
1992	31,264	28,167	31,264	31,264
1993	29,416	25,345	29,416	29,416
1994	32,264	28,173	32,264	32,264
1995	31,884	29,639	31,884	31,884
All years	381,511	350,575	215,639	254,556

signed by the appraiser was used instead of final score calculated by AJCA. Calculated final score was not included as a trait because it would not add information to a multitrait model that included the linear traits on which the final score was based. At least one score during first lactation (age <39 mo at first calving) was required. Scores after second lactation (age between 29 and 45 mo at second calving) were excluded; 381,511 records for 225,632 cows remained. Not all of the 16 traits were assigned for every record. Table 1 shows the distribution of observations across years and traits. Scoring started in 1988 for body depth and in 1987 for teat length. Final score assigned by the appraiser became optional in 1987 and has been missing from about 10 to 15% of records since then. Overall, observations were missing from 8% of records for final score, 43% for body depth, and 33% for teat length. There were 14,812 combinations of herd and date scored.

Type scores were adjusted for age and lactation stage with USDA multiplicative adjustment factors. Table 2 presents the means and standard deviations for the 16 traits after adjustment. Final score is expressed on a scale between 50 and 99; linear type traits are expressed on a scale between 1 and 50. Means for adjusted scores ranged from 22.0 for teat length to 30.9 for rear udder height; standard deviations ranged from 6.2 for teat length and thurl width to 7.9 for fore udder attachment.

Pedigrees were extracted from the USDA national database of lactation records. After elimination of animals without a type score and not related to at

least two other animals with type scores, 463,787 animals remained.

Model

A multitrait animal model for missing data was applied:

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

where \mathbf{y} = vector of type records; \mathbf{h} = vector of fixed effects of the interaction of herd and date scored (herd-date effect); \mathbf{c} = vector of fixed effects of the

TABLE 2. Means and standard deviations of type traits of US Jersey cows adjusted for age and lactation stage.

Trait	Records	\bar{X}	SD
	(no.)		
Final score	350,575	78.0	6.8
Stature	381,511	26.1	6.9
Strength	381,511	28.2	6.9
Dairy form	381,511	30.8	7.5
Foot angle	381,511	21.3	6.6
Rear legs (side view)	381,511	28.5	6.8
Body depth	215,639	28.9	6.5
Rump angle	381,511	26.7	6.5
Thurl width	381,511	27.6	6.2
Fore udder attachment	381,511	27.1	7.9
Rear udder height	381,511	30.9	6.5
Rear udder width	381,511	29.9	6.3
Udder depth	381,511	27.9	7.6
Udder cleft	381,511	28.6	6.2
Front teat placement	381,511	22.8	6.8
Teat length	254,556	22.0	6.2

TABLE 3. Estimated heritabilities and assumed variances for permanent environment and interaction of herd and sire relative to total variance for US Jersey type traits.

Trait	Heritability	Relative variance	
		Permanent environment	Herd-sire interaction
Final score	0.293	0.112	0.075
Stature	0.399	0.104	0.070
Strength	0.264	0.076	0.051
Dairy form	0.277	0.089	0.060
Foot angle	0.128	0.073	0.049
Rear legs (side view)	0.133	0.070	0.047
Body depth	0.273	0.081	0.054
Rump angle	0.314	0.121	0.080
Thurl width	0.223	0.065	0.044
Fore udder attachment	0.218	0.083	0.055
Rear udder height	0.275	0.110	0.073
Rear udder width	0.260	0.093	0.062
Udder depth	0.323	0.093	0.062
Udder cleft	0.199	0.098	0.065
Front teat placement	0.286	0.106	0.071
Teat length	0.306	0.106	0.071

interaction of year scored, parity, and age (year-parity-age effect); \mathbf{s} = vector of random effects of interaction of herd and sire (herd-sire effect); \mathbf{p} = vector of random effects of permanent environment; \mathbf{u} = vector of random additive genetic effects of animals and genetic groups; \mathbf{X} , \mathbf{H} , \mathbf{S} , \mathbf{Z} , and \mathbf{Z}^* = incidence matrices associating \mathbf{h} , \mathbf{c} , \mathbf{s} , \mathbf{p} , and \mathbf{u} , respectively, with \mathbf{y} ; and \mathbf{e} = vector of random residual effects.

Year-parity-age effect \mathbf{c} was included in the model because of concerns in recent years about the accuracy of estimates of genetic trend (1) that are related to problems with age adjustment and changes in maturity rates (19). Records were divided into 24 groups based on year scored (prior to 1983, 1983 through 1987, 1988 through 1992, and after 1992), parity (first or second lactation), and age within parity (<27 mo, 27 to 31 mo, and >31 mo for first lactation; <39 mo, 39 to 43 mo, and >43 mo for second lactation). Age adjustments had been changed on January 1, 1988; therefore, 1988 was chosen as a boundary for grouping of years scored. This approach is similar to the method used for US yield evaluations (19).

