

## Genetic Evaluations for Mixed-Breed Populations

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### ABSTRACT

An all-breed animal model was developed for routine genetic evaluations of US dairy cattle. Data sets from individual breeds were combined, and records from crossbred cows were included. About 1% of recent cows were first-generation crossbreds. The numbers of cows with records since 1960 ranged from 10 to 22 million for the 6 traits analyzed, which were milk, fat, protein, somatic cell score, productive life, and daughter pregnancy rate. Programs were modified to account for general heterosis, to group unknown parents separately by breed, to adjust variances separately by breed, and to adjust data to a 36-mo age equivalent instead of a mature equivalent. Convergence rate of the all-breed model was similar to that of the previous within-breed animal model. Estimated breed differences were similar to those obtained previously from phenotypic breed means or from studies of crossbred cows and their herd-mates. Genetic evaluations from the all-breed and within-breed systems had high correlations: >0.99 for recent Holsteins and slightly <0.99 for other breeds. Predicted transmitting abilities will be converted back to the within-breed bases for purebred animals and to the breed of sire base for crossbred animals so that most purebred breeders will not be affected by the change to a multibreed model. Evaluations of crossbred animals from the multibreed model can include accurate information for both parents. Reliabilities also increase for purebred relatives because of the additional crossbred records and in mixed breed herds because cows of other breeds are additional contemporaries. Another benefit of the multibreed model is that breed differences are routinely estimated and updated. More research and education may be needed on using the new evaluations in the design of breeding programs. Implementation is expected in May 2007.

**Key words:** genetic evaluation, multibreed, crossbreeding

### INTRODUCTION

Selection and mating systems across breeds can produce more profit than selection within breed if additive and nonadditive breed differences are well estimated. Most genetic evaluations have compared animals only within breeds. Exceptions for dairy cattle are the evaluations in New Zealand (Harris, 1994) and the Netherlands (Harbers, 1997; NRS, 2005). An all-breed model has also been used to evaluate US dairy goats since 1988 (Wiggans, 1989) and beef cattle in Ontario since 1994 (Sullivan et al., 1999). Across-breed evaluations could also be useful for poultry (Wei and van der Werf, 1995), swine (Lutaaya et al., 2002), and US beef cattle (Arnold et al., 1992; Pollak and Quaas, 2005).

Crossbreeding is of increasing interest to dairy producers and dairy geneticists (McAllister, 2002; Weigel and Barlass, 2003; Heins et al., 2006). Cole et al. (2005) included crossbred and purebred Brown Swiss and Holsteins in US evaluations for calving ease. The number of first-generation (**F1**) crossbred dairy cows with usable yield records was about 10,000 in 2001, the latest birth year with complete data. This exceeds the numbers of purebred Brown Swiss, Guernsey, Ayrshire, or Milking Shorthorn cows. Holsteins became popular in many countries because of superior milk production, but some crossbreds have economic merit that is comparable with purebred Holsteins and may exceed Holstein merit if calving ease, calf livability, cow fertility, and cheese yield pricing are considered.

Inclusion of data from crossbred animals can lead to more reliable evaluations of purebred relatives, more accurate comparisons of genetic merit among all potential mates, and improved breeding programs that identify the best gene combinations. Goals of this research were to compare methods for evaluating mixed-breed populations and then to apply the best methods for routine evaluation of US dairy cattle.

### MATERIALS AND METHODS

An all-breed animal model was applied to usable records from dairy cattle back to 1960, including records from crossbred cows. The total number of sire-identified cows with records was 22.6 million for milk and fat

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yield, 16.1 million for protein yield, 22.5 million for productive life (PL), 19.9 million for daughter pregnancy rate (DPR), and 10.5 million for SCS. The all-breed model developed was similar to that used for US goat evaluations (Wiggans, 1989). A main difference from the goat evaluation and the calving ease evaluation is that general heterosis is accounted for as in Harbers (1997). Estimates of heterosis were obtained from VanRaden and Sanders (2003) and were not reestimated in the present study. Modeling of specific heterosis (Harris, 1994) and recombination effects (Van der Werf and de Boer, 1989; Lidauer et al., 2006) would also be possible but was not attempted.

