Evaluation of Progeny Tests of Dairy Sires in Single Herds

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Abstract

First-lactation Holstein-Friesian HIR records of 37,890 animals were studied for the usefulness of average deviations of daughter records from contemporaries to estimate breeding values of sires whose daughters are in one herd. Breeding values based on daughters' deviations were termed unadjusted breeding values. The added usefulness of the dams' deviation from their contemporaries to adjust for selection of mates of sires also was examined. Breeding values adjusted for the deviations of the sires' mates were termed adjusted breeding values. Breeding values from Dairy Herd Improvement Association records including artificially sired daughters for 99 of the 1,355 sires involved were compared with the unadjusted and adjusted breeding values.

Comparisons of the unadjusted and adjusted breeding values with estimates of breeding values based on the average of daughter records indicated that both are more efficient than the daughter average. The adjusted had slightly more precision than the unadjusted breeding value, and it was corrected for possible effects of selection of dams. These effects do not appear to be important for comparisons among groups of sires with single-herd proofs, since rank correlations between unadjusted and adjusted breeding values were 0.978 for milk and 0.972 for per cent fat. Results of the theoretical and actual comparisons of the single-herd proofs with the breeding values from Dairy Herd Improvement Associations were in close agreement. The rank correlation between the single-herd proofs and the AIBV's for the 99 bulls was 0.51 for milk yield, and in theory the correlation was expected to lie between 0.45 and 0.51. The results of the investigation do not justify routine adjustment of regressed daughter deviations for the difference of their dams from their herdmates, even for single-herd progenies.

Introduction

Current practice in progeny testing is to utilize young sire sampling programs to provide multiherd proofs. Such programs require careful evaluation of young bulls whose pedigrees may include sires with single-herd proofs. Furthermore, numerous herds continue to use their own sires through natural service, and those naturally proven sires are a potential source of genetic material for artificial insemination.

Correlations between the estimates of breeding values based on single-herd proofs and those based on extensive multiple-herd proofs have generally been low (4, 5, 10). Comparison of the daughters of a sire with their paternally unrelated contemporaries seems to be the most promising method for evaluating even those sires with progeny in a single herd. Nonetheless, critical information is needed for assumptions usually made under artificial insemination conditions do not hold. Possible deviations from randomness in the choice of mates of sires also deserve investigation in estimating the breeding values of bulls from single-herd proofs.

This study was undertaken to examine the usefulness of the average deviation of daughter records from contemporaries for estimating the breeding value of sires whose daughters are in one herd and to evaluate the additional usefulness of the dams' average deviation from their contemporaries to adjust for the selection of dams.

Data and Procedures

Data. First lactations of 37,890 animals from 442 Holstein-Friesian HIR herds were expressed as 305-day, 2 ×, mature equivalent records. First lactations were the first available lacta-
tions initiated by cows at under 36 months of age. Contemporaries, other first-lactation cows calving in the same herd-year-season but excluding paternal sisters of the cow, were available for each of the records. Lactations were initiated from March, 1952, through April, 1961. They were divided into two seasonal groupings, October through April and May through September, as recommended by Tucker and Legates (12), a total of 16 year-season groupings.

When a sire had eight or more daughters in a single herd, they were defined as a single-herd progeny group. Only the first single-herd progeny group of a sire was studied (first herd with eight daughters completing records). There were 1,355 sires of such progeny groups.

In another phase of the study, the artificial insemination summaries compiled by the U.S. Department of Agriculture for December, 1962, to October, 1964, were utilized for 99 of the sires which had lactation records for at least 25 artificially sired daughters. These summaries from DHIA data included records from all lactations, with a seasonal grouping of herdmates based on a five-month moving average.

**Definition of breeding values.** Two methods were developed for estimating breeding values of sires with single-herd proofs. The first method utilized the regressed average deviation of the daughters from their herdmates, referred to as “unadjusted breeding value” (UBV). The second method, in addition to deviations of the daughters, included an adjustment for the deviations of the mates of the sires from their first-lactation herdmates. The breeding values estimated by this method were designated as “adjusted breeding values” (ABV).

The breeding value of a sire \( g \) expressed as a deviation from the mean, given a measurement \( z \) of the performance of his progeny, may be described by a model corresponding to a bivariate normal distribution (11). The expected value of \( g \) is

\[
E[g/z] = E[\hat{g}] + \frac{\sigma_g}{\sigma_z} (z - E[z])
\]

where \( E \) represents the mathematical expectation, \( \rho \) is the correlation between \( g \) and \( z \), and \( \sigma_z \) is the standard deviation of the measurement.