Herd-sire effect \mathbf{s} was included in the model to limit the effect of a single herd on a bull evaluation. A total of 70,281 groups were created to account for the interaction of herd and sire.

Genetic effects were defined as $\mathbf{u} = \mathbf{a} + \mathbf{Qg}$, where \mathbf{a} = vector of random additive genetic effects of animals expressed as deviations from group means, \mathbf{g} = vector of fixed effects of genetic group, and \mathbf{Q} = incidence matrix that links \mathbf{g} with \mathbf{u} . To account for differences in mean genetic merit of unknown ancestors as proposed by Westell et al. (18), 18 genetic groups were defined based on birth year (prior to 1961, 1961 to 1962, ..., 1991 to 1992, and after 1992).

(Co)variance Components

(Co)variance components were estimated by Gengler et al. (5) from a subset of the data with recent scores and no missing values by multiple diagonalization using a similar multitrait model but without a herd-sire effect. Of the estimated (co)variance matrix for permanent environment from their analysis, 40% was assigned to herd-sire interaction and the remainder to permanent environmental (co)variance matrix. This approach generated a herd-sire variance that was somewhat less than the 10% of total variance used with the previous sire model (13) and the 9% of total variance used by Holstein Association USA (Brattleboro, VT) with its current animal model for type traits (10). Table 3 shows the heritabilities and relative variances for permanent environment and interaction of herd and sire.

Computation of Solutions and Reliability

Solutions using a multitrait model and data with missing values were obtained with a canonical transformation that had been adapted to include several random effects (2, 4). Multiple diagonalization was used to diagonalize the four (co)variance matrices simultaneously. Using this transformation, the 16 correlated traits were transformed to 16 uncorrelated traits. Missing values were estimated during the iteration on the data (2) without backtransformation. When missing values for a transformed trait were updated, the most recently available solutions for other traits were used. Within a trait, second-order

Jacobi iteration (8, 9) was used because it does not require several sorted files as does Gauss-Seidel iteration (15). Inbreeding was included in the construction of the inverse of the relationship matrix using the method for US yield evaluations (20). If known, prior solutions were used to speed convergence. Squared relative change across the 16 transformed traits was the convergence criterion. Solutions on the original scale were obtained by backtransformation.

To account for missing values when reliability was computed, single-trait prediction error variances were computed for transformed traits (10, 12) using the reduction of information for missing values in original traits (4). Multitrait reliabilities were obtained through backtransformation (10).

Genetic Base

Solutions for additive genetic effects were expressed as PTA (half the estimates of \mathbf{u}) relative to the mean PTA for all cows born in 1990. This base was chosen because it was similar to the base used for yield traits in the US and in several other countries.

RESULTS AND DISCUSSION

Computational Environment

Computations were done on an IBM RISC System 6000 (Model 560; IBM Corp., Armonk, NY) workstation with 512 MB of memory. One round of itera-

TABLE 4. Solutions for effect of interaction of year scored, parity, and age for US Jersey type traits expressed as deviations from mean solutions for effect of parity and age within time period.

