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Impact of bovine somatotropin on ranking for genetic value of dairy sires for milk yield traits and somatic cell score

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ABSTRACT. Records of Holstein cows were used to examine how different models account for the effect of bovine somatotropin (bST) treatment on genetic evaluation of dairy sires for yield traits and somatic cell score. Data set 1 included 65,720 first-lactation records. Set 2 included 50,644 second-lactation records. Set 3 included 45,505 records for lactations three, four and five. Estimated breeding values (EBV) of sires were with three different animal models. With Model 1, bST administration was ignored. With Model 2, bST administration was used as a fixed effect. With Model 3, administration of bST was used to define the contemporary group (herd-year-month of calving-bST). Correlations for EBV of 1,366 sires with treated daughters between pairs of the three models were calculated for milk, fat and protein yields and somatic cell score for the three data sets. Correlations for EBV of sires between pairs of models for all traits ranged from 0.971 to 0.999. Fractions of sires with bST-treated progeny selected in common (top 10 to 15%)

were 0.94 and usually greater for all pairs of models for all traits and parities. For this study, the method of statistical adjustment for bST treatment resulted in a negligible effect on genetic evaluations of sires when some daughters were treated with bST and suggests that selection of sires to produce the next generation of sires and cows might not be significantly affected by how the effect of bST is modeled for prediction of breeding values for milk, fat and protein yields and somatic cell score.

Key words: Bovine somatotropin, Estimated breeding values, Genetic parameters, Somatic cell score, Milk yield ranking

INTRODUCTION

Effects of bovine somatotropin (bST) on milk production traits have been reported by several studies (Bauman et al., 1985; Peel and Bauman, 1987; Soderholm et al., 1988; Bauman, 1992; Weigel et al., 1998; Al-Jumaah, 2001). Jordan et al. (1991) showed that milk and protein yields increased 18.8 and 3.3%, respectively, for high-producing cows, but with no effect on somatic cell score (SCS). Hartnell et al. (1991) indicated that response of milk yield to bST treatment depends on the amount of bST injected. Reproductive performance has been found to be similar for treated and untreated cows (Eppard et al., 1985; Chalupa et al., 1988; Soderholm et al., 1988; Nytes et al., 1990; Bauman et al., 1999). Burnside and Meyer (1988) with a simulation study presented results of the effects of bST on bias of sire evaluation, on within herd variance, and on accuracy of genetic evaluation. They showed that if bST was administered equally to all cows in the herd, there would be no problem with genetic evaluation of sires. However, if adjustment for use of bST is not made and bST does influence genetic evaluation, then some cows could be selected to be bull-dams even though they were not genetically superior. As a consequence, a serious bias may occur in sire evaluation if some young sires evaluated by Animal Improvement Programs Laboratory have different fractions of treated daughters or their herdmates treated with bST. In addition, Weigel et al. (1998) determined the effects of bST on estimated breeding value (EBV) using animal models with bST injection ignored, with bST as part of the management group, and with bST treatment as a fixed effect. They reported that correlations between estimates of sire and cow breeding values between different models were 0.99. Frangione and Cady (1988), however, reported a significant effect of bST on ranking of sires. Tsuruta et al. (2000) from a study of test day records concluded that bias in genetic evaluation programs caused by ignoring bST treatment might be significant. Al-Jumaah (2001) suggested that failure to adjust for bST treatment would have a minimal effect on genetic evaluations of cows.

The objective of the present study was to compare rankings of sires on EBV with different models that attempt to account for effect of bST treatment on genetic evaluations for lactation yields for milk, fat and protein and somatic cell score from first, second and third and later lactations.

MATERIAL AND METHODS

Data for this study were provided by the Dairy Records Management System (DRMS) (Raleigh, NC), and consisted of milk yield adjusted to 305 days in lactation, twice a day milking, and to a mature equivalent basis for Holstein cows calving between 1990-2001. Although, recording of use of bST by DRMS began in 1994, cows born between 1990-1993 were included to be certain that records from cows receiving bST in later lactations were included. To assure more accurate identification, only records with official Holstein registration numbers were included. Three different data sets were used. Data set 1 included only first-lactation records. Data set 2 included only second-lactation records. Data set 3 included records from lactations 3 through 5. Approximately 10% of all lactation records included in the data sets were from cows treated with bST. Numbers of records in this study are shown in Table 1. The three data subsets contained 65,720, 50,644 and 45,505 records, respectively. The numbers of cows recorded as treated with bST at least three times during lactation and numbers of untreated cows are shown in Table 1. Lactation records considered treated with bST had to be from cows recorded as injected three or more times during lactation. Records of cows indicated as treated but less than three times during lactation were not used. Numbers of sires of cows with records with bST treatment in the three data sets were 1,366, 1,254 and 1,351, respectively. Percentages of herds using bST in the three data sets were 23, 25 and 26%, respectively. Records from herds with less than five cows treated with bST were not included.