Pedigrees for 46,603,162 dairy cattle were traced to the earliest ancestors recorded electronically, with a lower birth year limit of 1950 because earlier ancestors were not stored. Most animals (99%) had ancestors of only 1 breed, but 431,000 had ancestors of >1 breed. Of those, >350,000 had breed compositions with <94% of 1 breed and >6% of another breed because the crossbreeding occurred within the most recent 4 generations of the pedigree. Beginning in November 2005, the percentage of primary breed was reported for bulls and cows with pedigrees that contain more than 1 breed.

Breed composition of the cows with first lactations in 2004 included 90.9% Holsteins, 6.2% Jerseys, 0.8% Brown Swiss, 0.4% Guernseys, 0.3% Ayrshires, <0.1% Milking Shorthorns, 1.2% F1 crossbreds (coefficients of heterosis >50%), and 0.3% backcross cows (coefficients of heterosis >25%). Nearly all F1 cows had Holstein as one parent breed, and contributions from the other breeds were proportional to population size as reported by VanRaden and Sanders (2003). The number of F1 crossbreds doubled in the last 3 yr. For bulls born since 1997, only 4 Jerseys and 1 Brown Swiss had >25 crossbred daughters, and each of these bulls had >200 purebred daughters. More recently, semen from Scandinavian Red and French breeds was imported and the resulting daughters are nearly all F1 crossbreds. Since 1987, over 5,000 herds had at least 1 crossbred cow, and currently 1,377 herds were coded as mixed-breed herds containing >25% crossbreds or cows of a different breed.

Unknown-parent groups in the animal model were separated by breed, pedigree path (dams of cows, sires of cows, and parents of sires), national origin (US or foreign), and birth year. Groups were formed when they included at least 500 animals within a time period and at least 2,000 animals across all years. The grouping pattern was similar to that for Dutch evaluations (NRS, 2005), except that they required only 40 animals per group. Larger numbers are needed for traits with lower heritability. Crossbred ancestors with no records and only 1 progeny were kept in the relationship matrix

**Table 1.** Standard deviation ratios used as variance adjustment factors for yield traits and daughter pregnancy rate

Breed	Yield	Daughter pregnancy rate
Ayrshire	0.72	0.94
Brown Swiss	0.94	0.99
Guernsey	0.87	0.97
Holstein	1.00	1.00
Jersey	0.89	0.94
Milking Shorthorn	0.71	0.91

and treated as known so that the system of equations could link to animals with records back to purebred ancestor groups.

Heterogeneous variance adjustments (Wiggans and VanRaden, 1991) were modified for all-breed analysis of production traits and DPR. For mixed-breed herds, variance within herd would be overestimated if no account were taken of breed differences. Variance adjustments for milk, fat, and protein were previously based on ratios of milk variances, but variances of fat yield were used in the all-breed analysis. Variance adjustments were not used for all-breed PL and SCS evaluations because they had not been used previously in official within-breed evaluations.

Means, sums of squared deviations, and degrees of freedom were accumulated separately within herd, year, and breed. Those variance estimates within herd, year, and breed were combined with estimates within region, year, and breed to produce final variance adjustment factors. The regional estimate acted as a prior and received credit equal to 20 degrees of freedom. Data for other breeds were adjusted to make genetic variance equal to Holstein base cows. Variance adjustment factors are reported in Table 1.

Age-parity-season adjustment factors have adjusted yield traits to mature equivalence. However, economic comparisons are more precise if records are adjusted to younger or more central ages, because more cows have records at those ages and maturity differences may be inherited (McDaniel, 1973). Multiplicative pre-adjustment factors of Schutz (1994) for each breed were rescaled to 36 mo of age. As a result, adjusted yields were lower by about 5% for Guernseys, 10% for Holsteins, Jerseys, and Ayrshires, and 15% for Brown Swiss and Milking Shorthorns. Sire breed was used to adjust crossbred records. Holstein factors were applied if the sire was crossbred or if the cow's breed was not among the 6 listed above.