Under the assumption that the expected values of \( g \) and \( z \) are both equal to zero, the predicted breeding value of the sire (\( \hat{g} \)) is

\[
\hat{g} = \frac{\sigma_g}{\sigma_z} (z) = \beta (z).
\]

Predicted breeding values for the 1,355 sires were computed with individual \( \beta \)'s for each sire. These individual \( \beta \)'s took into account the numerator and distribution of daughters, dams, and herdmates, and the variances for the effects in the subsequent linear model. The model used to describe a record was

\[
Y_{ijkl} = \mu_j + h_i + s_k + e_{ijkl}
\]

where

\[
Y_{ijkl} \text{ is the first-lactation record of the } j^{th} \text{ cow by the } k^{th} \text{ sire in the } i^{th} \text{ year-season in the } j^{th} \text{ herd}, \mu_j \text{ is the mean for the population of all first lactations in the } j^{th} \text{ year-season, } h_i \text{ is the effect of the } i^{th} \text{ herd, } s_k \text{ is the effect of the } k^{th} \text{ sire, and } e_{ijkl} \text{ is a random effect peculiar to the } ijkl^{th} \text{ record, } l = 1, 2, \ldots, n_{ijk}.
\]

The herd, sire, and error effects are random and normally distributed with means equal to zero and variances \( \sigma^2_h, \sigma^2_s, \text{ and } \sigma^2_e \). No sire-by-herd interaction was included in the model, since a previous analysis of multiple-herd progenies from these data had shown them to be negligible (9).

Year-season means (Table 1) for the population were computed from all first-lactation records in the data. These means were assumed to have negligible sampling errors.

\[
\hat{\mu}_j = \frac{\sum_{i,j,k} Y_{ijkl}}{\sum_{i,j,k} n_{ijkl}} = \frac{\sum_{i,j} Y_{ij.}}{n_{.j}}.
\]

The adjusted herdmate average for a cow was computed by the procedure described by Heidhues et al. (6) and Van Vleck et al. (13). The adjusted herdmate average for the daughters of the \( k^{th} \) sire, in the \( j^{th} \) year-season in the \( i^{th} \) herd (\( \text{AHM}_{ijk} \)) was computed by

\[
\text{AHM}_{ijk} = \frac{\sum_{i,j,k} Y_{ijkl} - \text{AHM}_{ijk} - \mu_j}{n_{ij.} - n_{ijk} + 1}.
\]

We assumed that all sires of herdmates of a given cow in a herd-year-season group had the same number of daughters. The number of sires of the herdmates of the \( ijk^{th} \) progeny group was defined as \( r_{ijk} \), and the average number of daughters per sire of herdmates as

\[
\bar{n}_{ijk} = \frac{n_{ijk} - n_{ij.}}{r_{ijk}}.
\]

To derive the expected values we also assumed that the sires of herdmates were not repeated across seasons, and that no sire of daughters appeared as sire of herdmates for other cows.

In terms of the model, the adjusted herdmate average is

\[
\text{AHM}_{ijk} = \frac{(n_{ij.} - n_{ijk})h_i + \bar{n}_{ijk} \sum_{k} s_k + \sum_{k} e_{ijkl} + \mu_j}{n_{ij.} - n_{ijk} + 1}.
\]
Table 1. Number of records and the means for milk yield and fat per cent for each year-season.