Table 1. Numbers of records, herds, sires, cows, and herd-year-months of calving (HYM) for parities one and two and for lactations three and later for cows treated or not treated with bovine somatotropin (bST).

bST	Parity 1		Parity 2		Lactation 3⁺	
	Yes	No	Yes	No	Yes	No
Records	6,374	59,346	4,557	46,137	3,878	41,627
Herds	151	499	170	504	176	495
Sires	1,366	7,889	1,254	6,820	1,351	6,705
Dams	4,203	48,218	3,554	38,104	3,404	34,187
HYM	1,629	17,206	1,697	16,857	1,816	18,309

⁺Lactations three, four, and five.

Three different models were used to calculate EBV of cows and sires:

Model 1: bST treatment was ignored.

For data sets 1 and 2:

$$y_{ij} = HYM_i + a_j + e_{ij}$$

where y_{ij} is lactation record of cow *j* in contemporary group *i*,
HYM_i is fixed effect of herd-year-month of calving contemporary group *i*,
a_j is random additive genetic value of cow *j*, and
e_{ij} is random residual effect for record of cow *j* in contemporary group *i*.

For data set 3:

$$y_{ijk} = HYM_i + a_j + c_j + e_{ijk}$$

where y_{ijk} is the kth lactation record for cow j in contemporary group i,
HYM_i is fixed effect of the herd-year-month of calving contemporary group i,
a_j is a random additive genetic value of cow j,
c_j is random permanent environmental effect associated with cow j, and
e_{ijk} is random residual effect for lactation k of cow j in contemporary group i.

Model 2: bST treatment considered to be a fixed effect.
For data sets 1 and 2:

$$y_{ijk} = HYM_i + bST_j + a_k + e_{ijk}$$

where y_{ijk} is lactation record of cow k in contemporary group i,
HYM_i is fixed effect of the herd-year-month of calving contemporary group i,
bST_j is fixed effect of bST injection ($j = 1$ if bST given and $j = 2$ if not given bST),
a_k is random additive genetic value of cow k, and
e_{ijk} is random residual effect for record of cow k in contemporary group i with bST treatment j.

For data set 3:

$$y_{ijkl} = HYM_i + bST_j + a_k + c_k + e_{ijkl}$$

where y_{ijkl} is the lth lactation record of cow k in contemporary group i with bST treatment j,
HYM_i is fixed effect of the herd-year-month of calving contemporary group i,
bST_j is fixed effect of bST injection ($j = 1$ if given bST and $j = 2$ if not given bST),
a_k is random additive genetic value of cow k,
c_k is random permanent environmental effect associated with cow k, and
e_{ijkl} is random residual effect for lactation record l of cow k in contemporary group i with bST status j.

Model 3: bST administration used to create contemporary groups.
For data sets 1 and 2:

$$y_{ij} = HYMb_i + a_j + e_{ij}$$

where y_{ij} is lactation record of cow j in contemporary group i,
$HYMb_i$ is fixed effect of the combination of herd-year-month of calving and bST status (contemporary group i),
a_j is random additive genetic value of cow j, and
e_{ij} is random residual effect for record of cow j in contemporary group i.

For data set 3:

$$y_{ijk} = HYMb_i + a_j + c_j + e_{ijk}$$

where y_{ijk} is the kth lactation record of cow j in contemporary group i,
$HYMb_i$ is fixed effect of contemporary group i (herd-year-month of calving and bST status),
a_j is random additive genetic value of cow j,
c_j is random permanent environmental effect of cow j, and
e_{ijk} is random residual effect for lactation record k of cow j in contemporary group i.

The general equation for the animal model used for estimation of genetic parameters for data sets 1 and 2 was

$$y = X\beta + Za + e$$

where y is the vector of lactation records,
β is the vector of fixed effects,
a is the vector of random additive genetic values of the animals,
X and Z are known design matrices, and
e is the vector of random residual effects.

The general equation for the animal model used for estimation of genetic parameters for data set 3 was:

$$y = X\beta + Z_1a + Z_2c + e$$

where y is the vector of lactation records,
β is the vector of fixed effect,
a is the vector of random additive genetic effects of the animals,
c is the vector of permanent environmental effect of cows with records,
X , Z_1, and Z_2 are known design matrices, and
e is the vector of random residual effects.

The first moments for all models were assumed to be E(y) = Xβ. The first moments and second moments from the means for random effects for data sets 1 and 2 were:

$$\mathbf{E}\begin{bmatrix}\mathbf{a}\\\mathbf{e}\end{bmatrix}=\begin{bmatrix}\mathbf{0}\\\mathbf{0}\end{bmatrix} \qquad \text{and} \qquad \mathbf{Var}\begin{bmatrix}\mathbf{a}\\\mathbf{e}\end{bmatrix}=\begin{bmatrix}\mathbf{A}\sigma_a^2 & \mathbf{0}\\\mathbf{0} & \mathbf{I}_n\sigma_e^2\end{bmatrix}$$

First and second moments for parities 3 to 5 with one or more records for each animal were assumed to be:

$$\mathbf{E}\begin{bmatrix}\mathbf{a}\\\mathbf{c}\\\mathbf{e}\end{bmatrix}=\begin{bmatrix}\mathbf{0}\\\mathbf{0}\\\mathbf{0}\end{bmatrix} \qquad \mathbf{Var}\begin{bmatrix}\mathbf{a}\\\mathbf{c}\\\mathbf{e}\end{bmatrix}=\begin{bmatrix}\mathbf{A}\sigma_a^2 & \mathbf{0} & \mathbf{0}\\\mathbf{0} & \mathbf{I}_c\sigma_c^2 & \mathbf{0}\\\mathbf{0} & \mathbf{0} & \mathbf{I}_n\sigma_e^2\end{bmatrix}$$

where A is the matrix of numerator relationships among animals augmented for animals without records (such as sires) which contribute to relationships among animals with records,
I_c is an identity matrix with order equal to the number of cows with records,
I_n is an identity matrix with order equal to the number of records
σ^2_a is additive genetic variance,
σ^2_c is permanent environmental variance, and
σ^2_e is residual variance.