Additional age-parity-region-time factors were included in the animal models to account for gradual changes that might occur after the multiplicative pre-adjustments for age-parity were developed in 1995. These

were estimated separately in the within-breed animal model from the data for each breed, but were estimated as uniform effects across breeds in the all-breed model. Recent age effects indicated that cows of all breeds are more productive at early ages relative to mature ages when compared with estimates from past decades, continuing the trend reported by Norman et al. (1995) for Holsteins. Multiplicative preadjustments may need to be updated in the future if relative maturity rates of breeds change.

Research to simultaneously estimate breed-age-parity-region-time effects in the all-breed model was abandoned because of very poor convergence or divergence and after learning that the Netherlands had attempted similar research, also with poor results (G. de Jong, NRS, Arnhem, the Netherlands; personal communication, 2006). Differences among breeds in recent residual age-parity effects were large only when comparing SCS of Holsteins to other breeds. These differences were corrected by applying multiplicative factors of 1.00, 1.00, 0.98, 0.96, and 0.94 for parities 1 to 5 of Holstein SCS data after the previous official age-parity factors were already applied. Simultaneous estimation might be possible for the largest breeds but not for all breeds.

Management groups in the within-breed evaluation were separate for registered and grade Holsteins if at least 5 cows of each type were present, whereas cows within the other breeds were grouped together regardless of registry status. In the all-breed evaluation, crossbreds were grouped together with registered or grade cows to allow estimation of breed differences. Crossbred cows sired by Holstein bulls were treated as grades, but all cows sired by bulls of other breeds were treated as purebreds and grouped with purebred cows. Management groups for herds that maintain separate herd codes for cows of different breeds in theory could be combined if the owner name and ZIP code match (Garcia-Peniche et al., 2005), but groups in the present study were combined only if herd codes matched. For within-breed evaluations, heritability of yield traits for Jerseys and Brown Swiss was higher (0.35) than for other breeds (0.30). For the all-breed model, the higher heritability for daughters of Jersey and Brown Swiss sires was accounted for by adjusting their lactation-length weights.

Convergence of solutions was tested by comparing results after 300 rounds of iteration to results after additional rounds. Priors for unknown-parent groups were set to 0 initially, and group solutions after 300 rounds were used as priors for remaining rounds. Final PTA from the all-breed system was compared with the official USDA within-breed PTA from August 2005. The comparisons were not exact because the all-breed analysis included about 2 mo more data for yield traits and

SCS, and about 1 mo more data for PL, than did August 2005 evaluations.

Separate evaluations that included information from crossbred cows based on sire breed were also tested and compared with the within-breed evaluations. In the within-breed system, information from crossbred cows was used only if it was recorded in a grading-up program of a breed association. In the sire-breed evaluation, information from all crossbred daughters was included, but their pedigrees were truncated at the nearest purebred ancestor of another breed; more distant ancestors of other breeds were treated as unknown because the data file based on sire breed included no information for them. The minimum number of unknown dams per birth-year group was reduced to 150; separate groups for less numerous breeds were not estimated but instead were assumed to equal the primary breed.

Evaluations from an all-breed model can be reported with different genetic base options and including or excluding heterosis. An all-breed base was calculated using the mean of all cows born in 2000. Within-breed bases were calculated from the PTA of cows with coefficients of heterosis of <50% (i.e., F1 and backcross cows were not included). The PTA for each breed was adjusted to the within-breed base, as is done for goat evaluations and for current dairy cattle evaluations. Evaluations for crossbred animals with breed code XX will be reported on the base of the sire breed, which may cause some confusion because evaluations of animals from reciprocal crosses will be on different bases.

