Relationships of First Lactation Milk and Type Traits to Cow Survival and a Sire Index for Discounted Total Milk

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ABSTRACT
The probability of cow survival during each of six consecutive 13-mo periods after first calving was regressed on lactation milk yield and 15 type traits, each recorded during the first lactation. Adjusted coefficients of determination were small (.028 to .081). The ratio of variance in predicted cow survival probabilities due to milk only with that due to the 15 type traits was 12.6:1, 4.7:1, 2.5:1, .5:1, 0:1, and .02:1 for respective herdlife periods. Maximum effect of type traits on herdlife ranged from 11 to 109 d. Prediction equations for cow survival were incorporated into a sire index for discounted total milk yield of progeny. Type traits affected the sire index by their influence on the six predicted survival rates. Milk yield affected the discounted total milk index directly as well as through the survival rates. Simulated variation from milk estimated transmitting abilities for sires accounted for 99.9% of the total variation in the discounted total milk index. Since the effect of the type traits on cow survival rates was greatest during the later herdlife periods, too few animals would have survived to these later periods to reveal any significant effect from type on the discounted total milk index.

INTRODUCTION
The total return derived from an insemination used to produce progeny depends upon the expected milk yield per lactation and the expected number of lactations per cow. The average number of lactations per cow depends upon the rate of survival from one lactation to the next. A sire index for total return per insemination could be formulated using an index for milk yield in combination with indexes for a sequence of survival rates (8, 13).

The only nationally available sire index for total return from lifetime production of progeny is the net present value (PV$) index described by Wilcox et al. (20). This index assumes survival rates are equal among cow progeny groups. Only a few studies (4, 11, 19) have proposed that sire indexes for survival rates among cow progeny be included when calculating a total return sire index. Postponing sire selections to await progeny data on survival rates would unduly delay decisions and lengthen the average generation interval. Indirect predictions of herdlife or survival rates could be useful since production and conformation traits are routinely recorded during first lactation.

First lactation milk yield accounts for more variability in cow survival measures than any other first lactation trait (14, 15). Thirty-five percent to 132% more variation in cow survival was accounted for when first lactation type traits were jointly considered with yield traits (10, 14, 15).

The objectives for this study were 1) to develop prediction equations for the probability that a dairy cow survives each of the six adjacent herdlife periods using first lactation milk and type phenotypes, and 2) to incorporate the prediction equations into a sire index for discounted total milk yield of progeny.

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MATERIALS AND METHODS

Data

Subjective scores for 15 linearized type traits were recorded in a descriptive traits project (hereafter referred to as the Ohio project) initiated in 1972 and continued through August 1983. Cows recorded as disposed for dairy purposes or unknown reasons were deleted from the data set. Data included only first recorded calvings prior to 40 mo of age. The data set consisted of records on 8698 Holstein cows from 444 herds in Ohio. First lactation milk records (305 d, 2x, mature equivalent) for all cows were obtained from the Animal Improvement Programs Laboratory of the USDA. Milk records were expressed as deviations from 5-to-rolling herd-year contemporary averages.

Survival Variables

The productive herd life of each cow was defined as months between first calving date and the earliest following date: disposal date, last herd test period date, or project termination date. Herd life records were treated as censored when a herd stopped testing or the Ohio project ended. There were 1381 cows with censored herd life records.

Zero or one valued variables, denoted as $1$, $2$, $3$, $4$, $5$, $6$, were used to describe survival through the first six 13-mo periods of herd life (1 to 13, 14 to 26, 27 to 39, 40 to 52, 53 to 65, and 66 to 78 mo) after first calving. Cows surviving through each herd life period were coded as 1 or coded 0 otherwise. A cow that failed to survive a period was assigned a missing value for each survival variable following that period. If failure to survive was a result of record censoring, the survival variable corresponding to the censored herd life period was assigned a missing value. Only data coded as a 1 or 0 were included in the analyses of the survival variables. The fraction of cows surviving through each herd life period and the number of observations included are in Table 1.