<table>
<thead>
<tr>
<th>Year-season</th>
<th>Number records</th>
<th>Milk (kg)</th>
<th>Fat (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2,278</td>
<td>5,777</td>
<td>3.68</td>
</tr>
<tr>
<td>2</td>
<td>2,918</td>
<td>5,835</td>
<td>3.69</td>
</tr>
<tr>
<td>3</td>
<td>2,953</td>
<td>5,665</td>
<td>3.70</td>
</tr>
<tr>
<td>4</td>
<td>2,553</td>
<td>5,901</td>
<td>3.68</td>
</tr>
<tr>
<td>5</td>
<td>2,598</td>
<td>5,713</td>
<td>3.70</td>
</tr>
<tr>
<td>6</td>
<td>2,718</td>
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</tr>
<tr>
<td>7</td>
<td>2,783</td>
<td>5,781</td>
<td>3.72</td>
</tr>
<tr>
<td>8</td>
<td>2,840</td>
<td>5,868</td>
<td>3.69</td>
</tr>
<tr>
<td>9</td>
<td>2,726</td>
<td>5,793</td>
<td>3.73</td>
</tr>
<tr>
<td>10</td>
<td>2,664</td>
<td>6,089</td>
<td>3.78</td>
</tr>
<tr>
<td>11</td>
<td>2,558</td>
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</tr>
<tr>
<td>12</td>
<td>2,567</td>
<td>6,319</td>
<td>3.79</td>
</tr>
<tr>
<td>13</td>
<td>2,521</td>
<td>6,013</td>
<td>3.76</td>
</tr>
<tr>
<td>14</td>
<td>2,452</td>
<td>6,333</td>
<td>3.72</td>
</tr>
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<td>15</td>
<td>2,615</td>
<td>6,122</td>
<td>3.76</td>
</tr>
<tr>
<td>16</td>
<td>1,770</td>
<td>6,419</td>
<td>3.73</td>
</tr>
<tr>
<td>Total</td>
<td>40,944</td>
<td>5,965</td>
<td>3.71</td>
</tr>
</tbody>
</table>

The correlation between \( UB V_k \) and \( g_k \) is

\[
\rho = \frac{\sigma_{g_k}}{\sigma_{D_k}}
\]

and varies as the number of daughters, number of herdmates, number of sires of herdmates in each year-season, and the number of year-seasons affect \( \sigma_{D_k} \).

Individual unadjusted breeding values were computed for each of the 1,355 sires with single-herd progenies. The \( \sigma_{b_k}^2, \sigma_{c_k}^2 \), and \( \sigma_{e_k}^2 \) for the computation were from an analysis of variance of the 22,608 records in the single-herd progenies (9). These values were \( \hat{\sigma}_{b_k}^2 = 394,146 \) and 0.0200, \( \hat{\sigma}_{c_k}^2 = 148,619 \) and 0.0142, and \( \hat{\sigma}_{e_k}^2 = 913,277 \) and 0.0686 for milk yield and test.

Consideration of mates. Under single-herd conditions, a proof based on the daughter deviations may be subject to bias according to how the mates were chosen. To adjust for this potential bias and to give the appropriate weights to the information from daughters and dams, an index procedure (14) was used to estimate the sire’s breeding value from the combined information from daughters and dams. The procedure takes into account the environmental correlations between daughters, dams, and herdmates in single herds.

The estimated breeding value of a sire was described by \( \hat{g} = \beta_1 \overline{D} + \beta_2 \overline{M} \) corresponding to a multiple regression model where \( \overline{D} \) is the average deviation of the daughters from herdmates, \( \overline{M} \) is the average deviation from herdmates of the dams, of the cows in \( \overline{D} \) having first-lactation herdmates, and \( \beta_1 \) and \( \beta_2 \) are the partial regression coefficients of the sire’s breeding value on the daughter and dam average deviations. Solutions for the \( \beta \)'s are from the equations

\[
\beta_1 \sigma_{D_k}^2 + \beta_2 \sigma_{M_k}^2 + g_k = \sigma_{e_k} \overline{D} \overline{D}
\]

where

\( \sigma_{D_k}^2 \) is the variance of the average of daughter deviations,

\( \sigma_{M_k}^2 \) is the variance of the average of the dams’ deviations,

\( \sigma_{D_k, M_k} \) is the covariance of the daughter and dam average deviations,

\( \sigma_{e_k} \overline{D} \) is the covariance of the sire’s breeding value and \( \overline{D} \) and equals \( 2\sigma_{e_k} \overline{D} \), and

\( \sigma_{e_k} \overline{M} \) is the covariance of the sire’s merit with the average deviation of his mates. This covariance was assumed to be zero.
The solutions for the $\beta$'s are

\[ \beta_1 = \frac{-2\sigma_b^2 \sigma_{DM}^2}{\sigma_b^2 \sigma_{DM}^2 - (\sigma_{DM})^2} \text{ and } \]

\[ \beta_2 = \frac{2\sigma_b^2 \sigma_{DM}^2}{\sigma_b^2 \sigma_{DM}^2 - (\sigma_{DM})^2} = -\beta_1 \frac{\sigma_{DM}^2}{\sigma_b^2}; \]

then \[ \hat{D} = \frac{2\sigma_b^2 \sigma_{DM}^2}{\sigma_b^2 \sigma_{DM}^2 - (\sigma_{DM})^2} \left[ D - \frac{\sigma_{DM}^2}{\sigma_b^2} (\bar{M}) \right]. \]