Conversions between all-breed and within-breed bases involved both a mean and the standard deviation ratio from Table 1 for traits with variance adjustment that differed by breed:

$$\text{within-breed PTA} = (\text{all-breed PTA} - \text{breed mean}) \times (\text{breed SD}/\text{Holstein SD});$$

$$\begin{aligned} \text{all-breed PTA} = & \\ & (\text{within-breed PTA} \times \text{Holstein SD}/\text{breed SD}) \\ & + \text{breed mean.} \end{aligned}$$

The within-breed, sire-breed, and all-breed models compared can be described with notation similar to Wiggans (1989):

$$y - b_{\text{F}}\text{F} - b_{\text{H}}\text{H} = m + c + p + a + v + e;$$

where  $y$  is a record preadjusted for multiplicative factors to account for heterogeneous variance and for age, parity, season, lactation length, and number of times

**Table 2.** Breed differences from Holstein base estimated from an all-breed model, previously, and from national phenotypic means adjusted to 36 mo of age and previously estimated heterosis<sup>1</sup>

Source of estimate	Breed	Difference from Holstein					
		Milk, kg	Fat, kg	Protein, kg	SCS	Productive life, mo	Daughter pregnancy rate, %
All-breed EBV	Ayrshire	-2,390	-61	-59	-0.16	0.3	2.4
	Brown Swiss	-1,911	-36	-32	-0.10	0.8	1.1
	Guernsey	-2,776	-37	-62	0.07	-8.5	0.8
	Jersey	-2,962	-34	-47	0.19	3.2	5.5
	Milking Shorthorn	-3,230	-111	-90	-0.07	-2.2	4.5
Previous <sup>1</sup> EBV	Ayrshire	-2,118	-54	-53	-0.24	-1.0	1.8
	Brown Swiss	-1,914	-33	-29	-0.14	-0.6	0.2
	Guernsey	-3,014	-46	-70	-0.10	-6.0	2.0
	Jersey	-3,096	-33	-53	0.04	1.6	4.6
	Milking Shorthorn	-2,403	-83	-66	-0.12	-4.8	4.2
Phenotypic difference	Ayrshire	-2,988	-94	-80	-0.11	3.3	0.8
	Brown Swiss	-2,066	-44	-37	-0.15	1.9	-0.6
	Guernsey	-3,305	-65	-81	0.29	-1.3	-1.1
	Jersey	-3,115	-45	-54	0.26	4.9	5.0
	Milking Shorthorn	-3,819	-145	-109	0.12	1.5	3.3
Phenotypic mean	Holstein	10,480	382	315	3.07	28.1	25.5
Previous <sup>1</sup> heterosis	—	317	16	12	0.02	0.3	1.8

<sup>1</sup>VanRaden and Sanders (2003) estimates for all traits except daughter pregnancy rate, which was estimated by VanRaden et al. (2004).

milked daily that can vary by trait, time period, region, and breed; *m* is the management group mean; *c* is the interaction of herd with sire; *p* is the permanent environmental effect; *a* is the additive genetic effect; and *e* is the random residual. The animal model for bovines includes 3 new terms added since 1989: *v* is an age-parity-region-time effect (implemented in 1995); *b<sub>F</sub>F* is a regression of *y* on the cow's inbreeding coefficient (implemented in 2005); and *b<sub>H</sub>H* is a regression of *y* on the cow's coefficient of heterosis (used only in the all-breed model). The 3 models do not differ much in the terms they include, but rather in the data in *y*, the cows grouped in *m*, and the definitions of unknown-parent groups for missing ancestors in the relationship matrix.

## RESULTS

Additive genetic differences for breeds from the all-breed model were similar to previous estimates from national data (VanRaden and Sanders, 2003). The previous study included only herds containing crossbreds, whereas herds with multiple pure breeds but no crossbreds also contributed to breed comparisons in this study. Current estimates were also similar to breed phenotypic differences for yield traits of cows born during 2000. All 3 estimates are in Table 2 to provide confidence that estimated breed differences are reasonable. For PL and SCS, current estimates were more similar to phenotypic breed differences than to previous estimates. Reasons may be that previous PL estimates

were based on a previous definition of PL and cows that were born before 1990. Estimates of breed effects changed little with additional rounds of iteration. Variance of changes in the PTA as a fraction of PTA variance was  $3.2 \times 10^{-7}$  for milk and  $7.3 \times 10^{-7}$  for PL by round 300. The convergence limit of  $1 \times 10^{-8}$  was reached after 122 more rounds for milk and 656 rounds for PL. Statistical comparisons of unknown-parent solutions were not available, but the correlation of round 300 PTA with final PTA was extremely high (>0.999), which indicated good convergence of the system.

