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# Sire Evaluation by Only Extended Partial Milk and Fat Records

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## ABSTRACT

The standard of comparison for dairy production records is the 305-day lactation, and much research has been directed to estimating 305-day milk and fat records from incomplete or in-progress records. This study was to determine the effect of several methods of extending incomplete records on sire evaluation. Complete 305-day milk and fat records of first lactations of 73,724 daughters of 1,362 artificial insemination Holstein sires processed at the New York Dairy Records Processing Laboratory were used to compute sire proofs for yield of milk and fat. Partial records of two lengths (60 to 80 days and 130 to 160 days) on the same daughters were extended by three methods, and sire proofs were computed from these six sets of extended records. Correlations between sire proofs with complete records only and sire proofs with only extended incomplete records were .93 or .94 (for milk proofs) when the length of the part record was between 130 and 160 days, regardless of the method of extension. Correlations were less (.66 to .81 for milk proofs), as expected, when the length of the part record was between 60 and 80 days.

## INTRODUCTION

The 305-day lactation has been a standard for comparison of dairy production records and serves as the raw material for evaluation of genetic merit of production traits of sires and cows. The interval from the birth of a bull calf to completion of his daughters' first records is over 5 yr. To obtain daughter records earlier, much research has been directed to methods of

estimating 305-day milk and fat records from incomplete or in-progress records (1, 3, 5, 6, 7, 8, 9, 11).

Little is known of the effect of extended records on prediction of genetic merit of sires. Without such information, choice of a method of extension may be inexact. Examining relationships between sire evaluation and various methods of extending incomplete dairy records was the objective of this study. In addition, the effect of the length of in-progress records on sire evaluation was examined.

## MATERIALS AND METHODS

Test day records of 73,724 first lactations of daughters of 1,362 artificial insemination (AI) Holstein sires in the Northeast processed at the Dairy Records Processing Laboratory in Ithaca, NY, were in this study. Each record had nine or more test days. Records of cows whose sire had fewer than 40 daughters were excluded. For sires with more than 60 daughter records, 60 records were selected randomly such that each herd contributed at least one record. A further requirement was that 12-mo rolling herd averages be available for herds since two of the extension procedures required herd average milk production.

Initially, sire proofs for yield of milk and fat and percent fat were computed with complete first lactation records only. Computations followed the model of the Northeast Artificial Insemination Sire Comparison (NEAISC) (4). Three methods of extending incomplete records to 305-day equivalents representative of those recently developed or currently used were applied to part records of two lengths.

Until recently incomplete records in the Northeast were extended to 305-day equivalents by the following formula:

$$\hat{Y}_{305} = \text{Factor} \times Y_n \quad [1]$$

where  $Y_n$  is the cumulative production to day  $n$ , and  $\hat{Y}_{305}$  is estimated production for 305

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days. Determination of the appropriate factor is based on age of cow at calving (within lactation number), season of freshening, and n. For identification, this method is estimation by cumulative ratio factor (CRF).

Recently, a method extending incomplete lactation records from information on last test day has been studied (1, 3, 5). The prediction of 305-day equivalent is of the form:

$$\hat{Y}_{305} = Y_n + DR \times \text{Factor} \times LT \quad [2]$$

where DR is the number of days remaining from day n to day 305, LT is the last test-day production (milk or fat), and  $Y_n$  is the same as in [1]. Choice of the appropriate factor is based on age at freshening (in months), season of freshening, stage of lactation, and herd milk production (5). This method will be called estimation from last test day (LTD).

To reduce the number of stages of lactation required and to allow the factor to change with production, a third method was developed for use in the Northeast (11). Though complex in appearance, this method requires no more information than that required for the method of equation [2]. Prediction of 305-day equivalent is of the form:

$$\hat{Y}_{305} = Y_n + (b_1 LT + b_2 LT \times n + b_3 / LT + b_4 \times \sqrt{n/LT}) \times DR \quad [3]$$

where  $Y_n$ , DR, and LT are the same as defined above and the  $b_i$  ( $i = 1, 2, 3, 4$ ) are coefficients (factors) appropriate for each age at freshening, season of freshening, stage of lactation, and herd milk production. This method is referred to as the last-test day equation (LTDE).