Variance components for random effects were estimated using a derivative free REML algorithm (Graser et al., 1987) with the computer program (MTDFREML) developed by Boldman et al. (1995). Local convergence was considered to be met if the variance of the -2 log likelihoods in the simplex was less than 1×10^{-6}. After first convergence, restarts were made to find global convergence with convergence declared when the values of -2 log likelihood did not change to the second decimal. Breeding values were estimated for all animals for all data sets. The EBV for sires were examined for effect of models on ranking of sires.

Sires with bST-treated daughters were ranked from high to low based on the EBV for each model and trait. Fractions of sires in common for the high 10 to 25% of EBV were compared with the three models. Correlations were calculated for sires between EBV for pairs of models for all data sets.

RESULTS AND DISCUSSION

Correlations among estimated breeding values for milk yield for sires with daughters treated with bST for pairs of the three different models using the three data sets are shown in Tables 2, 3 and 4. Correlations between pairs of two models (1 and 2), (1 and 3) and (2 and 3) for parity one were 0.997, 0.989 and 0.991; for parity two were 0.998, 0.989 and 0.990, and for lactations 3 to 5 were 0.997, 0.988 and 0.991, respectively.

Table 2. Correlations among estimated breeding values for yield traits and somatic cell score for sires with the three models for parity one.

Traits	Models		
	1 and 2	1 and 3	2 and 3
Milk	0.997	0.989	0.991
Fat	0.998	0.989	0.992
Protein	0.996	0.988	0.991
Somatic cell score	0.999	0.994	0.994

For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

The fractions of sires having bST-treated progeny in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for milk yield for parity one are shown in Figure 1. The fractions to select based on ranking by EBV ranged from 0.10 to 0.25. The fractions of sires in common with Models 1 and 2 ranged from 0.965 to 0.985;

Table 3. Correlations among estimated breeding values for yield traits and somatic cell score for sires with the three models for parity two.

Traits	Models		
	1 and 2	1 and 3	2 and 3
Milk	0.998	0.989	0.990
Fat	0.999	0.991	0.992
Protein	0.998	0.988	0.990
Somatic cell score	0.999	0.993	0.993

For Model 1, bovine somatotropin (bST) injection was ignored; for model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

Table 4. Correlations among estimated breeding values for yield traits and somatic cell score for sires with the three models for lactations 3 to 5.

Traits	Models		
	1 and 2	1 and 3	2 and 3
Milk	0.997	0.988	0.991
Fat	0.997	0.988	0.991
Protein	0.996	0.987	0.990
Somatic cell score	0.979	0.971	0.991

For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

with Models 1 and 3, from 0.947 to 0.971, and with Models 2 and 3 from 0.959 to 0.974. For fractions selected by rankings on EBV from 0.14 to 0.19, fractions of sires in common between Models 1 and 3 and Models 2 and 3 were nearly identical.

For parity two, fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for milk yield are shown in Figure 2. Fractions in common with Models 1 and 2 were 0.977 to 0.989, for Models 1 and 3 were 0.949 to 0.962, and for Models 2 and 3 were 0.955 to 0.968. For fractions selected from 0.13 to 0.20, the fractions of sires in common between Models 1 and 3 and Models 2 and 3 were nearly identical.

For data set 3, fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for milk yield are shown in Figure 3. Fractions of sires in common with Models 1 and 2 were 0.964 to 0.978, with Models 1 and 3 were 0.935 to 0.956, and with Models 2 and 3 were 0.949 to 0.964.

Correlations among EBV for fat yield of sires with bST-treated daughters with the three models using the three data sets are also shown in Tables 2, 3 and 4. Correlations between EBV for pairs of two models (1 and 2), (1 and 3) and (2 and 3) for parity one were 0.998, 0.989 and 0.992; for parity two were 0.999, 0.991 and 0.992, and for lactations 3 to 5 were 0.997, 0.998 and 0.991, respectively.