Years, parity, and age	Solutions for type traits ¹															
	FS	ST	SR	DF	FA	RL	BD	RA	TW	FU	RH	RW	UD	UC	TP	TL
Before 1983																
Parity 1																
<27 mo	-0.4	-0.2	-0.3	-0.1	0.1	0.0	-0.1	0.0	0.0	0.0	0.0	-0.2	0.3	-0.1	0.0	0.1
27 to 31 mo	0.0	0.1	-0.1	0.0	0.1	0.0	0.1	0.0	0.3	0.0	0.2	0.1	0.2	0.0	0.0	0.0
>31 mo	0.1	0.2	0.2	0.1	0.1	0.0	0.1	0.0	0.2	0.2	0.0	0.1	0.2	0.0	0.0	0.1
Parity 2																
<39 mo	0.3	-0.3	-0.2	0.2	-0.1	0.0	0.0	0.0	-0.1	-0.1	0.0	0.3	-0.4	0.2	-0.2	-0.1
39 to 43 mo	0.1	0.2	0.0	0.0	0.0	0.0	0.0	0.0	-0.1	-0.2	0.0	0.0	-0.1	0.0	0.1	0.0
>43 mo	0.1	0.1	0.3	-0.1	-0.1	-0.1	-0.1	0.1	-0.4	-0.1	0.0	-0.2	-0.1	-0.1	0.0	0.0
1983 to 1987																
Parity 1																
<27 mo	-0.3	-0.1	0.3	-0.2	0.1	-0.4	-0.3	0.1	-0.6	0.8	0.1	-0.2	1.2	-0.2	-0.3	-2.0
27 to 31 mo	-0.4	0.0	-0.2	-0.4	0.1	0.1	-0.3	0.0	-0.5	0.6	-0.1	-0.3	0.5	-0.1	0.1	-1.1
>31 mo	-0.3	0.1	0.0	-0.4	0.2	0.1	-0.1	-0.1	-0.1	0.5	-0.1	-0.5	0.2	0.0	0.3	-0.5
Parity 2																
<39 mo	0.4	0.1	0.0	0.2	-0.1	-0.1	0.2	0.0	0.3	-0.4	0.2	0.3	-0.4	0.2	-0.1	1.1
39 to 43 mo	0.2	-0.1	-0.3	0.3	-0.1	0.1	0.1	0.0	0.3	-0.8	0.1	0.3	-0.8	0.0	-0.1	1.4
>43 mo	0.3	-0.1	0.0	0.4	0.0	0.1	0.3	-0.2	0.7	-0.7	0.0	0.2	-0.8	0.0	0.0	1.2
1988 to 1992																
Parity 1																
<27 mo	0.3	-0.2	-0.4	0.2	-0.2	-0.1	-0.3	0.6	-0.4	-0.2	0.0	-0.1	-0.5	-0.3	-0.3	0.0
27 to 31 mo	-0.1	0.1	-0.1	-0.1	0.0	0.0	-0.1	0.2	-0.1	-0.1	-0.1	0.0	-0.5	0.0	0.0	-0.1
>31 mo	-0.1	-0.1	0.0	0.0	0.1	0.0	0.0	0.7	0.0	-0.3	0.0	0.1	-1.7	-0.2	-0.3	-0.2
Parity 2																
<39 mo	-0.2	0.4	0.2	-0.4	-0.1	0.0	0.2	-2.0	0.2	0.9	-0.2	-0.2	3.7	0.6	0.9	0.3
39 to 43 mo	-0.1	0.0	0.2	0.0	0.1	0.1	0.1	-0.3	0.2	0.2	0.0	0.0	0.3	0.1	0.2	0.0
>43 mo	0.1	-0.3	-0.1	0.3	0.0	0.0	-0.1	0.6	0.1	-0.5	0.2	0.3	-1.4	-0.1	-0.6	-0.1
After 1992																
Parity 1																
<27 mo	0.8	-0.4	-0.4	0.6	0.5	-0.4	-0.2	0.7	-0.3	0.3	-0.2	0.0	0.6	-0.3	-0.2	-0.4
27 to 31 mo	0.4	-0.1	-0.2	0.5	0.2	-0.1	-0.1	0.3	0.0	0.0	0.0	0.2	0.0	0.0	0.0	-0.2
>31 mo	0.1	-0.2	-0.2	0.3	0.0	0.0	-0.4	0.8	-0.1	-0.5	0.2	0.3	-1.2	-0.2	-0.4	-0.3
Parity 2																
<39 mo	-0.6	0.7	0.5	-1.0	-0.4	0.0	0.6	-2.0	0.4	1.0	-0.5	-0.5	2.9	0.5	1.0	0.5
39 to 43 mo	-0.3	0.3	0.2	-0.4	-0.2	0.2	0.1	-0.3	0.2	0.0	0.1	-0.1	-0.2	0.1	0.2	0.1
>43 mo	-0.4	-0.1	0.1	0.1	-0.3	0.2	0.0	0.6	0.0	-0.1	0.5	0.3	-1.9	0.0	-0.5	0.2

¹FS = Final score, ST = stature, SR = strength, DF = dairy form, FA = foot angle, RL = rear legs (side view), BD = body depth, RA = rump angle, TW = thurl width, FU = fore udder attachment, RH = rear udder height, RW = rear udder width, UD = udder depth, UC = udder cleft, TP = front teat placement, and TL = teat length.

TABLE 5. Means, standard deviations, minimums, and maximums for multitrait animal model PTA¹ and reliabilities for type traits of 363,145 US Jersey cows born since 1971.

Trait	PTA				Reliability		
	\bar{X}	SD	Minimum	Maximum	\bar{X}	SD	Maximum
Final score	-0.93	1.19	-6.4	4.8	0.46	0.15	0.89
Stature	0.00	1.31	-7.1	6.7	0.51	0.17	0.91
Strength	0.06	0.92	-5.5	4.9	0.47	0.15	0.89
Dairy form	-1.37	1.49	-7.9	6.3	0.47	0.15	0.89
Foot angle	0.15	0.63	-3.4	3.1	0.38	0.12	0.85
Rear legs (side view)	-0.25	0.69	-4.0	3.8	0.36	0.11	0.85
Body depth	-0.09	0.92	-6.1	4.7	0.47	0.15	0.89
Rump angle	-0.10	1.06	-5.6	5.5	0.46	0.15	0.90
Thurl width	-0.15	0.79	-4.7	3.7	0.46	0.15	0.89
Fore udder attachment	-0.02	1.01	-6.2	4.7	0.45	0.14	0.88
Rear udder height	-0.86	1.07	-6.8	4.9	0.44	0.14	0.89
Rear udder width	-0.93	1.07	-5.7	4.4	0.45	0.15	0.89
Udder depth	0.37	1.23	-7.5	7.1	0.49	0.16	0.90
Udder cleft	-0.23	0.76	-4.6	4.4	0.41	0.13	0.87
Front teat placement	-0.19	1.05	-5.8	5.7	0.44	0.14	0.89
Teat length	0.18	0.93	-5.1	7.2	0.46	0.15	0.89