Conversion of Type Trait Scores

Type traits were scored on a discrete ordered scale of 1 to 3 or 1 to 4, representing one biological extreme to the other. A set of 15 type traits was chosen from the 60 traits scored in this project, described fully by Smith et al. (18). This set of 15 traits was chosen to correspond to the 15 primary type traits summarized by the Holstein-Friesian Association of America (HFAA). Descriptions for the 15 primary HFAA traits along with the corresponding traits chosen from the Ohio project are in Table 2.

Scores for the 15 traits were rescaled to a 50-point scale analogous to the HFAA linear system. Three steps were taken to convert the type traits from the scale used in the Ohio project to the 50-point scale. First, each original type trait score was reassigned as the mean of a subset of observations from a standard normal population according to its relative frequency and order on the original phenotypic scale. The recoded trait scores will be referred to as normal scores. Second, the normal scores were adjusted for describer, stage of lactation within describer, age at first calving within describer, and year-month of description within describer effects. Third, the adjusted normal scores were converted to a 50-point scale with a target mean of 25 and a target standard deviation of 6
<table>
<thead>
<tr>
<th>Trait</th>
<th>HFA System Code: description</th>
<th>Ohio project Code: description</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Rear foot angle, 3: Shallow, 2: Intermediate, 1: Deep</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Foot angle, 25: Intermediate, 45-50: Snug and strong</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Foot angle, 25: Intermediate, 45-50: Snug and strong</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Fore udder attachment, 1-5: Loose, 25: Intermediate, 45-50: Snug and strong</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Fore udder attachment, 1-5: Loose, 25: Intermediate, 45-50: Snug and strong</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Rear udder width, 3: Narrow, 25: Intermediate, 45-50: Wide</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Rear udder width, 3: Narrow, 25: Intermediate, 45-50: Wide</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Rear udder height, 4: Broken, 3: Loose, 2: Bulgy, 1: Smooth</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Rear udder height, 4: Broken, 3: Loose, 2: Bulgy, 1: Smooth</td>
</tr>
<tr>
<td>Udder support</td>
<td>1-5: Negative cleft, 25: Clearly defined halving, 45-50: Extreme cleft</td>
<td>Udder support, 3: Convex, 2: Flat, 1: Halved</td>
</tr>
</tbody>
</table>
TABLE 2. (continued) Definition of Holstein-Friesian Association (HFA) type traits and corresponding traits from the Ohio project.

<table>
<thead>
<tr>
<th>Trait</th>
<th>HFA System</th>
<th>Ohio project</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Trait Code: description</td>
<td>Trait Code: description¹</td>
</tr>
<tr>
<td>Angularity</td>
<td>1--5: Thick and coarse</td>
<td>Withers</td>
</tr>
<tr>
<td></td>
<td>25: Sharp and angular</td>
<td>3: Thick</td>
</tr>
<tr>
<td></td>
<td>45--50: Extremely sharp and angular</td>
<td>sharpness</td>
</tr>
<tr>
<td>Body depth</td>
<td>1--5: Shallow</td>
<td>Rear rib</td>
</tr>
<tr>
<td></td>
<td>25: Intermediate</td>
<td>3: Shallow</td>
</tr>
<tr>
<td></td>
<td>45--50: Deep</td>
<td>2: Intermediate</td>
</tr>
</tbody>
</table>

¹ Descriptive scale is listed to conform to the scale used in the HFA system.

for all traits. Details are discussed by Keller (12).

Regression Analyses

The general linear models procedure of the Statistical Analysis System (SAS) was used to complete a weighted least squares analysis of variance on each of the 6 survival variables. Weights were calculated as \(1/[s^*(1 - s^*)]\), where \(s^*\) is the predicted probability from the prior analysis. Results from the third iteration of each analysis were used. The initial model used for each survival variable was:

\[
S_{ij} = a + r y_j + b_1 D_{ij} + b_2 (D_{ij})^2 + b_3 \bar{M}_{ij} \\
+ b_4 (\bar{M}_{ij})^2 + b_5 (D_{ij}) (\bar{M}_{ij}) \\
+ b_6 (D_{ij})^2 (\bar{M}_{ij}) + b_7 A F C_{ij} \\
+ \sum_{n=1}^{15} [c_n X_{nij} + d_n (X_{nij})^2 + f_n \bar{X}_{nij} \\
+ g_n (\bar{X}_{nij})^2 + h_n (X_{nij}) (\bar{X}_{nij}) \\
+ k_n (X_{nij})^2 (\bar{X}_{nij}) + l_n (X_{nij}) (D_{ij}) \\
+ m_n (X_{nij})^2 (D_{ij})] \]  

where:

\(S = \) observed survival probability outcome, 0 or 1,
\(a = \) effect common to all observations,
\(r_y = \) the calendar year corresponding to the year the cow entered this herdlife period,
\(D = \) first lactation contemporary deviation milk yield,
\(\bar{M} = \) contemporary average milk,
\(A F C = \) age at first calving in months,
\(X_n = \) the score for the \(n^{th}\) type trait,
\(X = \) the herd average score for the \(n^{th}\) type trait.

The constants \(b_1, b_2, b_3, b_4, b_5, b_6, b_7, c_n, d_n, f_n, g_n, h_n, k_n, l_n, \) and \(m_n (n = 1, \ldots, 15)\) are regression coefficients. Risk year \((r_y)\) was included in the analyses to account for the mean difference in survival which would affect all cows across herds as culling practices vary among calendar years.

A total of 126 regression coefficients was computed using the initial model (Equation [1]). The number of coefficients was reduced by using an abbreviated step down procedure. Each type trait phenotype with a coefficient not significantly different from zero at 20% probability was removed from the initial model. Data were reanalyzed with a reduced form of the model. Results are reported for the analysis based on the reduced models.

Herdlife as a Function of Survival Probabilities

The expected length of herdlife in days was computed from the predicted survival probabilities using the following recursion equation:

\[
\text{Herdlife} = \sum_{i=1}^{9} \left[ \prod_{j=0}^{i-1} S_j \right] (1 - S_i) \\
\times [D_i + (i - 1) (C_i)] \]  

where $S_j$ and $S_i$ represent probabilities of survival during the $j$th and $i$th lactations. The probability of survival to start a first lactation was defined as 1 (i.e., $S_0 = 1$). The probability of survival during the first six lactations was predicted from the phenotypic regression Equation [1]. The probability of survival during the seventh and eighth lactations were defined as $.5$. All cows starting the ninth lactation were defined to be culled during this lactation (i.e., $S_9 = 0$). The $D_i$ values represent the average number of days in milk prior to removal in the terminal lactation and were 257, 254, 254, 253, 249, 245, 241, 240, and 240 for first to ninth lactation, respectively (7). The CI represents the average calving interval, which was assumed to be 396.5 d.

Relative Effects of Milk and Type on Survival

The comparative effects of first lactation milk and the set of 15 type traits on survival were determined by isolating their effect on the variation in each predicted survival probability. Each variance was computed from cow records including 1) milk and all 15 type traits, 2) milk alone, or 3) the set of 15 type traits. The trait record of each cow was assigned its mean value when excluded from the variance. Each variance was computed using only the cows that started a specific herdlife period. The variances due to milk alone and the set of 15 type traits alone were each expressed relative the variance using all traits.

Discounted Total Milk Index

A prediction of the total milk yield produced by a bull's daughters may be calculated from his estimated transmitting ability (ETA) indexes for milk and 15 type traits. Discounted total milk (DTM) was defined from a composite of the milk ETA and the survival predictions as well as constants describing a production system. The milk ETA index was equated to the production expected in a standard lactation. Both the milk ETA and 15 type ETA indexes were used to define predictions of the probability to survive six herdlife periods. Equation [1] was the specific function used to calculate the predicted probability. When trait ETA index values replace their respective cow records in Equation [1] the functional form becomes a prediction of the survival probability for a bull's daughters.

The following constants and assumptions were used to define the production system.