Holstein bull PTA changed little when across-breed PTA and official within-breed PTA were compared (Table 3). For bulls with high within-breed reliability ( $\geq 99\%$ ), correlations exceeded 0.999 for Holsteins and 0.97 within other breeds. The PTA changed more for breeds with smaller populations, for bulls with fewer daughters, and for cows. Among other breeds, correlations tended to be lowest for Milking Shorthorns and highest for Jerseys. Correlations for PTA fat and PTA protein are not shown but were similar to those for PTA milk. Recent bulls were defined as those born since 1995 with daughters in  $\geq 10$  herds and within-breed reliability of  $\geq 70\%$  for yield or  $\geq 40\%$  for SCS, PL, or DPR. Recent cows were defined as those born since 1998 and reliability of  $\geq 40\%$  for yield or  $\geq 30\%$  for SCS, PL, or DPR.

The largest changes in PTA were for bulls and cows with pedigrees that included >1 breed, and reliabilities also increased for those animals. Gains in reliability



**Table 3.** Correlations of PTA from across-breed and within-breed analyses by trait

PTA trait	Breed	Bulls with high reliability <sup>1</sup>	Recent bulls <sup>2</sup>	Recent cows <sup>3</sup>
Milk	Ayrshire	0.990	0.963	0.943
	Brown Swiss	0.990	0.960	0.942
	Guernsey	0.991	0.988	0.969
	Holstein	>0.999	0.994	0.989
	Jersey	0.997	0.988	0.972
	Milking Shorthorn	0.997	0.986	0.947
Productive life (PL)	Ayrshire	—	0.941	0.966
	Brown Swiss	0.980	0.953	0.957
	Guernsey	—	0.983	0.972
	Holstein	0.999	0.997	0.994
	Jersey	0.999	0.986	0.984
	Milking Shorthorn	—	0.906	0.916
SCS	Ayrshire	—	0.975	0.969
	Brown Swiss	0.989	0.969	0.963
	Guernsey	0.999	0.972	0.979
	Holstein	>0.999	0.994	0.994
	Jersey	0.974	0.976	0.977
	Milking Shorthorn	—	0.988	0.961
Daughter pregnancy rate (DPR)	Ayrshire	—	0.962	0.962
	Brown Swiss	0.984	0.946	0.974
	Guernsey	—	0.989	0.988
	Holstein	>0.999	0.995	0.995
	Jersey	0.998	0.980	0.979
	Milking Shorthorn	—	0.956	0.915
Numbers of animals with milk PTA	Ayrshire	18	39	9,159
	Brown Swiss	41	89	26,116
	Guernsey	30	68	13,432
	Holstein	714	7,878	2,925,402
	Jersey	81	427	200,387
	Milking Shorthorn	5	5	3,615

<sup>1</sup>Born since 1985 with  $\geq 99\%$  reliability for Holsteins,  $\geq 98\%$  for Jerseys, and  $\geq 95\%$  for other breeds. A value of dash (—) indicates that <5 bulls in the breed had evaluations with high reliability.

<sup>2</sup>Born since 1995 with daughters in  $\geq 10$  herds and a reliability of  $\geq 70\%$  for yield or  $\geq 40\%$  for SCS, PL, or DPR.

<sup>3</sup>Born since 1998 and a reliability of  $\geq 40\%$  for yield or  $\geq 30\%$  for SCS, PL, or DPR.

were small for sires of crossbred cows because most already had hundreds or thousands of purebred daughters. Only 25 Jersey and Brown Swiss bulls born since 1997 had  $\geq 10$  crossbred daughters. Because many purebred animals have no crossbred progeny, changes in their PTA might also be explained by changes in the grouping of unknown dams and the addition of other breeds and crossbred cows to the management groups in mixed-breed herds. Those additional herd mates should increase accuracy but might also cause some bias if management of different breeds is not the same within herd.