¹Genetic base was all cows born in 1990.

tion (16 × 774,554 estimations) required approximately 23 min. The exact number of rounds that were needed to obtain convergence was not available because solutions from a preliminary analysis were used as starting values. Theoretically, slightly over 50 rounds of iteration would have been needed to obtain a relative squared difference of approximately 10⁻⁸. Use of prior solutions reduced the number of rounds of iteration required by about 15. After diagonalization, the low relative off-diagonals (ratio of squared off-diagonals to the product of diagonals) of 0.036% for herd-sire and permanent environment and 0.012%

for genetic covariance matrices indicated the success of the multiple diagonalization.

Effects of Year Scored, Parity, and Age

To allow comparison across time periods, solutions for year-parity-age effect (Table 4) were expressed as deviations from mean solutions for parity-age within a time period. Solutions for more recent time periods would have been inflated because of confounding with herd-date effect. Range of solutions was >1.0 for final score, stature, dairy form, rump angle, fore udder

TABLE 6. Means, standard deviations, minimums, and maximums for multitrait animal model PTA¹ and reliabilities for type traits of 11,982 US Jersey bulls born since 1971.

Trait	PTA				Reliability		
	\bar{X}	SD	Minimum	Maximum	\bar{X}	SD	Maximum
Final score	-1.01	1.11	-5.3	4.2	0.45	0.20	0.99
Stature	0.01	1.22	-4.8	5.3	0.48	0.21	0.99
Strength	0.04	0.83	-4.0	3.4	0.46	0.20	0.99
Dairy form	-1.65	1.50	-6.7	5.9	0.46	0.20	0.99
Foot angle	0.21	0.60	-2.5	3.1	0.39	0.18	0.99
Rear legs (side view)	-0.31	0.69	-3.2	3.6	0.38	0.18	0.99
Body depth	-0.14	0.83	-4.4	3.4	0.46	0.20	0.99
Rump angle	-0.32	1.01	-4.5	4.4	0.45	0.20	0.99
Thurl width	-0.16	0.71	-3.6	2.8	0.45	0.20	0.99
Fore udder attachment	0.23	1.00	-5.3	5.0	0.44	0.20	0.99
Rear udder height	-0.94	0.99	-5.8	3.9	0.44	0.20	0.99
Rear udder width	-1.06	1.02	-5.0	4.0	0.45	0.20	0.99
Udder depth	0.68	1.16	-7.0	6.3	0.47	0.20	0.99
Udder cleft	-0.30	0.71	-3.2	2.6	0.42	0.19	0.99
Front teat placement	-0.06	0.96	-4.0	5.2	0.44	0.20	0.99
Teat length	0.14	0.87	-4.3	6.7	0.45	0.20	0.99

¹Genetic base was all cows born in 1990.

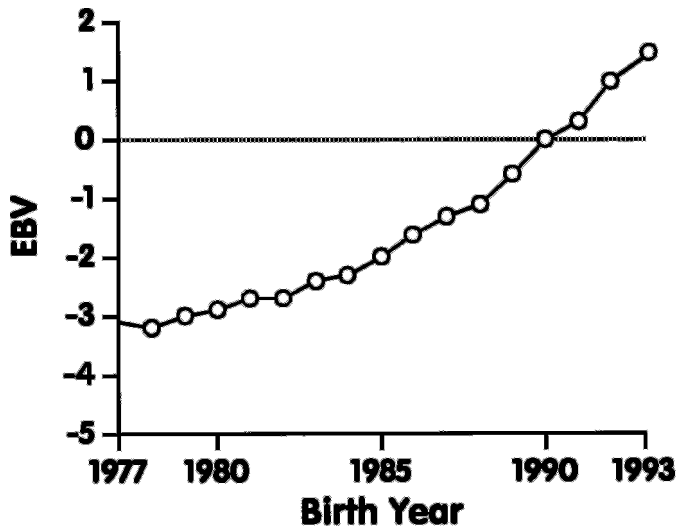


Figure 1. Genetic trend for final score of US Jersey cows born during 1977 through 1993.

