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# Bias in Genetic Evaluations by Records of Cows Treated with Bovine Somatotropin<sup>1</sup>

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## ABSTRACT

Records from Dairy Records Management Systems in Raleigh were used to estimate effects of bovine somatotropin (bST) treatment and to predict breeding values for milk production traits. The data comprised 5245 test-day records of bST-treated cows and 126,223 test-day records of untreated cows in first lactation for milk, fat, and protein yields. Fixed effects of bST treatment were estimated from test-day animal models with herd-test-date as another fixed factor. Percentage increases due to bST treatment ranged from 7 to 8% for test-day milk, fat, and protein yields. Random regression coefficients for additive genetic and permanent environmental effects were included in the model. To assess the potential for bias in genetic evaluations when some and not all cows are treated with bST, breeding values predicted by the test-day model with and without effects of bST treatment were compared for cows and sires. Correlations between breeding values predicted from models with and without effects of bST treatment were 0.99. However, relatively large bias was found for individual animals. This result suggests that bias in genetic evaluation caused by ignoring bST treatment may be significant.

(**Key words:** dairy cattle, milk yield, breeding values)

**Abbreviation key:** DRMS = Dairy Records Management Systems, MAD = maximum absolute difference, MAE = mean absolute errors, PBV = predicted breeding value, TD = test day.

## INTRODUCTION

The administration of bST affects milk production traits, depending on how much and how often bST is used for lactating cows. Increases of 20 to 40% in milk

yield for dairy cows receiving bST were shown by Bauman et al. (3). Jordan et al. (9) found that bST treatment for high-producing cows increased milk yield and protein percentage by 18.8 and 3.3%, respectively, but that there were no effects on SCC and BW. A review by Bauman (2) reported that bST increased milk yield, cows remained healthy, the composition of milk was not changed and that milk response to bST would be negligible if bST-treated cows were not stressed, underfed, or sick because of poor management.

Burnside (4) indicated that recording bST administration would be necessary for analyses of data for cow and sire evaluations if bST is widely used. Currently, for the USDA genetic evaluations, calculation of PTA for milk production does not consider that bST was used in 305-d lactation records (11). However, if bST treatment affects predicted breeding values (PBV) of cows and sires, then accounting for the effect of bST on milk production in genetic evaluations may be more effective with test-day (TD) records than with 305-d records. If enough records for bST-treated cows are used in genetic evaluation, PBV for production traits of dairy cattle may be biased. If a young sire evaluated by the Animal Improvement Programs Laboratory of USDA has only daughters receiving bST and their herdmates do not receive bST, a serious bias could arise in comparison with bulls that have no or fewer treated daughters and with bulls whose daughters and their herdmates have received bST. Also, if only one cow were injected with bST regularly in a dairy herd and no adjustment for response to bST is made, she may be selected as a bull-dam to produce a young bull in the next generation even though she is not genetically superior. Peel and Bauman (13) summarized similarities between genetically superior cows and bST-treated cows. In their simulation study, Burnside and Meyer (5) found that if interaction of bST by genetic potential of cows existed, sire evaluations will be biased and warned that the systematic use of bST may cause serious errors in sire evaluations. Whether or not the response to bST is heritable, if daughters

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of a specific sire receive bST treatment, the ranking of animals by their genetic merit could be biased. Gallo et al. (8) found interactions between both genetic and nongenetic effects and response in milk yield to bST. However, several authors reported that the interaction of genetic potential by bST treatment was not significant (12, 17, 21). Simianer and Wollny (15) conducted a simulation study to assess the impact of different strategies of bST administration and found that accuracy of sire and dam evaluations would not be detrimentally affected. As a result of a simulation study, Colleau (6) indicated that large biases in genetic evaluation may occur when bST is administered only to the best cows. If bST-treated cows have genetic responses different from untreated cows, the effects of bST should be considered in the genetic evaluation model. A study of bST on genetic evaluation was conducted recently by Weigl et al. (21). They predicted breeding values of sires and cows including lactation records of cows treated with bST provided by Dairy Records Management Systems (DRMS) Raleigh and concluded that bST treatment had little impact on genetic evaluation. However, their results might have been underestimated or biased because they used incomplete records of bST treatment in the first year, 1994, when the system of recording of bST treatment started. They did not consider TD records reported with or without bST information. For genetic evaluation when not all cows receive bST, a TD model may be a way to adjust for effects of bST treatment because the date of bST injection on DHI records is uncertain and because the lactation curve could be distorted from the curve expected without use of bST. Stanton et al. (16) estimated lactation curves for milk, fat, and protein using a TD model and suggested that the TD model has the potential to provide more accurate genetic evaluations than a lactation model. Although genetic evaluation with a TD model requires more memory storage and more processing time, one of the main advantages of a TD model is that it accounts for the herd environment condition on each test day. Ptak and Schaeffer (14) described some advantages for TD models compared with lactation models such as, no need to extend records and greater accuracy of evaluations. Therefore, a TD model would have an advantage for genetic evaluations if information about bST treatment could be obtained for each TD record. Swalve (18) examined the possibility of comparing lactation curves to distinguish between bST-treated and other cows, but he concluded that because individual variation of TD records is so large, it would be difficult to detect bST treatment and preferential treatment simultaneously. His conclusion suggests that the responses of milk production for lactating cows to bST treatment and to preferential treat-