Crossbred animal PTA should be much more accurate with an all-breed than with a within-breed analysis because the relationship matrix can link to reliable sire PTA for breeds in both the maternal and paternal ancestry. For example, crossbred cows with the highest PTA PL each lived for several lactations and had a sire with high PTA PL and a grandsire with high PTA PL

of another breed. If crossbred data are included only within sire breed for the data set, management group mates and genetic evaluations for maternal ancestors of other breeds are ignored.

The sire-breed model produced PTA very similar to official PTA from the within-breed model. Correlations were generally  $>0.999$  for bulls with high reliability and also for recent bulls. Correlations for recent cows were about 0.995, and all of the largest changes were for F1 crossbred cows. A few crossbred cows were officially evaluated if enrolled in breed association grade-up programs, but most (93%) were not. The sire-breed model is an intermediate step between the current model and the all-breed model because records of crossbred cows are used, but many of their known ancestors and relatives of other breeds are treated as missing. Both the sire-breed and all-breed models add information from crossbred relatives but introduce some possibility of bias as compared with strictly purebred models.

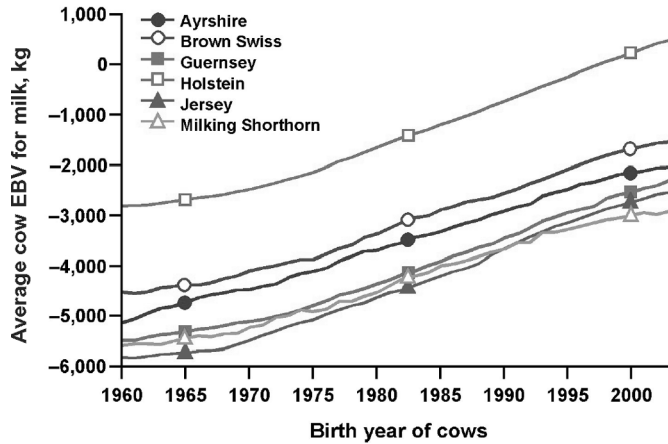


Figure 1. Genetic trend for milk (kg/lactation) on the all-breed base.

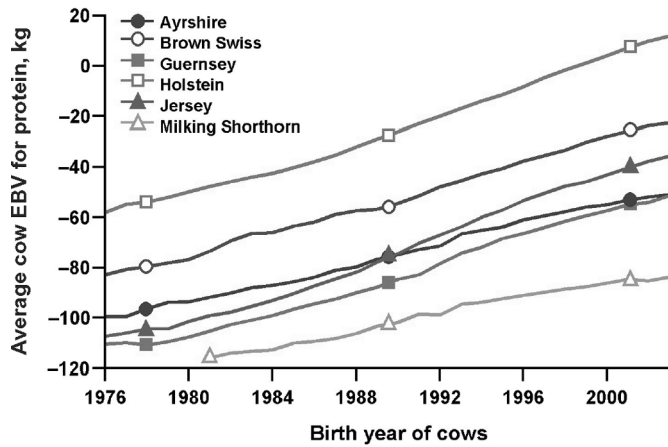


Figure 2. Genetic trend for protein (kg/lactation) on the all-breed base.

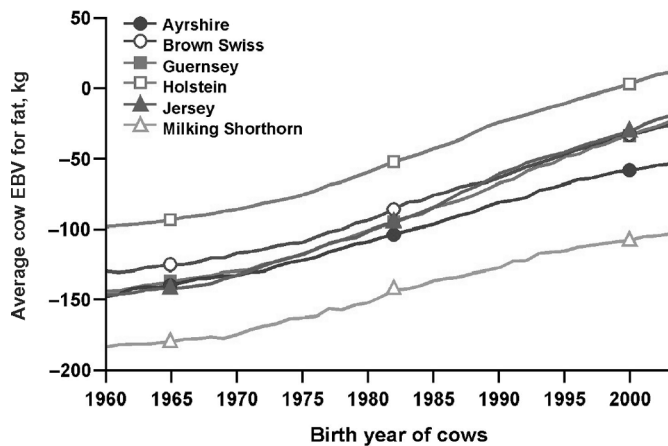


Figure 3. Genetic trend for fat (kg/lactation) on the all-breed base.