1) The probabilities of conception and female calf from an insemination were each .5. 2) The probability of pregnancy resulting in a live calf was .8. 3) The fraction of a bull's additive genetic merit transmitted from generation to generation was .5. 4) Age at first calving was 26 mo, and calving interval was 13 mo. 5) Mature equivalent age correction factors were 1.22, 1.12, 1.04, 1.01, and 1 for lactations 1, 2, 3, 4, and 5 or greater. 6) The contemporary average lactational milk production was 7273 kg, and the herd average for each type trait was 25. 7) Probabilities of survival from birth to 13 mo, and from 13 to 26 mo of age were .93 and .94. 8) The probability of survival from 78 to 92 mo of productive herdlife was .5. 9) All cows were culled from the herd at 93 mo of productive herdlife. 10) The discount rate per 12-mo period was 5%. 11) Milk yield of a bull's descendants was accumulated over 11 consecutive 13-mo periods and discounted back to the time of insemination.

The DTM index differed among sires only through differences in their index values for milk yield and the 15 type traits. The amount of DTM expected from one insemination was calculated as follows:

$$ DTM = \sum_{t=1}^{11} w^t c^t p^t m $$

where:

- $t$ is the number of 13-mo periods since the time of insemination,
- $w = [0 \ 0 \ .82 \ .89 \ .96 \ .99 \ 1 \ 1 \ 1 \ 1]$ is a row vector of fractions of a bull's genetic merit, which give the actual milk yield difference produced by a bull's daughters in each 13-mo age interval (i.e., the reciprocal of the corresponding mature equivalent age correction factor),
- $c = [1/(1 + .05)]^{12/12}$, is the discount rate per 13-mo period,
which is a matrix of probabilities of conception, female calf, and survival as well as the fraction of a bull's genetic merit transmitted from generation to generation.

The elements $S_{I1}$ through $S_{I6}$ represent sire indexes for the probability of survival during the first six consecutive 13-mo periods of productive herdlife. The first row and column of $p$ correspond to time of semination. The remaining rows and columns of $p$ correspond to 10 consecutive 13-mo periods in the female life cycle.

\[
p = \begin{bmatrix}
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
.2 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & .93 & 0 & .2 & .2 & .2 & .2 & .2 & .2 & .2 \\
0 & 0 & .94 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & SI_1 & 0 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & SI_2 & 0 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & SI_3 & 0 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & SI_4 & 0 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & SI_5 & 0 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & SI_6 & 0 \\
0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & .5 \\
\end{bmatrix}
\]

which is a vector incorporating the sire's index for milk yield. $S_{Im}$ was assumed to be the difference in mature milk yield produced by the sire's daughters relative to herd average.

\[
m = [SI_m \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0]
\]

which is a matrix of probabilities of conception, female calf, and survival as well as the fraction of a bull's genetic merit transmitted from generation to generation.

The elements $SI_1$ through $SI_6$ represent sire indexes for the probability of survival during the first six consecutive 13-mo periods of productive herdlife. The first row and column of $p$ correspond to time of semination. The remaining rows and columns of $p$ correspond to 10 consecutive 13-mo periods in the female life cycle.

\[
m = [SI_m \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0]
\]

which is a vector incorporating the sire's index for milk yield. $S_{Im}$ was assumed to be the difference in mature milk yield produced by the sire's daughters relative to herd average.

Relative Effects of Milk and Type
on the Discounted Total Milk Index

The effects of milk and the 15 type traits on the DTM index were summarized by comparing the variance of DTM due to each set of traits. Variability expected in sire indexes for milk and the 15 type traits was mimicked by using the product of the milk and type records (expressed as deviations) from 1000 randomly chosen cows and:

\[
\sqrt{\frac{nh^2}{4 + (n-1)h^2}} \left(\frac{h^2}{4}\right)
\]

This product would have variation comparable to the variation expected among 1000 analogous sire indexes for the same traits. The sire indexes were simulated on means of 100 daughters with records on all 16 traits \((n=100)\) and heritabilities \((h^2)\) equal to .3 for milk, and .2 for each type trait. The variance in the DTM index was partitioned by computing a variance due to milk ETA's only, and type ETA arrays only by selectively setting all cow deviation records to their mean value for those traits excluded from the variance.