**Table 1.** Number of records in first lactation analyses and number with bST treatment.

	Number of records (bST treatment)
Test-day records	131,468 (5245)
Cows	12,745
Sires	2330
Herds	126
Herd-test dates	11,057

ment are similar and that if bST treatment were not reported, the effects of bST treatment on milk production could not be estimated. Since the FDA approved the use of bST in dairy cows in 1993, records for bST-treated cows have accumulated at DRMS. Data on cows with bST treatment have become available from the Raleigh DRMS, although at the time of this study, the data were limited to 3 yr and certain states. However, the records should be of sufficient quantity to estimate the effects of bST treatment and additive genetic effects of cows and sires and to determine whether the effects of bST treatment are ignored, in which serious problems in genetic evaluations of cows and sires may result.

The objectives of this study were to estimate the effects of bST treatment on production traits, to predict breeding values using TD models with and without considering effects of bST treatment, and to compare those PBV to assess the potential for bias in genetic evaluations when some but not all cows are treated with bST.

## MATERIALS AND METHODS

First-lactation records of Holstein cows from Raleigh DRMS were used in this analysis. The original data were collected in DHI herds from northeastern and eastern states, but no records of bST-treated cows were found for some states. The numbers of records used in this study are shown in Tables 1, 2, and 3. The data comprised 126 herds and 131,468 TD records of 12,745 cows for milk, fat, and protein yields. The system of recording bST treatment at DHIA started in 1994, but to secure more information, DHI records collected from 1990 to 1996 were also analyzed. The number of records for each year and the average 305-d yields are shown in Table 2. To reduce environmental variation among herds and to compare cows with and without bST treatment within the same herd, only data from herds in which at least one record was sampled from bST-treated cows were extracted. Table 3 shows that no first TD records of bST-treated cows were reported and few records for the second TD. After

**Table 2.** Number of herds, cows, and average 305-d yields (kg) by calving year.

Calving year	Herds	Cows		Average 305-d yields		
		No bST	bST	Milk	Fat	Protein
1990	89	1601	0	7409	265	236
1991	90	1684	0	7531	276	240
1992	97	1941	0	7749	283	249
1993	100	2099	75	8014	290	258
1994	97	1903	210	8160	292	263
1995	85	1668	613	8071	293	260
1996	66	948	3	8119	292	261

the peak of lactation, more cows were treated with bST. Only first-lactation records were used in this study because the small number of records for bST-treated cows in second lactation. Each cow with data was required to have known sire identification and a 305-d lactation record from two times a day milking. Three times a day milking records were not used because the number of such records with bST treatment was limited. Incomplete (in progress) 305-d records were removed. Complete 305-d records with at least eight TD records during the first lactation were extracted from the original data set. In addition, herds that had fewer than five tested cows were eliminated.