Since $\sigma_{DM}^2/\sigma_b^2$ is the regression of the dams' average deviation on the daughters' average deviation, the adjusted daughter average deviation for the $k^{th}$ sire in the $i^{th}$ herd may be defined as

\[ \overline{AD}_{ik} = \bar{D}_{ik} - \frac{\sigma_{DM}^2}{\sigma_b^2} (\bar{M}_{ik}) \]

where $\bar{M}_{ik}$ is the average deviation of the mates of the $k^{th}$ sire in the $i^{th}$ herd.

Since $\beta_1$ can be defined as the regression of the sire's breeding value on the adjusted daughter average deviation ($\beta_1 = \overline{AD}_k$), the adjusted breeding value of the sire may be expressed as

\[ ABV_j = \beta_{kj} \overline{AD}_k \]

The expected correlation between $ABV_k$ and the true merit of the sire is

\[ \rho_{k,\sigma} = \frac{\rho_{n_{ijk}}}{\sqrt{\frac{1}{h^2} + \frac{4(n_{ijk} - 1)\rho_{n_{ijk}}}{\Sigma n_{ijk}(n_{ijk} - 1)\rho_{n_{ijk}}}/n_{ijk}}}. \]

The expected correlation between each of the different estimates ($\sigma$, UBV, ABV) of breeding value and the true breeding value of the sire were computed for varying amounts of information in the proof.

Comparison of single herd and Artificial Insemination proof. The estimated breeding value of the $k^{th}$ sire as a deviation from the population mean and from the AI proof in DHIA was $AIBV_k = 2(PDA_k - PM)$ where $PDA_k$ is lactation records were not available to be included in the average.

The efficiency of the actual average of daughter records ($\sigma$) as an estimator of breeding value from single-herd sire proofs also was examined.

The following quantities were defined:

\[ n_{ijk} = \text{number of daughters of the } k^{th} \text{ sire in the } i^{th} \text{ year-season } \]

\[ h^2 = \frac{\sigma_{h}^2}{\sigma_{h}^2 + \sigma_{n}^2 + \sigma_{g}^2 + \sigma_{e}^2}; \]

\[ p = \frac{\sigma_{h}^2 + \sigma_{g}^2}{\sigma_{h}^2 + \sigma_{n}^2 + \sigma_{g}^2 + \sigma_{e}^2}; \]

\[ q = \frac{\sigma_{n}^2 + \sigma_{e}^2}{\sigma_{h}^2 + \sigma_{n}^2 + \sigma_{g}^2 + \sigma_{e}^2}. \]

The expected correlation between the single-herd daughter average and the sire's true merit is

\[ \rho_{k,\sigma} = \frac{n_{i_{jk}}h^2}{\sqrt{1 + \frac{4(n_{i_{jk}} - 1)h^2}{\Sigma n_{i_{jk}}(n_{i_{jk}} - 1)p + 2\Sigma n_{i_{jk}}n_{j_{ik}}q}}}. \]
the predicted daughter average in the USDA list, and PM is the population mean in the most recent published summary for the sire. These means, the years included, and the lists in which they appeared are given in Table 2.

The regression of the breeding value of the sire on the daughter measurement used by the U.S. Department of Agriculture is \( 2n/(n + t^2) \) when n is the number of daughters of the sire. The expected correlation between the AIBV and the sire's true merit is \( \rho = \sqrt{n/(n + 12)} \).

To compare the UBV and ABV with each other and with the AIBV from DHIA data, the means and standard deviations were computed for 99 sires for which the three types of proof were available. These sires had a minimum of eight daughters and five dams in a single herd and at least 25 artificial-insemination daughters.

Simple correlations between the measurements used as predictors (D and AD) in the single-herd proof, the dam average deviation (M), and the AIBV were computed for the same 99 sires. The multiple correlation coefficients of the D and M with the AIBV were also computed. Rank correlations of the estimated breeding values of the sires in the sample were obtained for milk yield and fat per cent.