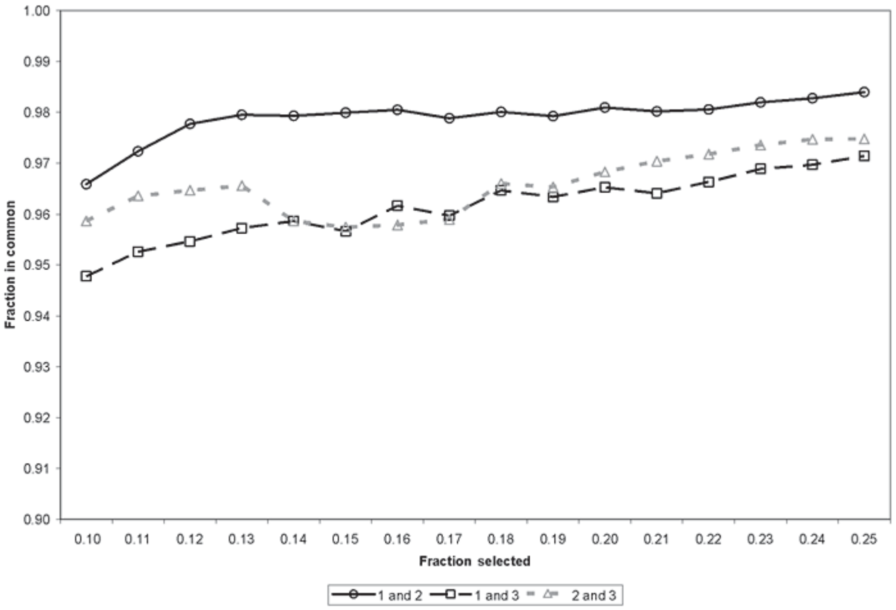

Figure 1. Fractions of sires (1,366 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for parity one. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

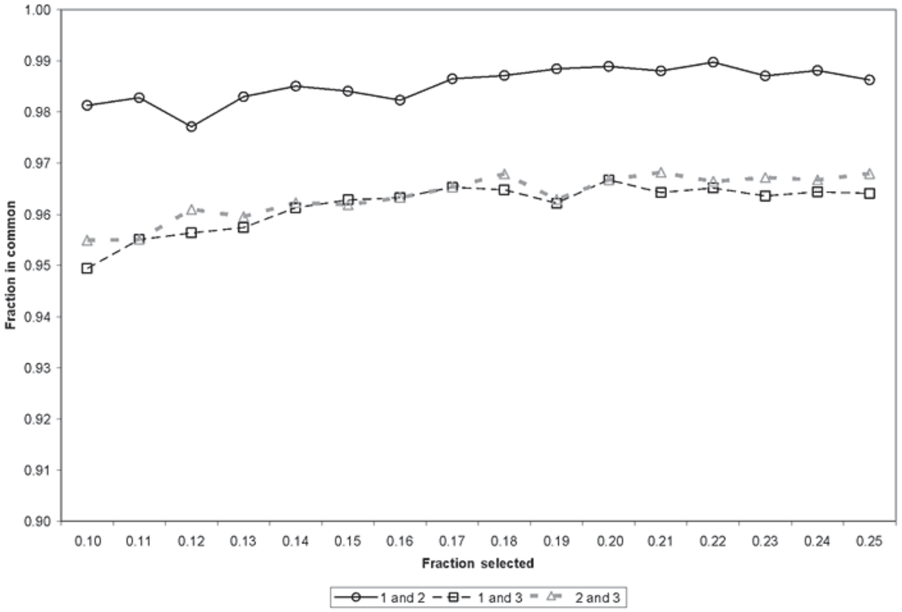

Figure 2. Fractions of sires (1,254 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for parity two. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

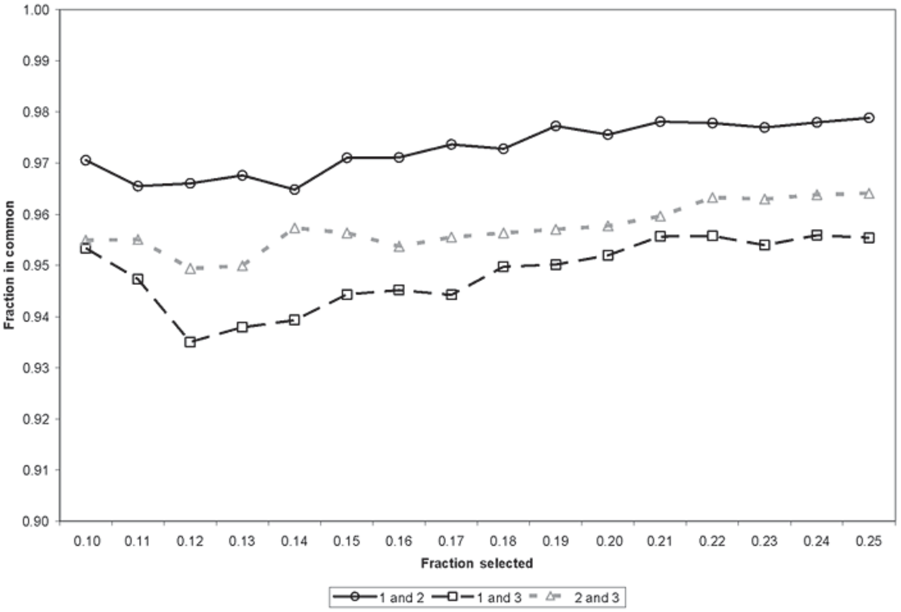

Figure 3. Fractions of sires (1,351 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for lactations 3 to 5. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

Fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for fat yield for parity one are shown in Figure 4. The fractions of sires in common with Models 1 and 2 were from 0.984 to 0.992, with Models 1 and 3 were from 0.952 to 0.969, and with Models 2 and 3 were from 0.949 to 0.974.