We chose two stages of lactation from which part records would be extended to 305-day milk and fat equivalents by these three methods. The first stage was 60 to 80 days postpartum; the second stage was 130 to 160 days postpartum. These three methods were applied to part records from two stages of lactation, creating six sets of estimated first lactation records which were used to compute six estimates of sires' transmitting abilities through the NEAISC procedure.

The model for the  $ijkl$ th record is:

$$Y_{ijkl} = \mu + h_i + g_j + s_{jk} + e_{ijkl}$$

where  $\mu$  is an unknown constant;  $h_i$  is the effect of the  $i$ th herd-year-season of freshening;  $g_j$  is the effect of the  $j$ th sire group (grouping by sire identification number);  $s_{jk}$  is the effect of the  $k$ th sire within the  $j$ th group; and  $e_{ijkl}$  represents all other variation not specified in the model for the  $l$ th record. The herd-year-season and group effects are fixed while  $s_{jk}$  and  $e_{ijkl}$  are random variables distributed

$$\begin{bmatrix} s \\ e \end{bmatrix} \sim \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \quad \begin{bmatrix} A\sigma_s^2/\sigma_e^2 & 0 \\ 0 & I \end{bmatrix} \sigma_e^2$$

where A is the numerator relationship matrix among sires. Heritability of milk yield is .25, and the ratio  $\sigma_e^2/\sigma_s^2 = 15$ . The estimate of .5 of a sire's genetic merit (sire proof) is  $\hat{g}_j + \hat{s}_{jk}$ , where the ^ signifies a solution to mixed model equations. The constraint imposed to obtain a solution used LaGrange multipliers to set a function of sire proofs to zero. This function is chosen so that the mean evaluation of sires of 2-yr-old cows freshening in 1968 weighted by number of daughters would be zero.

The six sets of sire proofs from extended

TABLE 1. Means (kg) and standard deviations (SD) for sire proofs of milk and fat.

Extension method	Milk		Fat	
	$\bar{X}$	SD	$\bar{X}$	SD
	----- Complete records -----			
	542	793	18.1	13
	----- Records extended from 60 to 80 days -----			
CRF <sup>a</sup>	595	343	19.5	16
LTD <sup>b</sup>	582	339	20.0	11
LTDE <sup>c</sup>	596	396	20.4	9
	----- Records extended from 130 to 160 days -----			
CRF	572	760	19.1	14
LTD	571	745	18.6	14
LTDE	582	784	19.5	13

<sup>a</sup>Cumulative ratio factors.

<sup>b</sup>Last test day method.

<sup>c</sup>Last test day equation method.

lactation records were compared to proofs for only complete lactations of the same cows. Correlations between sets of sire proofs evaluated how well the methods of extending incomplete lactations matched in sire evaluation.

### RESULTS AND DISCUSSION

Table 1 presents means and standard deviations of sire proofs for milk and fat. Inspection of the means of milk proofs reveals a tendency among all extension methods to inflate sire proofs above those from only complete records. This is true, albeit less, for means of fat proofs. The nature of this result is particularly disturbing because means of projected milk and fat records in Table 2 do not show a similar increase over complete records. Although an analytic explanation for the inflated proof means is not possible, recall that each set of sire proofs is computed with the same sires, the same relationship matrix and group definitions, and the same number of progeny. The only change is the observation vector,  $y$ . Note that the results of Table 1 are presented as sire proofs, which are computed as the sum of a sire's group

TABLE 2. Means (kg) and standard deviations (SD) for daughter records of milk and fat.