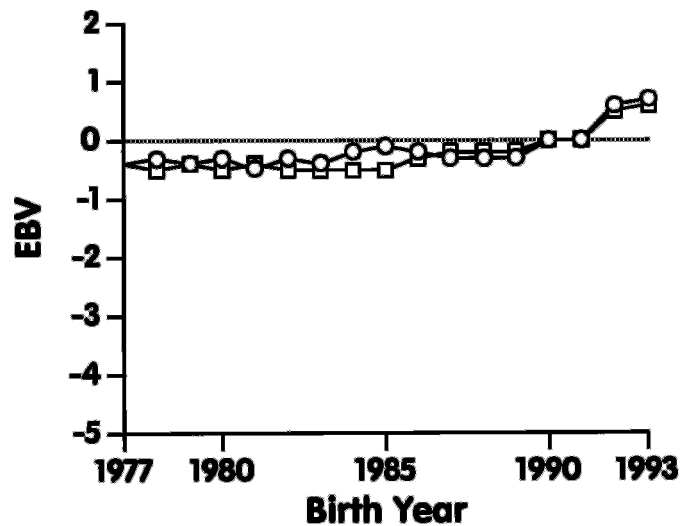


Figure 3. Genetic trend for rump traits of US Jersey cows born during 1977 through 1993: rump angle (○) and thurl width (□).

attachment, udder depth, and front teat placement for scores after 1992; for rump angle, fore udder attachment, and front teat placement for scores from 1988 through 1992; and for thurl width, udder depth, and teat length for scores from 1983 through 1987. The most extreme ranges were observed for udder depth after 1987 (5.4 for scores from 1988 through 1992 and 4.8 for scores after 1992). These differences reflect lack of fit of current age adjustments. Importance of this effect could be reduced somewhat by changing

the herd-date effect to a herd-date-parity effect. Because an age effect was included in the analysis, the evaluations were not biased by age differences.

PTA

Means, standard deviations, minimums, and maximums for multitrait animal model PTA and their reliabilities are shown in Table 5 for cows and in Table 6 for bulls. For 363,145 cows born since 1971 (Table 5), final score had a mean PTA of -0.93 (standard deviation of 1.19) and a mean reliability of 0.46 (standard deviation of 0.15). For linear type traits of cows, mean PTA ranged from -1.37 for dairy form to 0.37 for udder depth; standard deviations for PTA ranged from 0.63 for foot angle to 1.49 for dairy form. Mean reliabilities for cow PTA ranged from 0.36 for rear legs to 0.51 for stature (standard deviations from 0.11 for rear legs to 0.17 for stature). These results reflected the different heritabilities of the traits. For 11,982 bulls born since 1971 (Table 6), mean PTA and reliability and their standard deviations for final score were similar to those for cows. For linear type traits, mean PTA of bulls ranged from -1.65 for dairy form to 0.68 for udder depth; mean reliabilities ranged from 0.38 for rear legs to 0.48 for stature. For bulls, standard deviations for both PTA and reliability were somewhat lower than those for cows. No minimum number of daughters was imposed for bulls.

Correlations between PTA with and without inbreeding considered were high (>0.99). However, when inbreeding was considered, some PTA changed by up to 0.2, which caused some rerankings.

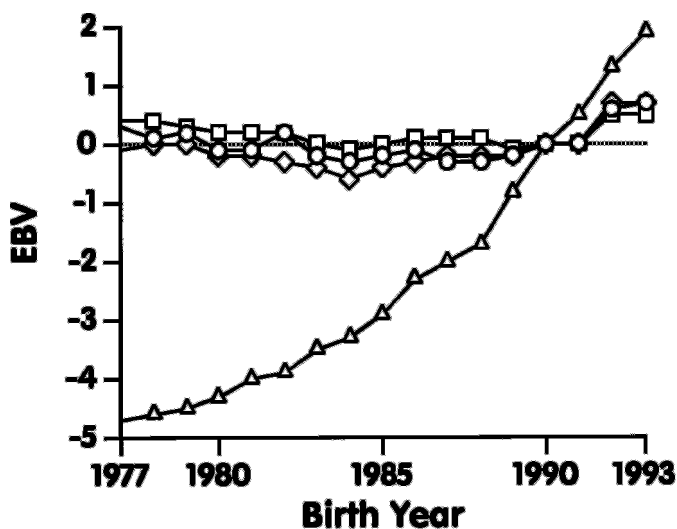


Figure 2. Genetic trend for body form traits of US Jersey cows born during 1977 through 1993: stature (○), strength (□), dairy form (△), and body depth (◇).

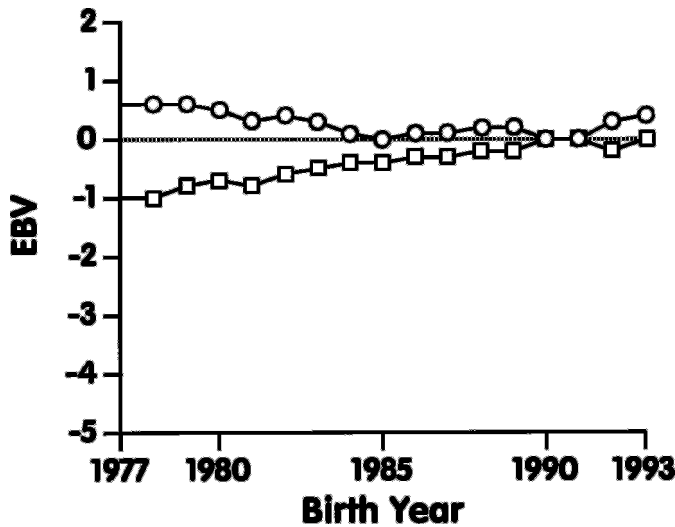


Figure 4. Genetic trend for feet and leg traits of US Jersey cows born during 1977 through 1993: foot angle (○) and rear legs (side view) (□).