For parity two, fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for fat yield are shown in Figure 5. Fractions of sires in common with Models 1 and 2 were 0.984 to 0.992, with Models 1 and 3 were 0.946 to 0.971, and with Models 2 and 3 were 0.949 to 0.974.

For lactations 3 to 5, fractions of sires in common with pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for fat yield are shown in Figure 6. Fractions of sires in common with Models 1 and 2 were 0.966 to 0.984, with Models 1 and 3 were 0.957 to 0.974, and with Models 2 and 3 were 0.962 to 0.977.

Correlations among estimated breeding values for protein yield of sires with bST-treated daughters with the three models using the three data sets are also shown in Tables 2, 3 and 4. Correlations between EBV for pairs of two models (1 and 2), (1 and 3) and (2 and 3) were: for parity one 0.996, 0.988 and 0.991; for parity two 0.998, 0.988 and 0.990, and for lactations 3 to 5 0.996, 0.987 and 0.990, respectively.

Fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for protein yield for parity one are shown in Figure 7. The fractions of sires in common with Models 1 and 2 were from 0.974 to 0.983, with Models 1 and 3 were from 0.945 to 0.967, and with Models 2 and 3 were from 0.953 to 0.970.

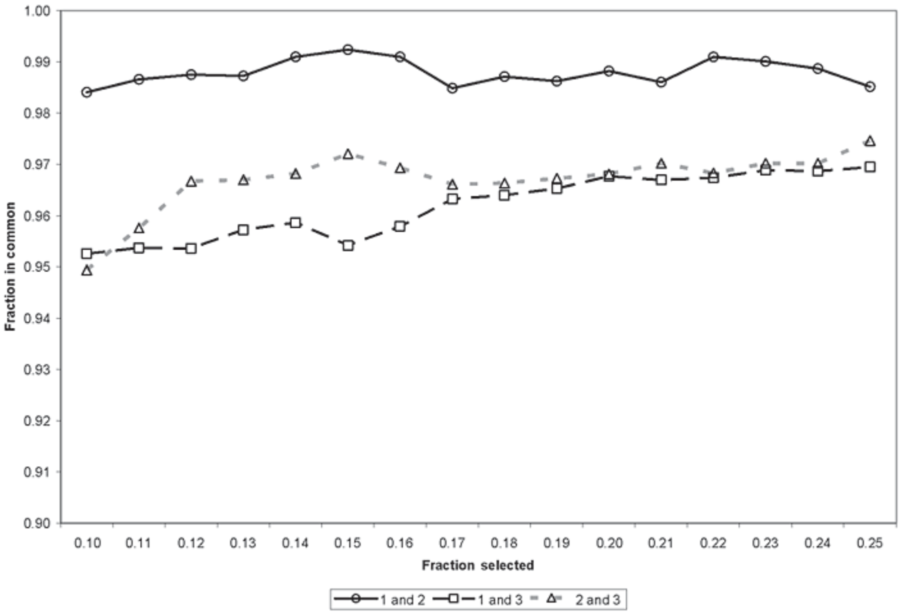

Figure 4. Fractions of sires (1,366 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for parity one. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

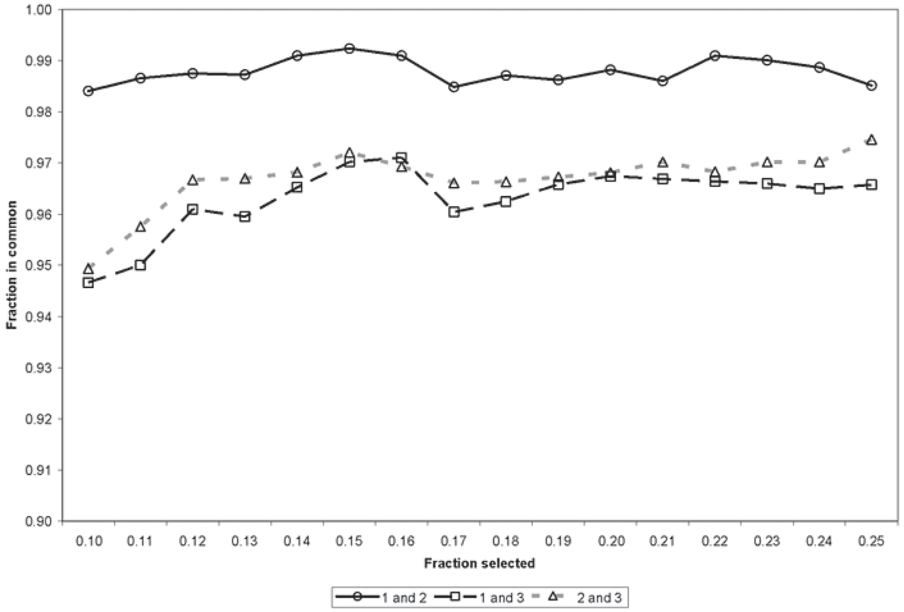

Figure 5. Fractions of sires (1,254 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for parity two. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