### Results and Discussion

Expected correlations between the daughter average (O) and the sire's merit (g) for equal numbers of daughters across year-seasons, and for varying numbers of daughters are given in Table 3. Values of \( h^2, p, \) and \( q \) from the data and used in the computations were 0.37, 0.34, and 0.25 for milk yield and 0.53, 0.23, and 0.19 for fat per cent.

The values in Table 3 confirm that the average of daughter records is not a good predictor of the merit of sires proven in single herds and that the improvement in efficiency of the estimates with increasing number of daughters is small, even when the daughters are distributed in several year-seasons. The absolute magnitude of even these values is high, since the heritability of 0.37 in these and subsequent comparisons in Table 4 is much above the more commonly found 0.20 to 0.25.

When the average of daughter deviations, or the same value adjusted for average of their dams' deviations, is used for the evaluation of sires, a large number of variables must be considered. This makes it difficult to provide a simple tabulation of the expected correlations between the estimated and the true breeding values. However, to provide an indication of the magnitude of those correlations, a series of sample cases from the data has been listed in Table 4. Several bulls with the same number of daughters have been listed to show the variation in the expected correlations. This variation...
TABLE 4. Examples of expected correlations between the true merit of sires and their unadjusted and adjusted breeding values for varying number and distribution of daughters and dams in year-season for single-herd proofs.

<table>
<thead>
<tr>
<th>Daughter Number</th>
<th>Number year-season</th>
<th>Number dams</th>
<th>$\rho_{e,UBV}$</th>
<th>Fat</th>
<th>$\rho_{e,ABV}$</th>
<th>Fat</th>
</tr>
</thead>
<tbody>
<tr>
<td>8</td>
<td>3</td>
<td>3</td>
<td>.602</td>
<td>.655</td>
<td>.623</td>
<td>.655</td>
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<td>20</td>
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<td>.896</td>
<td>.876</td>
<td>.904</td>
</tr>
</tbody>
</table>

may be due to number of herdmates, of sires of herdmates, of sires of dams, etc.

A comparison of the expected correlations in Table 4 with those in Table 3 indicates that deviations from adjusted herdmate averages markedly improve the efficiency of the estimates of breeding value, both for small and large numbers of daughters. If the number of herdmates per daughter is large and the daughters are distributed in several seasons, the upper limit of the expected correlations (as the number of daughters increases without limit) is much closer to unity than for the average of daughter records.

The expected relative gain in precision from ABV over and above the precision of the UBV's is $\rho_{e,ABV}/\rho_{e,UBV} = 1/(1 - \rho_{D,M}^2)$. This is identical to the expression given by Lush (7).

Table 4 shows the means and standard deviations for milk yield and per cent fat for the UBV, ABV, and AIBV for the 99 sires for which the three estimates of breeding values were available. The mean breeding values for milk yield from the single-herd estimates were higher than the AI estimate. A similar situation was reported by Meek and Van Vleck (8) in contrasting non-AI herdmate comparisons with AI proofs. A similar situation was reported by Meek and Van Vleck (8) in contrasting non-AI herdmate comparisons with AI proofs. It is likely that an interval of 3 to 4 years elapsed between the first lactations of

TABLE 5. Means and standard deviations of estimated breeding values for milk yield and fat per cent for sires with the three estimates of breeding value.

<table>
<thead>
<tr>
<th>Number sires</th>
<th>Means (kg)</th>
<th>Standard deviations</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>UBV</td>
<td>ABV</td>
</tr>
<tr>
<td>Milk</td>
<td>99</td>
<td>309</td>
</tr>
<tr>
<td>Fat %</td>
<td>99</td>
<td>.038</td>
</tr>
</tbody>
</table>
the natural-service daughters and the AI daughters. Thus, the effect of genetic trend in the population could become important and make the later sire proof lower than the initial proof. Burnside and Legates (3) reported genetic trends in these HIR Holstein herds from 0.75 to 0.92% of the average milk yield, or 45 to 55 kg of milk per year. Such a trend could account for much of the difference between the single-herd and AI estimates (UBV - AIBV = 188 kg and ABV - AIBV = 133). A further reason for the differences between them and the AIBV's could be that the single-herd data may have been the major basis for choosing the sire for artificial insemination.