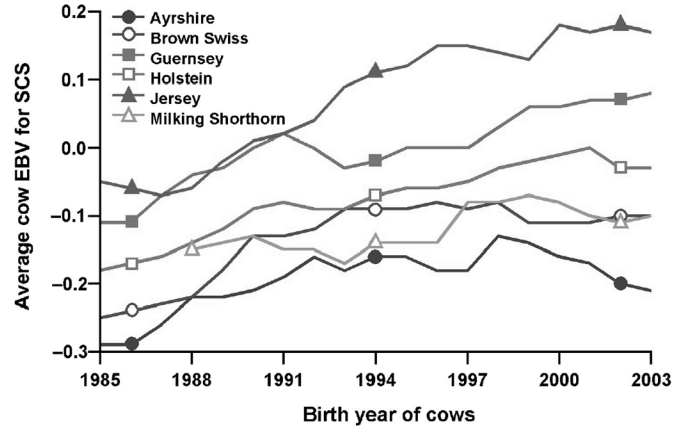


Figure 4. Genetic trend for SCS on the all-breed base.

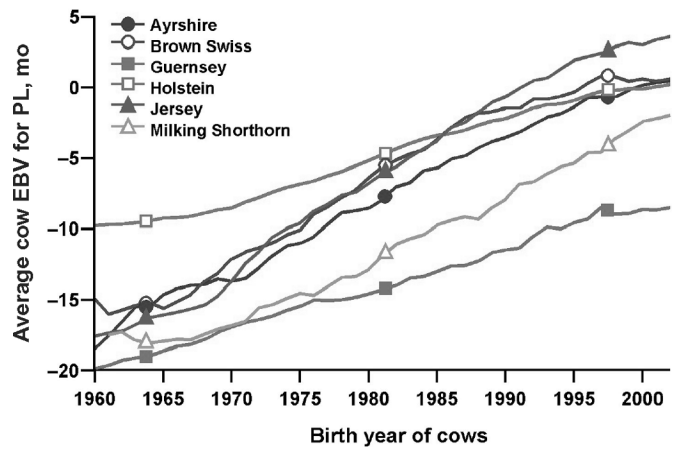


Figure 5. Genetic trend for productive life (PL; mo) on the all-breed base.

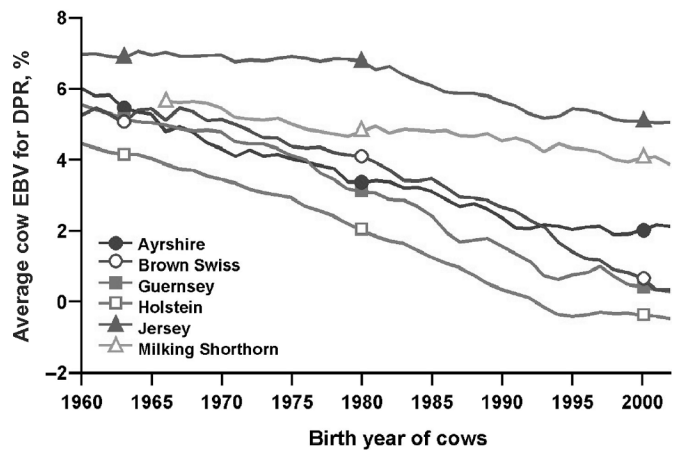


Figure 6. Genetic trend for daughter pregnancy rate (DPR; %) on the all-breed base.