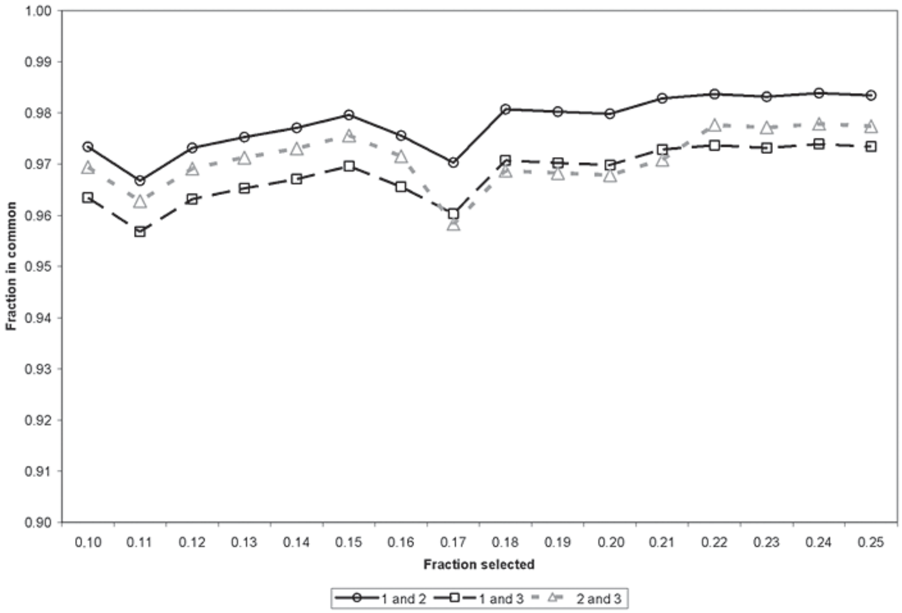

Figure 6. Fractions of sires (1,351 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for lactations 3 to 5. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

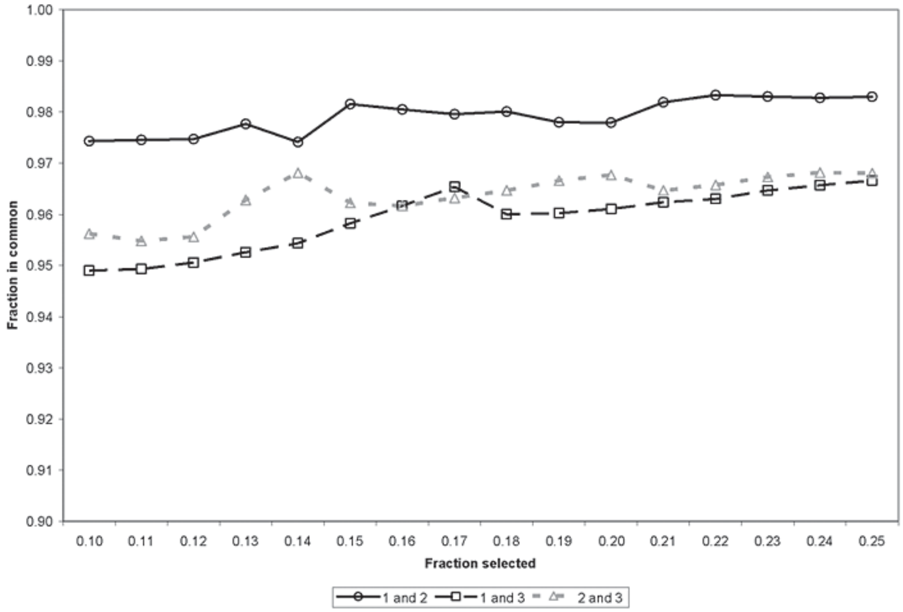

Figure 7. Fractions of sires (1,366 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for parity one. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

For parity two, fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for protein yield are shown in Figure 8. Fractions in common with Models 1 and 2 were 0.974 to 0.984, with Models 1 and 3 were 0.953 to 0.967, and with Models 2 and 3 were 0.960 to 0.972.

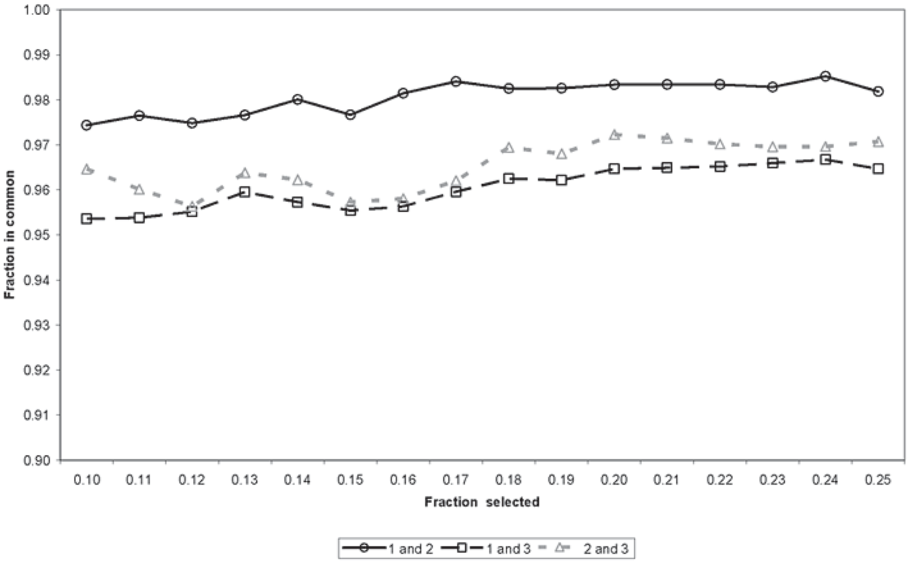

Figure 8. Fractions of sires (1,254 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for parity two. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