The larger mean for milk yield for the UBV's than for the ABV's indicates that, on the average, the sires in the sample were mated to cows above their contemporaries. The unweighted average of the dams' averages for the group of sires was 259 kg of milk above herdmates, and the difference between the UBV and the ABV means was 55 kg. The quotient (55/259) = 0.21 gives an indication of the average weight given to the dams' deviations (M) in the computation of the ABV's.

The means for fat percent suggest that this situation is different from that for milk yield. The highest mean percentage fat was obtained for the ABV's, and the lowest was for the ABV's. Differences were small and might be attributed to genetic differences between the DHIA and HIR populations. On the average, the deviation of the dams from their contemporaries was essentially zero for fat per cent and the difference between the means of the UBV's and the ABV's was negligible.

Standard deviations for the estimated breeding values were in good agreement with their theoretical expectations (ρp2). The standard deviations for milk yield in the single-herd proofs were higher than the AI standard deviation. However, the estimate of genetic variance for milk yield in the HIR data was higher than has been reported for DHIA data. For fat per cent the standard deviation of the AIBV's was higher than those of the single herd estimates.

The simple correlations between D, M, and AD and AIBV for milk yield and test are in Table 6, as well as the multiple correlation coefficients of D and M with AIBV.

The procedure to develop the ABV was based on the assumption that the true merit of the sire and the deviation of his mates from their contemporaries (M) were uncorrelated. The correlations of M and AIBV (−.11 and 0.09) were not significantly different from zero and substantiated the validity of that assumption. The correlations between the single-herd predictors and the AIBV's are in agreement with their expectations when the number of daughters in the proof is considered.

For a group of bulls, the expected correlation between different estimates (P1 and P2) of breeding value (after Bereskin and Lush, 2) is

\[ \rho_{P_1P_2} = k = \frac{1}{N} \sum_{i=1}^{N} \rho_{g_{i}g_{i}} \rho_{g_{i}g_{k}} \rho_{g_{k}} \]

with \( N \) = the number of bulls in the group. For milk yield, the minimum expected correlation between the single-herd and the AI proofs with 8 and 25 daughters, respectively, is approximately 0.45. This minimum increases to about 0.51 when the number of AI daughters is 100. Meek and Van Vleck (8) reported values (0.47 to 0.69) for the correlation of non-AI herdmate comparisons with the Cornell daughter level and the uncorrected USDA-AI daughter-herdmate difference that were similar to values in this study.

Only small differences were found between the two single-herd predictors. This suggested that, on the average, no appreciable precision was gained by including the dams’ average deviation from herdmates in the estimates of the sires’ breeding values. From comparing the simple correlation coefficients with the multiple correlation coefficients, even when the optimum weight was given to the dams' deviation, the gain in precision was extremely small. Consequently, when weights other than the optimum ones for a particular sample are used, as in the

<table>
<thead>
<tr>
<th>AIBV milk</th>
<th>AIBV % fat</th>
</tr>
</thead>
<tbody>
<tr>
<td>D*</td>
<td>0.514</td>
</tr>
<tr>
<td>M</td>
<td>−.11</td>
</tr>
<tr>
<td>D,M</td>
<td>0.517*</td>
</tr>
<tr>
<td>AD</td>
<td>0.503</td>
</tr>
</tbody>
</table>

*D is average deviation from herdmates of daughters; M is average deviation from herdmates of dams; D,M is the combination of the above two variables for multiple correlation and AD is the average of daughter deviations adjusted for their dams.

*Multiple correlation coefficients.
Table 7. Rank correlations of estimates of breeding value for milk yield and fat per cent.

<table>
<thead>
<tr>
<th></th>
<th>AIBV versus</th>
<th>AIBV versus</th>
<th>UBV versus</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk yield</td>
<td>.507</td>
<td>.507</td>
<td>.978</td>
</tr>
<tr>
<td>Fat %</td>
<td>.732</td>
<td>.727</td>
<td>.972</td>
</tr>
</tbody>
</table>

adjusted average of daughter deviations, the correlation could be lower for the adjusted than for the unadjusted estimates of breeding value.

From Table 7, the rank correlations between the AIBV and the two types of single-herd estimates of breeding value were essentially the same, further indicating that there was little difference in precision between the adjusted and unadjusted estimates of breeding value. Previous reports in the literature (1, 7, 14) have also indicated that little is gained by including the dams in the sire-appraisal procedures, especially when deviations from herdmates are used.

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References