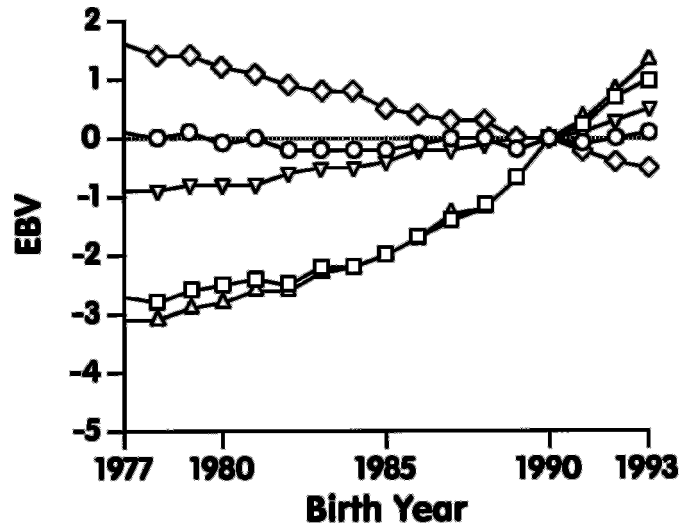


Figure 5. Genetic trend for udder traits of US Jersey cows born during 1977 through 1993: fore udder attachment (○), rear udder height (□), rear udder width (△), udder depth (◇), and udder cleft (▽).

Comparison of Multitrait Animal and Sire Models

Correlations of multitrait animal model and sire model PTA were calculated by birth year (Table 7) for US Jersey cows and bulls with >40 progeny. For cows, no correlations were computed for body depth and teat length because sire model PTA were not available for those traits. Correlations increased over time and were higher for bulls with >40 progeny than

for cows born during the same years. Traits with missing values generally had lower correlations than did other traits; correlations for final score decreased slightly for bulls born after 1984, and correlations for body depth and teat length were lower for bulls born before 1980.

Differences between solutions from multitrait animal and sire models could have been caused by differences in 1) data included, 2) use of information

TABLE 7. Correlations between PTA from multitrait animal and sire models for US Jersey type traits by birth year of animal.

Trait	Birth year							
	Cows			Bulls with >40 progeny				
	1975 to 1979 (n = 30,739)	1980 to 1984 (n = 70,923)	After 1984 (n = 147,856)	1970 to 1974 (n = 181)	1975 to 1979 (n = 188)	1980 to 1984 (n = 231)	After 1984 (n = 192)	
Final score	0.56	0.76	0.88	0.67	0.82	0.91	0.88	
Stature	0.67	0.86	0.92	0.83	0.90	0.93	0.95	
Strength	0.62	0.81	0.87	0.79	0.83	0.91	0.91	
Dairy form	0.59	0.79	0.90	0.74	0.83	0.93	0.90	
Foot angle	0.65	0.82	0.88	0.73	0.81	0.85	0.88	
Rear legs (side view)	0.65	0.86	0.89	0.82	0.81	0.88	0.90	
Body depth	0.50	0.63	0.82	0.92	
Rump angle	0.69	0.83	0.91	0.85	0.91	0.93	0.93	
Thurl width	0.56	0.77	0.84	0.76	0.84	0.91	0.90	
Fore udder attachment	0.64	0.77	0.83	0.76	0.86	0.91	0.88	
Rear udder height	0.61	0.80	0.91	0.74	0.86	0.91	0.91	
Rear udder width	0.58	0.78	0.90	0.71	0.84	0.89	0.90	
Udder depth	0.61	0.71	0.83	0.79	0.83	0.89	0.86	
Udder cleft	0.66	0.84	0.88	0.81	0.87	0.88	0.89	
Front teat placement	0.63	0.85	0.91	0.81	0.87	0.92	0.92	
Teat length	0.78	0.80	0.77	0.75	

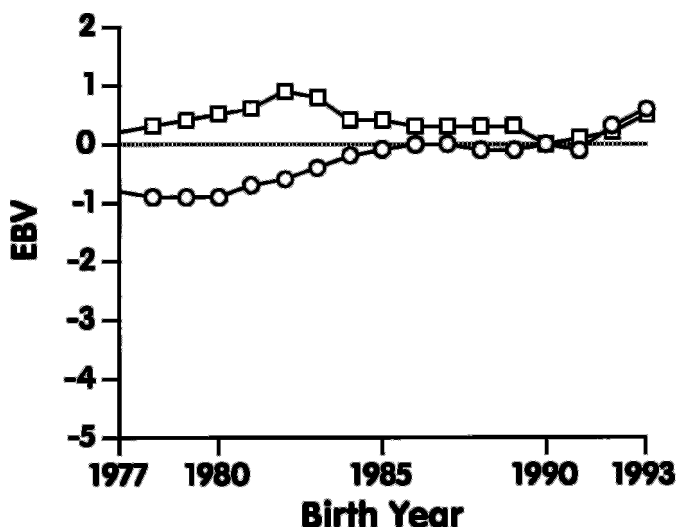


Figure 6. Genetic trend for teat traits of US Jersey cows born during 1977 through 1993: front teat placement (\circ) and teat length (\square).