Extension method	Milk		Fat	
	$\bar{X}$	SD	$\bar{X}$	SD
	————— Complete records —————			
	5457	2496	199.6	100
	————— Records extended from 60 to 80 days —————			
CRF <sup>a</sup>	5581	1987	209.1	76
LTD <sup>b</sup>	5334	1955	196.0	83
LTDE <sup>c</sup>	5444	2035	200.5	81
	————— Records extended from 130 to 160 days —————			
CRF	5483	2292	201.4	90
LTD	5376	2283	196.4	96
LTDE	5440	2306	198.7	89

<sup>a</sup>Cumulative ratio factors.

<sup>b</sup>Last test day method.

<sup>c</sup>Last test day equation method.

TABLE 3. Method 1 estimates of variance components ( $kg^2$ ) for daughter milk records in a herd-year-season by sire model.

Extension method	$\hat{\sigma}_e^2$ ( $\times 10^6$ )	$\hat{\sigma}_s^2$ ( $\times 10^5$ )	$h^2$	$\hat{\sigma}_e^2/\hat{\sigma}_s^2$
	————— Complete records —————			
	2.712	2.270	.309	11.95
	————— Records extended from 60 to 80 days —————			
CRF <sup>a</sup>	2.282	2.182	.349	10.46
LTD <sup>b</sup>	2.418	2.207	.335	10.96
LTDE <sup>c</sup>	2.178	2.135	.357	10.20
	————— Records extended from 130 to 160 days —————			
CRF	1.872	2.224	.425	8.42
LTD	1.971	2.264	.412	8.71
LTDE	1.707	2.212	.459	7.72

<sup>a</sup>Cumulative ratio factors.

<sup>b</sup>Last test day method.

<sup>c</sup>Last test day equation method.

solution (as deviated from the base group) and the individual sire solution. When examined separately, the average individual sire solution (within and across groups) as well as the average group solutions are overestimated also in comparison to the predictions made with complete records only. That this should occur is not surprising, but it is a cause for concern.

One should not expect the average sire proofs (or average group or sire solutions) to remain constant from one evaluation to the next. If, on the average, the predicted mean of progeny records of a sire are over- or underestimated, in comparison to the actual progeny mean, the average sire and group solutions will be altered similarly. Thus, although the average of predicted records is equivalent to the average of complete records (Table 2), sire proofs can be overestimated if particular individual sires have overestimated progeny records. When relationships are included in the equations, overestimation of one sire can augment prediction of another sire through the off-diagonal terms of the relationship matrix. Note, however, that comparison of proof means is valid only in this example where the group definition is the same for all evaluations. Because the

TABLE 4. Phenotypic correlations between sire proofs for milk computed with daughter records extended to 305-day equivalents by several methods.

			CRF	LTD	LTDE	CRF	LTD	LTDE
		(1)	A	A	A	B	B	B
		(1)	(2)	(3)	(4)	(5)	(6)	(7)
Complete	(1)	1.00	.81	.79	.66	.94	.94	.93
CRF <sup>a</sup>	A <sup>b</sup> (2)		1.00	.97	.96	.82	.82	.83
LTDC	A (3)			1.00	.95	.84	.81	.80
LTDE <sup>d</sup>	A (4)				1.00	.83	.83	.81
CRF	B <sup>c</sup> (5)					1.00	.98	.97
LTD	B (6)						1.00	.99
LTDE	B (7)							1.00

<sup>a</sup>Cumulative ratio factors.

<sup>b</sup>Records extended with a part length of 60 to 80 days.

<sup>c</sup>Last test day method.

<sup>d</sup>Last test day equation method.

<sup>e</sup>Records extended with a part length of 130 to 160 days.

mean sire proof is a nonestimable function, this comparison is not always valid.

Variance component estimates, under an assumed completely random model, i.e., Method 1(10), are in Table 3. Their presentation is intended for those readers interested in the use of extended in-progress records for sire evaluation. Throughout this investigation, computations were carried out with  $\sigma_e^2/\sigma_s^2 = 15$ . As evidenced by Table 3, this assumption may not be valid for extended in-progress records. Al-

though computing sire proofs with an overestimate of the variance ratio  $\sigma_e^2/\sigma_s^2$  will not bias the prediction of sire proofs, use of the incorrect ratio will increase the mean square error of prediction.