RESULTS AND DISCUSSION

Regression of Cow Survival on Milk
and Type Traits

The regression coefficients remaining in the reduced model from the original 126 numbered: 59, 76, 58, 45, 50, and 35, respectively,
for the six survival variables. The coefficients of multiple determination ($R^2$) from each survival variable analysis, calculated after adjustment for risk year effects, were .08, .06, .05, .03, .04, and .05. The $R^2$ values were adjusted to be independent of the number of parameters estimated (5). The average $R^2$ was .05 and smaller than comparable values in other studies. Other studies averaged near .11, ranging from .063 to .214 (6, 10, 14, 15). The use of binary survival codes for the dependent variables in this study probably lowered the $R^2$ values. The average $R^2$ value in the last three periods was only 60% as large as the average for the first three periods. However, during the fourth herdlife period the $R^2$ was lower than those thereafter. The longer interval between the later herdlife periods and the time when the phenotypes were recorded probably leads to a declining reliance on early records when culling occurs during the later phases of the productive cycle. The effectiveness of an early record would only approach the effectiveness of a later record among traits having a high repeatability. Clearly, first lactation milk and type reflect only a small fraction of all the factors contributing to the survival of individual cows during any of the six herdlife periods.

Relationship of Cow Survival with First Lactation Milk

The predicted survival probability as a function of first lactation milk yield is presented in Figure 1 for each of the six herdlife periods. The figure illustrates the relationships defined by the respective regression equations as functions of the first milk record alone while setting all other cow and herd average records to their mean value. Survival probability was generally positively related to the milk yield deviation. Survival probabilities peaked at a deviation less than the largest in 3 of the 6 herdlife periods. Hinks (9) found similar results. The average survival fractions decreased as the herdlife periods advanced. The slope of the probabilities on first lactation yield declined with the later herdlife periods. This was in agreement with others (2, 6) who found that culling was associated mostly with yield from the most recent lactation rather than the first lactation.

To summarize the magnitude of milk's impact on survival, maximum differences in predicted survival rates and expected herdlife due to differences in first lactation milk were computed. Predicted survival rates and expected herdlife values were compared over a range of deviation milk values from $-1814$ to 1995 kg. This range corresponds to the central 90% of the phenotypic distribution of deviation milk records. The milk scale was restricted in this manner to avoid exaggerated effects from rare extreme phenotypes. Maximum differences in survival rates from milk were 24, 45, 21, 9, 8, and 1% for the six herdlife periods. Maximum difference in expected herdlife from milk was 722 d.

Relationship of Cow Survival on First Lactation Type Traits

Predicted survival probability equations for each type trait and survival period were defined in the same manner as the equations for milk. The type trait scores that lead to the highest survival probabilities and expected herdlife are in Table 3. Descriptions of the scale directions in Table 2 are necessary to interpret the results in Table 3. For example, the shortest rump length score, 1, had the highest predicted survival probability during three of the first four herdlife periods. The composite herdlife curve was also highest at the shortest rump length score.

Figure 1. Regression curves of each survival variable on first lactation deviation milk yield. $S1$ to $S6$ represent survival rates during the following periods of herdlife: 1 to 13 mo, 14 to 26 mo, 27 to 39 mo, 40 to 52 mo, 53 to 65 mo, 66 to 78 mo, respectively. $\square = S1$, $\times = S2$, $\circ = S3$, $\# = S4$, $\bigcirc = S5$, $\bigstar = S6$. 
TABLE 3. First lactation type trait scores with highest predicted survival probabilities and length of herdlife.

<table>
<thead>
<tr>
<th>Trait</th>
<th>Survival rate during herdlife periods, mo</th>
<th>Length of herdlife</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>1—13</td>
<td>14—26</td>
</tr>
<tr>
<td>Rump length</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Udder depth</td>
<td>25</td>
<td>...</td>
</tr>
<tr>
<td>Rear udder suspensory</td>
<td>50</td>
<td>35</td>
</tr>
<tr>
<td>Leg set</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Rear teat placement</td>
<td>34</td>
<td>28</td>
</tr>
<tr>
<td>Withers sharpness</td>
<td>...</td>
<td>29</td>
</tr>
<tr>
<td>Height</td>
<td>...</td>
<td>21</td>
</tr>
<tr>
<td>Rear udder height</td>
<td>...</td>
<td>34</td>
</tr>
<tr>
<td>Heel depth</td>
<td>50</td>
<td>16</td>
</tr>
<tr>
<td>Rump width</td>
<td>...</td>
<td>50</td>
</tr>
<tr>
<td>Chest width</td>
<td>...</td>
<td>20</td>
</tr>
<tr>
<td>Fore udder smoothness</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>Rear rib depth</td>
<td>50</td>
<td>24</td>
</tr>
<tr>
<td>Rear udder width</td>
<td>...</td>
<td>...</td>
</tr>
<tr>
<td>Rump angle</td>
<td>23</td>
<td>29</td>
</tr>
</tbody>
</table>