from relatives, 3) effect of one trait on correlated traits, 4) genetic parameters, 5) use of unknown-parent groups, or 6) consideration of inbreeding. For the multitrait animal model, no appraisals before 1980 or after second lactation were included, and a score during first lactation was required. In addition, no calculated final scores were included in animal model evaluations; for cows with missing final scores, PTA were based on pedigree and correlated traits. All relatives affected animal model evaluations; sons and dams contributed to bulls, and progeny contributed to cows. Because animal model PTA resulted from a multitrait analysis, information from one trait affected PTA of all correlated traits. Heritabilities were higher, and repeatabilities were lower, for the animal model (5) than for the sire model. The animal model included unknown-parent groups, which were assigned by birth year and should enable better estimation of genetic trend. The inverse of the relationship matrix for the animal model was constructed with inbreeding considered. Even though the overall effect of including inbreeding was low, some animals with high inbreeding coefficients were reranked.

Genetic Trend

Genetic trends were computed from EBV ($2 \times$ PTA) for 302,219 cows born between 1977 and 1993. The EBV rather than PTA was used because EBV is the total estimated genetic merit of an animal, not just the half that is transmitted to a descendant. Earlier birth years were not considered because cow records were not available. Figures 1 through 6 show

the genetic trend for type traits of US Jersey cows. For final score (Figure 1), genetic trend was greatest during the most recent years. For type traits related to body form (Figure 2), genetic trend was observed only for dairy form, but no trend was observed for the other traits (stature, strength, and body depth), except for a slight increase during 1992 and 1993. Also, no change in genetic merit, except during 1992 and 1993, was apparent for rump traits (Figure 3). For feet and leg traits (Figure 4), EBV for foot angle decreased until 1990 and then began to increase slightly. The EBV for rear legs increased slightly over time; rear legs tended to become more sickled. Genetic trends for udder traits (Figure 5) generally were larger than for other traits. Rear udder traits showed an important positive genetic trend, and udder cleft showed a moderate, positive trend. Udder depth EBV decreased steadily, which is an unfavorable trend. Because udder depth receives the most weight in the functional type trait index of AJCA, its negative trend probably reflects its negative genetic correlation of -0.59 with milk yield (14). Fore udder attachment showed no genetic trend. For teat traits (Figure 6), a modest trend toward closer teats was found for front teat placement, but no genetic trend was found for teat length.

Quadratic regression equations were fit for mean EBV by birth year. If the quadratic effect was nonsignificant ($P < 0.05$), a linear equation was used. The difference between the mean EBV of cows born during 1992 and 1993 indicates recent genetic trend (Table 8), and results are similar to the trend shown in

TABLE 8. Differences between EBV of cows born in 1992 and 1993 (trend) from linear or quadratic fit of mean EBV by birth year for type traits of 302,219 US Jersey cows born during 1977 through 1993.

Trait	Trend ¹	Equation	R ²
Final score	0.55	Quadratic	99.8
Stature	0.18	Quadratic	67.8
Strength	0.10	Quadratic	59.7
Dairy form	0.77	Quadratic	99.7
Foot angle	0.06	Quadratic	75.3
Rear legs (side view)	0.02	Quadratic	96.5
Body depth	0.21	Quadratic	85.7
Rump angle	0.16	Quadratic	74.4
Thurl width	0.17	Quadratic	93.7
Fore udder attachment	0.05	Quadratic	36.1
Rear udder height	0.50	Quadratic	99.1
Rear udder width	0.52	Quadratic	99.6
Udder depth	-0.13	Linear	99.3
Udder cleft	0.12	Quadratic	97.3
Front teat placement	0.08	Linear	85.0
Teat length	-0.02 ²	Linear	12.9

¹Mean EBV of cows born during 1993 minus mean EBV of cows born during 1992.

²Nonsignificant ($P = 0.09$).

Figures 1 through 6. Genetic trend was greater for dairy form than for final score or rear udder traits. Almost no trend was evident for feet and leg traits and for fore udder attachment; the trend for udder depth was negative. The regression equations explained $\geq 60\%$ of total variance for all traits except fore udder attachment (36%) and teat length (13%), which were traits that showed no trend.

CONCLUSIONS

For linear type traits, canonical transformation can be used to transform correlated traits to uncorrelated traits to reduce computational requirements. This study showed that the extension of this approach to multiple random effects and missing values and to account for inbreeding in the inverse of the relationship matrix can be done at reasonable computer costs. An effect for stage of lactation could be included in the model to replace adjustment of records for stage of lactation but would complicate the model; addition of such an effect is being considered as a future enhancement to the model.