Variance of sire proofs and daughter records (in comparison to complete records) associated with 305-day equivalents where the part record was between 60 and 80 days in length was decreased. This directly results from prediction of 305-day equivalents. Extending in-progress

TABLE 5. Phenotypic correlations between sire proofs for fat computed with daughter records extended to 305-day equivalent by several methods.

			CRF	LTD	LTDE	CRF	LTD	LTDE
		(1)	A	A	A	B	B	B
		(1)	(2)	(3)	(4)	(5)	(6)	(7)
Complete	(1)	1.00	.72	.68	.70	.87	.85	.86
CRF <sup>a</sup>	A <sup>b</sup> (2)		1.00	.85	.86	.70	.63	.66
LTDC	A (3)			1.00	.97	.68	.63	.63
LTDE <sup>d</sup>	A (4)				1.00	.69	.64	.65
CRF	B <sup>c</sup> (5)					1.00	.96	.97
LTD	B (6)						1.00	.99
LTDE	B (7)							1.00

<sup>a</sup>Cumulative ratio factors.

<sup>b</sup>Records extended with a part length of 60 to 80 days.

<sup>c</sup>Last test day method.

<sup>d</sup>Last test day equation method.

<sup>e</sup>Records extended with a part length of 130 to 160 days.

TABLE 6. Genetic correlations between sire proofs for milk computed with daughter records extended to 305-day equivalent by several methods.

			CRF	LTD	LTDE	CRF	LTD	LTDE
	(1)		A	A	A	B	B	B
	(1)	(2)	(2)	(3)	(4)	(5)	(6)	(7)
Complete	(1)	1.00	.82	.80	.81	1.15	1.16	1.16
CRF <sup>a</sup>	A <sup>b</sup>	(2)	1.00	1.13	1.16	.75	.76	.77
LTD <sup>c</sup>	A	(3)		1.00	1.13	.73	.76	.76
LTDE <sup>d</sup>	A	(4)			1.00	.73	.74	.74
CRF	B <sup>e</sup>	(5)				1.00	1.18	1.18
LTD	B	(6)					1.00	1.18
LTDE	B	(7)						1.00

<sup>a</sup>Cumulative ratio factors.

<sup>b</sup>Records extended with a part length of 60 to 80 days.

<sup>c</sup>Last test day method.

<sup>d</sup>Last test day equation method.

<sup>e</sup>Records extended with a part length of 130 to 160 days.

records where the part record is between 60 and 80 days has less information than for part records of 130 to 160 days, and, therefore, the variance of the prediction is reduced.

Relationships between sire proofs from complete daughter records and proofs based on extended incomplete records are in Tables 4 and 5. Table 4 presents phenotypic correlations among sets of sire proofs for milk production. Not surprisingly, Table 4 shows that sire proofs computed from incomplete records of 130 to

160 days in length were associated more closely with complete lactation proofs than sire proofs predicted from daughter records of 60 to 80 days in length. Table 5, which contains correlations for sire proofs for daughter fat production, presents similar results. Also important, however, is that the several methods of extending part records are associated closely, particularly for part records of lengths between 130 to 160 days.

Genetic correlations between the seven sets of sire proofs are in Tables 6 and 7 for milk and

TABLE 7. Genetic correlations between sire proofs for fat computed with daughter records extended to 305-day equivalent by several methods.

			CRF	LTD	LTDE	CRF	LTD	LTDE
	(1)		A	A	A	B	B	B
	(1)	(2)	(2)	(3)	(4)	(5)	(6)	(7)
Complete	(1)	1.00	.87	.90	.86	.96	1.02	1.01
CRF <sup>a</sup>	A <sup>b</sup>	(2)	1.00	.99	1.14	.81	.75	.80
LTD <sup>c</sup>	A	(3)		1.00	1.04	.80	.74	.72
LTDE <sup>d</sup>	A	(4)			1.00	.82	.75	.73
CRF	B <sup>e</sup>	(5)				1.00	1.14	1.17
LTD	B	(6)					1.00	1.16
LTDE	B	(7)						1.00

<sup>a</sup>Cumulative ratio factors.