For lactations 3 to 5, fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for protein yield are shown in Figure 9. Fractions of sires in common with Models 1 and 2 were 0.958 to 0.976, with Models 1 and 3 were 0.943 to 0.954, and with Models 2 and 3 were 0.956 to 0.964.

Correlations among estimated breeding values for SCS of sires with bST-treated daughters with the three models using the three data sets are also shown in Tables 2, 3 and 4. Correlations between pairs of two models (1 and 2), (1 and 3) and (2 and 3) were: for parity one 0.999, 0.994 and 0.994; for parity two 0.999, 0.993 and 0.993, and for lactations 3 to 5 0.979, 0.971 and 0.991, respectively.

Fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for SCS for parity one are shown in Figure 10. Fractions of sires in common with Models 1 and 2 were from 0.993 to 0.998, with Models 1 and 3 were from 0.967 to 0.982, and with Models 2 and 3 were from 0.967 to 0.983.

For parity two, fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for SCS are shown in Figure 11. Fractions of sires in common with Models 1 and 2 were 0.993 to 0.997, with Models 1 and 3 were 0.963 to 0.979, and with Models 2 and 3 were 0.963 to 0.978.

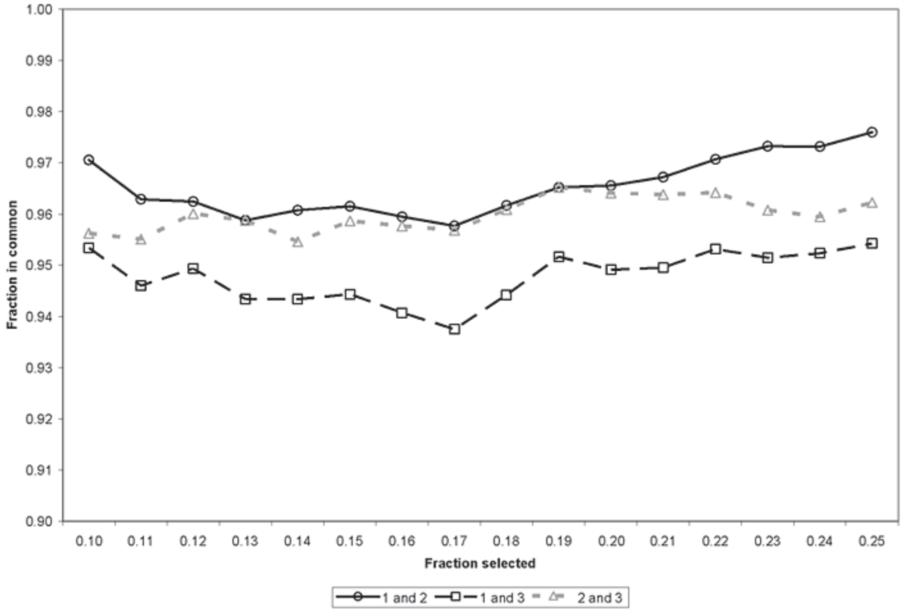

Figure 9. Fractions of sires (1,351 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for lactations 3 to 5. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

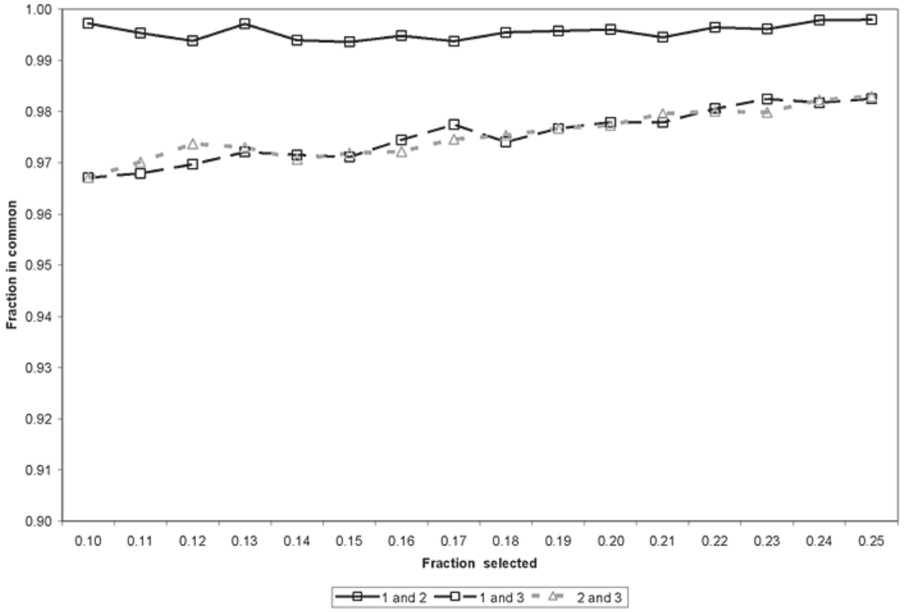

Figure 10. Fractions of sires (1,366 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for parity one. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