Comparison of animal and sire model evaluations showed large differences, especially for traits for which scoring was recently introduced. Correlations between animal and sire model PTA were higher for bulls than for cows and generally increased with later birth year. However, for teat length, which has missing values for earlier years, correlations generally decreased with later birth year.

Genetic trends were strongly positive for dairy form, final score, and rear udder traits. For most other traits, genetic trend was small, and a slight positive increase occurred during 1992 and 1993. The most important negative trend was for udder depth, which clearly tended toward deeper udders.

The methodology developed in this study for calculating PTA for type traits of dairy cattle should give US Jersey breeders the advanced tools they need to make more accurate genetic selections for final score and linear type traits.

ACKNOWLEDGMENTS

The authors acknowledge the financial support of AJCA and information from T. J. Lawlor, Holstein Association USA, and I. Misztal, University of Georgia. Manuscript review by R. E. Pearson, Virginia Polytechnic Institute and State University; G. W. Rogers, The Pennsylvania State University;

and S. M. Hubbard, Animal Improvement Programs Laboratory, ARS, USDA, is appreciated.

REFERENCES

- 1 Bonaiti, B., D. Boichard, A. Barbat, and S. Mattalia. 1993. Problems arising with genetic trend estimation in dairy cattle. Proc. Open Session INTERBULL Annu. Mtg., Aarhus, Denmark, August 19–20, 1993. Int. Bull. Eval. Serv. Bull. No. 8, Dep. Anim. Breed. Genet., SLU, Uppsala, Sweden.
- 2 Ducrocq, V., and B. Besbes. 1993. Solution of multiple trait animal models with missing data on some traits. *J. Anim. Breed. Genet.* 110:81.
- 3 Flury, B. N., and G. Constantine. 1985. Algorithm AS211: the F-G diagonalization algorithm. *Appl. Stat.* 34:177.
- 4 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.
- 5 Gengler, N., G. R. Wiggans, J. R. Wright, H. D. Norman, and C. W. Wolfe. 1997. Estimation of (co)variance components for Jersey type traits using a repeatability model. *J. Dairy Sci.* 80:1801.
- 6 Jensen, J., and I. L. Mao. 1988. Transformation algorithms in analysis of single trait and of multitrait models with equal design matrices and one random factor by trait: a review. *J. Anim. Sci.* 66:2750.
- 7 Lin, C. Y., and S. P. Smith. 1990. Transformation of multitrait to unitrait mixed model analysis of data with multiple random effects. *J. Dairy Sci.* 73:2494.
- 8 Misztal, I., and D. Gianola. 1987. Indirect solution of mixed model equations. *J. Dairy Sci.* 70:716.
- 9 Misztal, I., D. Gianola, and L. R. Schaeffer. 1987. Extrapolation and convergence criteria with Jacobi and Gauss-Seidel iteration in animal models. *J. Dairy Sci.* 70:2577.
- 10 Misztal, I., T. J. Lawlor, and T. H. Short. 1993. Implementation of single- and multiple-trait animal models for genetic evaluation of Holstein type traits. *J. Dairy Sci.* 76:1421.
- 11 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.
- 12 Misztal, I., and G. R. Wiggans. 1988. Approximation of prediction error variance in large-scale animal models. *J. Dairy Sci.* 71(Suppl. 2):27.
- 13 Norman, H. D., B. G. Cassell, G. J. King, R. L. Powell, and E. E. Wright. 1979. Sire evaluation for conformation of Jersey cows. *J. Dairy Sci.* 62:1914.
- 14 Norman, H. D., R. L. Powell, J. R. Wright, and B. G. Cassell. 1988. Phenotypic and genetic relationship between linear functional type traits and milk yield for five breeds. *J. Dairy Sci.* 71:1880.
- 15 Schaeffer, L. R., and B. W. Kennedy. 1986. Computing strategies for solving mixed model equations. *J. Dairy Sci.* 69:575.
- 16 VanRaden, P. M. 1992. Accounting for inbreeding and crossbreeding in genetic evaluation of large populations. *J. Dairy Sci.* 75:3136.
- 17 Weller, J. I., G. R. Wiggans, and T. J. Lawlor, Jr. 1987. Genetic evaluation of dairy goat does for milk and fat as an extension of buck evaluation. *J. Dairy Sci.* 70:681.
- 18 Westell, R. A., R. L. Quaas, and L. D. Van Vleck. 1988. Genetic groups in an animal model. *J. Dairy Sci.* 71:1310.
- 19 Wiggans, G. R., and P. M. VanRaden. 1994. Effect of including parity-age classes on estimated genetic trend for milk and component yields. *J. Dairy Sci.* 77(Suppl. 1):267.(Abstr.)
- 20 Wiggans, G. R., P. M. VanRaden, and J. Zuurbier. 1995. Calculation and use of inbreeding coefficients for genetic evaluation of United States dairy cattle. *J. Dairy Sci.* 78:1584.