**Table 4.** Genetic trends per year for the all-breed model and changes in trend between the all-breed and within-breed models<sup>1</sup>

Breed	Statistic	Milk, kg	Fat, kg	Protein, kg	SCS	PL, mo	DPR, %
Ayrshire	Trend	53	1.6	1.5	-0.004	0.31	0.01
	Change	8	0.1	0.4	0.002	0.09	-0.02
Brown Swiss	Trend	69	2.7	2.8	0.003	0.15	-0.20
	Change	-25	-0.2	0.5	0.007	0.00	-0.06
Guernsey	Trend	68	2.8	2.1	0.007	0.18	-0.08
	Change	-5	0.0	0.0	0.004	0.04	-0.01
Holstein	Trend	97	2.9	3.0	0.006	0.14	-0.06
	Change	-3	-0.2	-0.1	0.002	0.01	-0.02
Jersey	Trend	72	2.7	2.7	0.011	0.30	-0.02
	Change	-5	0.0	0.0	0.004	0.05	-0.02
Milking Shorthorn	Trend	41	1.3	1.0	0.004	0.40	-0.06
	Change	8	0.2	0.1	-0.002	0.10	-0.05

<sup>1</sup>PL = productive life; DPR = daughter pregnancy rate.

### Genetic Trends

Genetic trends for each breed and trait in the all-breed system are presented in Figures 1 to 6. Three trend validation tests (Interbull, 2004) were performed for each of 5 breeds (excluding Milking Shorthorn) and 5 traits (except that test 1 does not apply to PL). Interbull requires trend tests to be within 2 standard errors of 0.01 genetic standard deviations per year. Few biases were detected. For 64 of the 70 tests, 95% confidence intervals included the range of -0.01 to +0.01 genetic standard deviations per year.

Trends were then converted back to within-breed scales and compared with the previous official estimates. Trends and differences over the last decade (2002 minus 1992 birth year means) are in Table 4. Most changes in Holstein trends were accounted for by a coding error in the within-breed animal model that was corrected during development of the all-breed software. This affected all traits except PL. Estimates of trends in the other breeds were also improved by proper accounting for crossbred animals that had been treated as purebred animals in the within-breed model. Most trend estimates changed by <0.01 genetic standard deviation per year. Changes for SCS and DPR seem large relative to trends because all breeds had small SCS and DPR trends during the last 10 yr. Brown Swiss had the largest changes in trends, but all new trends seem reasonable.

Heterosis was subtracted in the all-breed model so that breed solutions reflect purely additive genetic effects. The effect of heterosis should be added to PTA of crossbreds and of other breeds when those are expressed on a purebred base because such animals contribute heterosis when randomly mated to purebreds (VanRaden, 1992). Similarly, adjustments for expected future inbreeding should differ depending on the breed

of mates in the base. Because PTA are officially expressed on only one base, expected future inbreeding was obtained using the mean relationship of the animal to purebred cows of that breed. Alternatively, Holsteins and Holstein-sired crossbreds could have a PTA reported on the Holstein base, and all other animals could have 2 evaluations: 1 on their breed base and 1 on the Holstein base. Breeders may desire PTA on the Holstein base if the number of crossbred cows increases and for breeds such as Scandinavian Red, with nearly all crossbred daughters, and such PTA will include both the additive difference from Holsteins and the heterosis when mated to Holsteins. Ideally, breeders should consider both additive and nonadditive merit in their selection and mating programs.

### CONCLUSIONS

National genetic evaluation programs were modified to include data from crossbred animals. An all-breed evaluation system was compared with previous within-breed evaluations. Genetic differences among breeds seemed to be estimated well, and convergence was fairly rapid, which indicated sufficient within-herd connections among purebred and crossbred groups. Joint evaluation of all breeds and crossbred animals can provide more information but does not greatly change rankings for animals that have herdmates and most relatives from the same breed. Changes were largest for breeds with small populations. Additional herdmates of another breed can add accuracy but can also cause bias if they are managed differently or if genetic effects are not modeled properly. An alternative was to include data from crossbred cows based only on sire breed. Under that alternative, changes in PTA were much smaller for purebred animals, but the merit of dams of crossbred cows was more difficult to estimate. Daughters of cross-

bred or foreign-breed sires such as Swedish Red or Montbeliarde would be difficult to evaluate in a sire-breed model because few purebred cows of the same breed would be available for comparison. The within-breed model did not use information from crossbred cows, and the sire-breed model did not provide accurate estimates of breed differences. Breeders can compare breeds and design crossbreeding programs using information from the all-breed evaluation. Implementation is expected in May 2007.

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