**Test-Day Model with Random Regressions**

A single-trait animal model was used in the present study because estimation of variance components for multiple trait random regression models is computationally demanding at this time. The data were analyzed with the following mixed model:

$$y = Xb + Z_1a + Z_2p + e$$

where **y** is a vector of TD records, **b** is a vector of fixed effects including fixed regressions, **a** is a vector of animal additive genetic effects for random regres-

sions, **p** is a vector of animal permanent environmental effects for random regressions, **e** is a vector of residual effects, **X** is incidence matrix for fixed effects, and **Z**<sub>1</sub> and **Z**<sub>2</sub> are incidence and covariate matrices for additive genetic and permanent environmental random effects. The (co)variances were defined as

$$V = V \begin{pmatrix} a \\ p \\ e \end{pmatrix} = \begin{pmatrix} G \otimes A & 0 & 0 \\ 0 & P \otimes I_p & 0 \\ 0 & 0 & R \end{pmatrix}$$

with the normality assumptions that  $\begin{pmatrix} a \\ p \\ e \end{pmatrix} \sim N(0, V)$

where **G** is a 3 × 3 covariance matrix of additive genetic random regressions, ⊗ is Kronecker product function, **A** is the numerator relationship matrix, **P** is a 3 × 3 covariance matrix of permanent environmental random regressions, **I**<sub>p</sub> is an identity matrix with order the number of cows, and **R** is a diagonal matrix with residual variance, σ<sub>e</sub><sup>2</sup>. The model for a TD observation was

$$y_{ijklmq} = h_i + ag_j + mo_k + bST_1 + \sum_{n=0}^2 \beta_n z_{nq} + \sum_{n=0}^2 \alpha_{mn} z_{nq} + \sum_{n=0}^2 \gamma_{mn} z_{nq} + e_{ijklmq},$$

where h<sub>i</sub> = fixed effect of herd-test date i; ag<sub>j</sub> = fixed effect of age group j (age at calving; 20 to 24, 25 to 28, 29 to 32, 33 to 36, 37 to 44 mo); mo<sub>k</sub> = fixed effect of calendar month of calving k, bST<sub>1</sub> = fixed effect of whether bST treatment is in the model or not; β<sub>n</sub> = fixed regression coefficients, α<sub>mn</sub>; and γ<sub>mn</sub> = random regression coefficients for additive genetic effects of animal, m, and permanent environmental effects of cow, m; z<sub>0</sub> = 1; z<sub>1</sub> = DIM; z<sub>2</sub> = exp(c × DIM) with constant, c = -0.05; and y<sub>ijklmq</sub> = test-day record q for herd-test date i, age group j, month of calving k, bST l, and cow m. The covariate part of these models was based on

**Table 3.** Number of records and percentage with bST treatment by test day.

Test day	no bST	bST	%
1	10,849	0	0.0
2	12,119	6	0.0
3	12,529	109	0.9
4	11,939	275	2.3
5	12,129	429	3.4
6	11,731	549	4.5
7	11,933	668	5.3
8	11,505	696	5.7
9	11,663	741	6.0
10	9448	668	6.6
11	7244	599	7.6
12	3134	505	13.9

**Table 4.** Estimates of variance components (kg) due to residual, permanent environmental, and additive genetic effects estimated from test-day models with and without effects of bST for milk, fat, and protein yields.

Test day	Milk		Fat		Protein	
	With	Without	With	Without	With	Without
Additive genetic variance components						
1	8.2	8.2	0.015	0.015	0.007	0.007
2	8.8	8.8	0.013	0.013	0.008	0.008
3	9.0	9.0	0.013	0.013	0.009	0.009
4	9.3	9.3	0.013	0.013	0.009	0.009
5	9.8	9.8	0.013	0.013	0.009	0.009
6	10.4	10.4	0.013	0.013	0.010	0.010
7	11.2	11.2	0.014	0.014	0.010	0.010
8	12.2	12.2	0.015	0.015	0.011	0.011
9	13.4	13.4	0.016	0.016	0.013	0.013
10	14.7	14.8	0.018	0.018	0.014	0.014
Permanent environmental variance components						
1	30.8	30.9	0.063	0.063	0.027	0.027
2	29.0	29.1	0.038	0.038	0.022	0.023
3	25.9	26.0	0.036	0.036	0.022	0.022
4	23.5	23.4	0.033	0.033	0.020	0.020
5	21.9	21.9	0.030	0.030	0.019	0.019
6	21.4	21.4	0.029	0.029	0.019	0.019
7	22.0	21.9	0.029	0.029	0.020	0.020
8	23.7	23.5	0.031	0.030	0.022	0.022
9	26.4	26.2	0.033	0.033	0.026	0.026
10	30.2	30.0	0.038	0.038	0.031	0.030
Residual variance components						
	20.0	20.1	0.054	0.054	0.023	0.023
Heritability						
Average	0.19	0.19	0.14	0.14	0.18	0.18
Repeatability						
Average	0.64	0.64	0.48	0.48	0.59	0.59