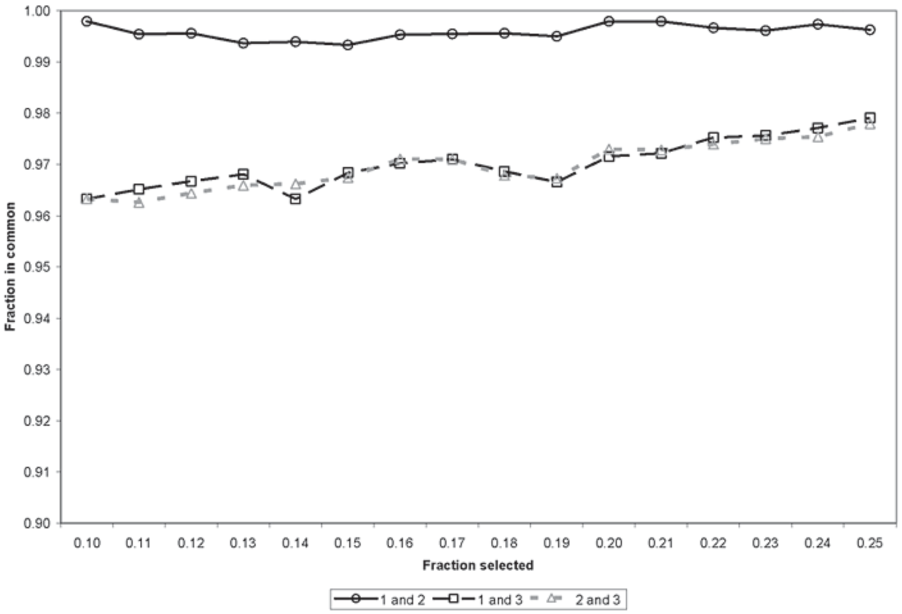

Figure 11. Fractions of sires (1,254 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for parity two. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

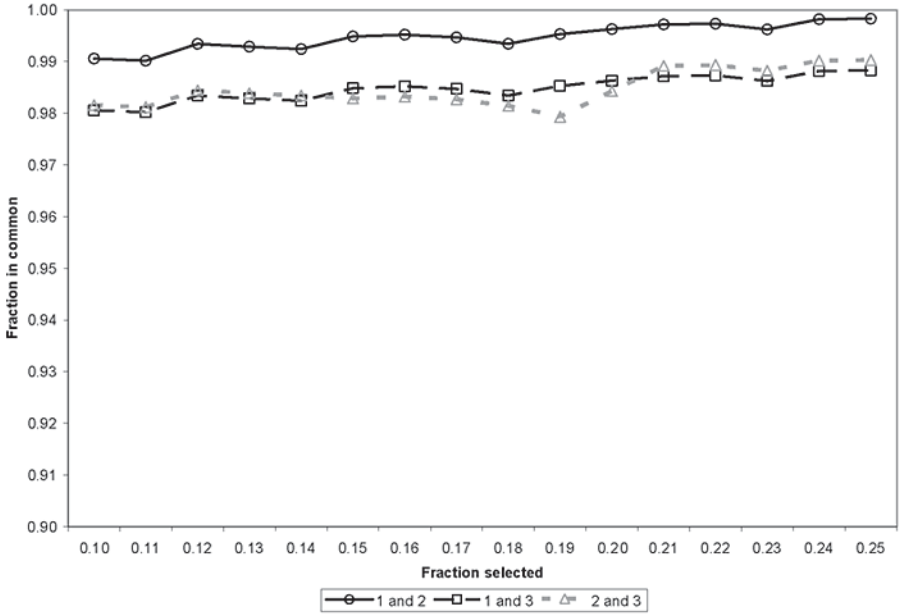

Figure 12. Fractions of sires (1,351 total sires) in common for different fractions selected based on rankings on estimating breeding values with pairs of the three models (1 and 2), (1 and 3) and (2 and 3) for milk yield for lactations 3 to 5. For Model 1, bovine somatotropin (bST) injection was ignored; for Model 2, bST injection or not was a fixed effect, and for Model 3, bST injection or not was used to form contemporary groups.

For lactations 3 to 5, fractions of sires in common based on rankings with EBV for pairs of the three different models (1 and 2), (1 and 3) and (2 and 3) for SCS are shown in Figure 12. Fractions in common with Models 1 and 2 were 0.990 to 0.998, with Models 1 and 3 were 0.980 to 0.988, and with Models 2 and 3 were 0.981 to 0.990.

The overall high correlations among estimated breeding values of sires with different models for effect of bST on yield traits and on somatic cell score with the three data sets (parity one, parity two, and lactations 3 to 5) show that differences in the three models had little impact on which sires would have been selected.

Future research should be designed to examine the effects of bST on estimates of the genetic parameters including genetic correlations between production traits and SCS for the three ways of including bST effects in the animal models.

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