1 Defined in text (Equation [2]).

2 Indicates the trait was not included in the reduced model analysis of the corresponding survival variable.

In general, the values in Table 3 for the body traits rump length, pins width, height, chest width, and rear rib depth showed a tendency for smaller cows to have longest herdlife. Udder traits consistently showed that intermediate scores were associated with the highest survival rates. The nonlinear survival relationships for udder traits may justify the selection of special mating pairs in extreme cases (1).

Inconsistencies among the scores that maximize survival across periods may be in part due to the different sets of traits included in the final regression analyses reported. Partial regression coefficients can be expected to differ according to whether some traits were held constant by the model. Also, large disproportionate shifts in the relative frequencies between the original score categories (e.g., 1, 2, 3, or 4) from one herdlife period to another probably affected the regression relationships. Because there were only three or four scores on the original trait scale, shifts in relative frequencies at the extreme ends of the original score scale could influence the calculated regression coefficients.

Maximum differences in predicted survival rates and expected herdlife values due to differences in each type trait are in Table 4. The maximum differences were computed using a method analogous to that described previously for milk yield. The interval of trait scores was restricted to values from 15 to 35 inclusive to cover the central 90% of the phenotypic distribution of type scores. Maximum differences in predicted survival rates from individual type traits ranged from less than .5% to 15%. Most of the differences in Table 4 are less than 5%. Only in herdlife periods 5 and 6 did maximum differences in survival rates due to individual type traits exceed the comparable differences due to milk yield. The largest difference among all type traits in days of expected herdlife was 109 d favoring shorter rump length. This is much smaller than the difference of 722 d due to milk yield. The average maximum herdlife difference among type traits was 53 d.

Comparative Effects of Milk and Type on Survival

Figure 2 presents the variances in the predicted survival probabilities due to milk alone, the set of 15 type traits alone, and milk and all type traits combined. The variances for each probability included nonlinear interaction terms and covariances between milk and type. As a consequence, the variance due to milk and all type traits did not equal the simple sum of the variance due to milk alone plus the variance due...
TABLE 4. Maximum differences in predicted percent surviving and days of herdlife between trait scores with extreme effects. 1

<table>
<thead>
<tr>
<th></th>
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<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>(%)</td>
<td>(%)</td>
<td>(%)</td>
<td>(%)</td>
<td>(%)</td>
<td>(%)</td>
<td>(d)</td>
</tr>
<tr>
<td>Rump length</td>
<td>4</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>...</td>
<td>3</td>
<td>109</td>
</tr>
<tr>
<td>Udder depth</td>
<td>0^4</td>
<td>...</td>
<td>10</td>
<td>...</td>
<td>11</td>
<td>...</td>
<td>86</td>
</tr>
<tr>
<td>Rear udder suspensory</td>
<td>3</td>
<td>2</td>
<td>2</td>
<td>7</td>
<td>...</td>
<td>83</td>
<td></td>
</tr>
<tr>
<td>Leg set</td>
<td>0</td>
<td>8</td>
<td>2</td>
<td>5</td>
<td>...</td>
<td>81</td>
<td></td>
</tr>
<tr>
<td>Rear teat placement</td>
<td>4</td>
<td>3</td>
<td>...</td>
<td>...</td>
<td>5</td>
<td>...</td>
<td>79</td>
</tr>
<tr>
<td>Withers sharpness</td>
<td>...</td>
<td>7</td>
<td>...</td>
<td>...</td>
<td>...</td>
<td>69</td>
<td></td>
</tr>
<tr>
<td>Height</td>
<td>...</td>
<td>3</td>
<td>...</td>
<td>...</td>
<td>5</td>
<td>2</td>
<td>55</td>
</tr>
<tr>
<td>Rear udder height</td>
<td>...</td>
<td>4</td>
<td>...</td>
<td>4</td>
<td>...</td>
<td>50</td>
<td></td>
</tr>
<tr>
<td>Heel depth</td>
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<td>4</td>
<td>6</td>
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<tr>
<td>Rump width</td>
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<td>3</td>
<td>1</td>
<td>11</td>
<td>2</td>
<td>36</td>
</tr>
<tr>
<td>Chest width</td>
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<td>...</td>
<td>2</td>
<td>5</td>
<td>6</td>
<td>3</td>
<td>30</td>
</tr>
<tr>
<td>Fore udder smoothness</td>
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<td>...</td>
<td>...</td>
<td>6</td>
<td>...</td>
<td>...</td>
<td>24</td>
</tr>
<tr>
<td>Rear rib depth</td>
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<td>1</td>
<td>...</td>
<td>...</td>
<td>15</td>
<td>...</td>
<td>19</td>
</tr>
<tr>
<td>Rear udder width</td>
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<td>...</td>
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<td>...</td>
<td>1</td>
<td>...</td>
<td>14</td>
</tr>
<tr>
<td>Rump angle</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>1</td>
<td></td>
<td>...</td>
<td>11</td>
</tr>
</tbody>
</table>