Wilmink's (22) model, which used the constant  $-0.05$ , corresponding to the peak of lactation at approximately 50-d postpartum. Due to few records of bST treatment in the first two test days, minimal effect by setting 50 d in the Wilmink  $s$  function is expected. Van der Werf and Schaeffer (20) showed that Ali's model (1), which has five covariates, had relatively high accuracy and low mean absolute error, but that Ali's model and Wilmink's model, which has three covariates, differed little. Wilmink's model is also computationally less demanding for estimation of variance components because, when applied to these models, Ali's model needs 31 parameters (15 for additive genetic effects, 15 for permanent environmental effects, and one for the residual effect), whereas Wilmink's model needs only 13 parameters.

The REMLF90 program (10) was used to estimate the effects of bST and to predict breeding values of cows and sires for milk, fat, and protein yields after convergence of estimates of the (co)variance components.

## RESULTS AND DISCUSSION

Estimates of the effects of bST treatment were  $1.88 \pm 0.11$  kg,  $0.066 \pm 0.005$  kg, and  $0.063 \pm 0.004$  kg for test-day milk, fat, and protein yields, respectively (significant at  $P < 0.01$ ). The DHI records do not show when bST was used on a particular cow during lactation. They show only that bST was injected at least once, some day between this test day and the previous test day. If the injection was given right after the previous test day (about 30 d prior to this test day), the effect of bST treatment would be underestimated, although the use of bST was reported. Lack of information on time of treatment might have led to underestimation of the effects of bST treatment. Some possible reasons for the smaller responses due to bST in this study compared with results from other papers are: 1) some variances or some effects were not accounted for in the model, 2) unknown amount and frequency of bST treatment, 3) unknown dates of bST injection, 4) possibly poor management for cows with bST treat-

**Table 5.** Correlations, mean absolute errors (MAE), and maximum absolute differences (MAD) between breeding values for cows and sires for milk yield predicted from test-day models with and without effects of bST.

Test day	Correlations		MAE (kg)		MAD (kg)	
	Cows	Sires	Cows	Sires	Cows	Sires
1	0.999	0.999	0.03	0.02	0.37	0.36
2	0.999	0.998	0.03	0.02	0.41	0.39
3	0.999	0.998	0.03	0.02	0.46	0.41
4	0.999	0.998	0.03	0.03	0.50	0.42
5	0.998	0.998	0.04	0.03	0.54	0.44
6	0.998	0.998	0.04	0.03	0.59	0.46
7	0.998	0.998	0.04	0.03	0.63	0.47
8	0.998	0.998	0.04	0.03	0.67	0.58
9	0.998	0.998	0.05	0.03	0.71	0.69
10	0.998	0.998	0.05	0.04	0.75	0.80

ment, and 5) the small number of bST-treated cows in the early stages of lactation.

Table 4 shows variance components for each random effect estimated with the model that included effects of bST and the other model that ignored the effects of bST. The variance components for additive genetic effects and permanent environmental effects for TD yields were calculated for each TD. The variance component estimates were similar when considering and ignoring the effects of bST treatment for all traits. The few records of bST-treated cows might have been “swamped” by all the records of untreated cows for variance component estimation.

Correlations between breeding values predicted from the model with effects of bST and the model without effects of bST were 0.998 to 0.999 for TD milk yield for cows and sires (Table 5). These correlations were similar to the results from Weigel et al. (21), although they did not take TD records into account. The correlations were 0.995 to 0.999 and 0.987 to 0.995 for fat and protein yields, respectively (Tables 6 and 7). These results suggest little bias in PBV from a model that does not include effects of bST, but these high correla-