<sup>b</sup>Records extended with a part length of 60 to 80 days.

<sup>c</sup>Last test day method.

<sup>d</sup>Last test day equation method.

<sup>e</sup>Records extended with a part length of 130 to 160 days.

fat, respectively. Computation of these coefficients required proper adjustment of the phenotypic correlations in Tables 4 and 5 (2). Appeal-

ing to introductory selection index methodology, the following approximate expectations of the parts of the correlations may be derived.

$$E(\hat{r}_{ij}) = \frac{\sum_k b_{ik} b_{jk} \sigma_{s_i s_j}}{\left\{ \left[ \sum_k b_{ik}^2 \left( \sigma_{s_i}^2 + \frac{\sigma_{e_i}^2}{n_{ik}} \right) \right] \left[ \sum_k b_{jk}^2 \left( \sigma_{s_j}^2 + \frac{\sigma_{e_j}^2}{n_{jk}} \right) \right] \right\}^{.5}} \quad [4]$$

where

- E = expectations taken separately for the calculated covariances and variances,
- $\hat{r}_{ij}$  = estimated phenotypic correlation between traits *i* and *j* (here, *i* and *j* are different sets of sire proofs based on different methods of extending incomplete records),
- $\sigma_{s_i s_j}$  = one-fourth of the additive genetic covariance between traits *i* and *j*,
- $\sigma_{s_i}^2, \sigma_{s_j}^2$  = one-fourth of the additive genetic variances for traits *i* and *j*,
- $\sigma_{e_i}^2, \sigma_{e_j}^2$  = residual variances for traits *i* and *j*, and
- $b_{ik}$  =  $n_{ik} / [n_{ik} + (\sigma_{e_i}^2 / \sigma_{s_i}^2)]$  for  $n_{ik}$  = number of daughters of the *k*th sire for the *i*th trait.

Substituting the above expression for  $b_{ik}$  and  $b_{jk}$  into [4] yields, after some algebra:

$$E(\hat{r}_{ij}) = \left[ \frac{\sum_k b_{ik} b_{jk}}{(\sum_k b_{ik} \sum_k b_{jk})^{.5}} \right] \left[ \frac{\sigma_{s_i s_j}}{\sigma_{s_i} \sigma_{s_j}} \right] \quad [5]$$

As a result, the "correction factor" to obtain approximate genetic correlations from the phenotypic correlations of Tables 4 and 5 is

$$\frac{(\sum_k b_{ik} \sum_k b_{jk})^{.5}}{\sum_k b_{ik} b_{jk}} \quad [6]$$

for  $b_{ik} = n_{ik} / [n_{ik} + (\sigma_{e_i}^2 / \sigma_{s_i}^2)]$ .

Inspection of Tables 6 and 7 demonstrates the same relationships in the phenotypic correlations of Tables 4 and 5. These results indicate a strong genetic relationship among sire proofs based on complete records and based on extended records from any of the three methods, particularly when lengths of incomplete records exceed 130 days.

**CONCLUSIONS**

The goal of this investigation was to examine the accuracy of sire proofs based entirely on extended incomplete lactation records of two lengths of lactation as compared to proofs of only complete records. Little accuracy in estimation of a sire's genetic merit was lost when part records of approximately 5 mo were used to replace information from complete lactations. Sire proofs entirely from extended incomplete records were overestimated. However, the moderately high correlation between sire proofs from complete records and proofs from extended 5-mo records indicates the usefulness of including in-progress records in estimation of the genetic merit of sires. The use of 5-mo in-progress records might be more beneficial if they were included in the sire evaluation process unextended as a separate and distinct trait.

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