1 Maximum differences computed from alternative type trait scores restricted to range from 15 to 35.
2 Defined in text (Equation [2]).
3 Indicates the trait was not included in the reduced model analysis of the corresponding survival variable.
4 Zero indicates difference was less than .5%.

to the type traits. First lactation milk yield became less important for the prediction of survival during later herdlife periods. This agrees with reports (3, 16) where the frequency of low production as the primary reason for removal decreased with cow age. Ratios of the variance due to milk alone and the variance due to the set of 15 type traits were 12.6:1, 4.7:1, 2.5:1, .5:1, 0:1, and .02:1 for herdlife periods 1 through 6. The 15 type traits accounted for more variability in survival rates beyond 40 mo of productive herdlife than first lactation milk yield.

Comparative Effects of Milk and Type on the Discounted Total Milk Index

The overall mean DTM index value was 29 kg with a variance of 529 kg^2 due to the mimicked differences from sire ETA indexes for milk and the 15 type traits. Variation in DTM indexes from milk alone accounted for 99.9% of the total variation from all 16 traits. Similarly, Johnson et al. (11) found sire milk and fat indexes accounted for 99% of the variation in a sire index for total economic value that included type.

The effect of 15 type traits on the DTM index was negligible compared with effect on milk even though the type traits had large effects relative to milk on survival beyond 40 mo of productive herdlife. There are several reasons for this result. First, differences in sire indexes from the 15 type traits had to affect
the DTM index through their influence on survival rates, whereas differences in milk yield affected the index directly as well as through survival. Second, type traits had their largest relative effects on survival beyond 40 mo of herdlife. Variations in survival rates late in herdlife from type are manifested among only the small fraction of animals expected to survive beyond 40 mo of herdlife. Also expected yields in later herdlife were discounted to the time of insemination which diminished variations in lifetime milk yield due to type’s effects on survival in later herdlife. The effects of the type traits on survival rates during the later herdlife periods occur too late and affect too few animals to have a significant influence on total lifetime milk yield.

CONCLUSIONS

Predicted survival rates from milk and type traits recorded in first lactation provide an early alternative to waiting for indexes from observed survival rates in bull evaluation. Further, an economic index such as the DTM index developed in this study could be published with each bull’s first evaluation on separate traits. The formulation of the DTM index aggregated the sire indexes for milk and 15 individual type traits into a single index to rank potential service sires. This formulation incorporates the role of type traits into a total productivity measure for dairy cattle using the influence of type traits on survival.

Further understanding of the properties necessary to support continued productivity at later stages of herdlife is required if phenotypes recorded early in the life cycle are to be more useful as predictors of survival later in life. The relationship of traits recorded in the first lactation with survival later depends on the degree the first lactation records represents the same trait later in life. Studies such as that of Smith and Allaire (17) on the durability of trait scores are needed.

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