tions might have been due to failure of a model to account for effects of bST and genotype by bST interaction or a consequence of the large fraction of records from untreated cows. Crooker and Otterby (7) and Bauman (2) have indicated that if interaction between management and response to bST treatment for lactating cows exists, then the shape of the lactation curve will vary from farm to farm. Therefore, different parameters may be required to estimate individual lactation curves, although that would not be practical. To detect serious bias for individual sires or cows, maximum absolute difference (MAD), which was the largest difference between PBV, was calculated. To investigate global bias, mean absolute errors (MAE) were calculated by dividing the sum of absolute differences by the total number of animals. For TD milk yield, MAE were small, 0.02 to 0.05 kg, which are equivalent to 6 to 15 kg for 305-d milk yield, but MAD were relatively large, 0.36 to 0.80 kg (equivalent to 110 to 244 kg per 305 d). The MAE for TD fat and protein yields were 0.001 to 0.002 kg and 0.001 to 0.005 kg (equivalent to 0.3 to 0.6 kg and 0.3 to 1.5 kg per 305 d), while the MAD were 0.011 to 0.028 kg and

**Table 6.** Correlations, mean absolute errors (MAE), and maximum absolute differences (MAD) between breeding values for cows and sires for fat yield predicted from test-day models with and without effects of bST.

Test day	Correlations		MAE (kg)		MAD (kg)	
	Cows	Sires	Cows	Sires	Cows	Sires
1	0.999	0.999	0.001	0.001	0.013	0.011
2	0.999	0.999	0.001	0.001	0.015	0.014
3	0.999	0.998	0.001	0.001	0.017	0.015
4	0.998	0.998	0.001	0.001	0.018	0.015
5	0.998	0.998	0.001	0.001	0.020	0.015
6	0.998	0.997	0.002	0.001	0.021	0.016
7	0.997	0.997	0.002	0.001	0.022	0.018
8	0.997	0.996	0.002	0.001	0.024	0.019
9	0.996	0.996	0.002	0.001	0.025	0.024
10	0.996	0.995	0.002	0.001	0.026	0.028

**Table 7.** Correlations, mean absolute errors (MAE), and maximum absolute differences (MAD) between breeding values for cows and sires for protein yield predicted from test-day models with and without effects of bST.

Test day	Correlations		MAE (kg)		MAD (kg)	
	Cows	Sires	Cows	Sires	Cows	Sires
1	0.995	0.994	0.002	0.001	0.018	0.014
2	0.994	0.993	0.002	0.002	0.021	0.015
3	0.993	0.992	0.003	0.002	0.024	0.016
4	0.993	0.992	0.003	0.002	0.027	0.016
5	0.992	0.991	0.003	0.002	0.030	0.016
6	0.991	0.990	0.004	0.002	0.033	0.017
7	0.990	0.989	0.004	0.003	0.036	0.018
8	0.990	0.989	0.004	0.003	0.038	0.021
9	0.989	0.988	0.005	0.003	0.041	0.024
10	0.988	0.987	0.005	0.003	0.043	0.026

0.014 to 0.043 kg (equivalent to 3.3 to 8.5 kg and 4.3 to 13.1 kg per 305 d), respectively. The correlations did not show much bias because the few bST-treated cows might not have had much influence on the correlations, or they indicate only a linear relationship between breeding values predicted from two models. On the other hand, the results of MAD suggest that PBV from a model excluding effects of bST treatment might have serious bias for individual sires.

If a repeatability model or a multiple lactation model with TD records is considered for genetic evaluation, the effects of bST in subsequent lactations should be investigated. Tsuruta (19) showed that responses to bST treatment for production traits might be different in subsequent lactations. Therefore, when sufficient data have been collected for such an analysis in the near future, further studies should be done.

### CONCLUSIONS

Average responses (7.2, 7.0, and 7.6% for milk, fat, and protein yields, respectively) to bST treatment were smaller (but statistically significant) than results published in other papers. The estimates of responses might have been greater or more accurately estimated if the dates of bST injection or frequencies of injection had been reported in DHI programs. This study was conducted assuming that all records of bST-treated cows were reported correctly and that no cows were given other preferential treatment. If these assumptions were not correct, the results could be underestimated.

The influence on PBV of including bST treatment in the model was small. It would be more difficult for a sire's PBV to be affected by bST than the PBV of a potential dam of a sire because a sire would need to have many daughters treated with bST to cause much of a bias. However, the results of MAD indicate relatively large bias in PBV of some animals although the

correlations were close to unity. If more bST treatments are used for particular cows or for the majority of a sire's daughters, larger bias in PBV might be expected.

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