GENETICS AND BREEDING

Genetic Evaluation of Length of Productive Life Including Predicted Longevity of Live Cows

P. M. VanRADEN
Animal Improvement Programs Laboratory
Agricultural Research Service, USDA
Beltsville, MD 20705-2350

E.J.H. KLAASKATE[1]
Department of Animal Sciences
University of Maryland
College Park 20742

ABSTRACT

Complete longevity data are available too late for most sire selection. Earlier selection is possible using correlated traits, nonlinear evaluation of censored data, or predicted longevities for live cows in addition to completed longevity data. Completed longevity was defined as total months in milk by 84 mo of age. Predicted longevity was computed by multiple regression from cows alive at six different ages. Variables included age at first calving, standardized first lactation milk yield (optional), lactation status (dry or milking), current months in milk, current months dry, and cumulative months in milk. Completed longevity data for dead cows were then merged with predicted longevity data for live cows. A total of 1,984,038 Holstein cows born from 1979 to 1983 were included and represented 1911 sires, each with at least 70 daughters. Heritability of longevity increased gradually from .03 at 36 mo to .08 at 84 mo. Phenotypic correlations of early with completed longevity ranged from .59 to .99; genetic correlations ranged from .92 to 1.00. Inclusion of yield for projection increased heritability at 36 mo substantially but decreased genetic correlation with complete longevity information. Expansion and weighting factors will allow predicted records to be used in longevity evaluations, which is similar to the procedures that allow predicted 305-d yields to be included in yield evaluations.

(**Key words**: longevity, length of productive life, genetic evaluation)

Abbreviation key: MIM84 = total months in milk by 84 mo of age, **SM1** = standardized first lactation milk yield.

INTRODUCTION

Lifetime income may be factored into income per unit of time and length of productive life. Genetic rankings for income per lactation have been computed routinely, but longevity has not been evaluated. An exception is the evaluation for stayability (ability to survive to 48 mo of age) in the northeastern United States (9). For USDA evaluations, only the percentage of daughters culled during first lactation is reported as a phenotypic summary (14). Improved statistical methods and reduced cost of computing now allow routine national genetic evaluations of longevity.

Highest profits come from high yielding cows that are able to remain in the herd for several lactations (1, 10). Herd life has greatest value when feed costs are high or when beef prices are low (1, 5, 13). Cows leave herds for many reasons, including low yield, mastitis and other health problems, reproductive failure, sales for dairy purposes, and death (2, 4, 6). Many of the traits that affect longevity are not currently evaluated. Some natural selection for longevity occurs because cows that live longer usually have more progeny. Artificial

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[1] Present address: Department of Animal Breeding, PO Box 338, Wageningen Agricultural University, Wageningen 6700H, The Netherlands.

selection for longevity can increase profitability if longevity measures are obtained early in life and if genetic variation is sufficient (18).

The coefficient of variation for longevity is larger than that for milk yield per lactation, but most estimates of heritabilities for measures of longevity have been low (3, 7, 8, 11, 17, 19). Estimates (.06 to .13) were slightly higher from continuous rather than discrete measures of longevity and use of nonlinear statistical models (8, 18). Nonlinear procedures directly use the dates that cows are culled as the information becomes available and treat records of cows still alive as censored. The observed, nonnormally distributed data are modeled as a nonlinear function of normal, underlying variables.

A simpler, linear model approach treats longevity records for cows still alive as incomplete records and extends them. Complete and incomplete longevity data are then included in one standard analysis. Milk yields <305 d are included for evaluation by prediction of the 305-d yield, expansion of genetic variance of incomplete yields to match that of completed yields, and reduced weighting of expanded yields compared with complete records for the evaluation (20). Rapid acceptance by the dairy industry might be expected if the statistical techniques currently used for yield traits work as well for longevity.

Breeders may select for herd life using correlated traits such as type if evaluations for longevity are not available. Although type is measured earlier than longevity, indirect selection offers slow or moderate progress because of low correlations of most type traits with longevity (3, 15, 17). If multiple-trait analysis of all such traits is not feasible, selection index procedures might be used to combine the separate single-trait evaluations. The correlated traits gradually would receive less emphasis as the cows become older and as more actual longevity information becomes available.

Because lowest yielding cows are culled, phenotypic and genetic correlations often are favorable between yield and longevity (11, 17). Nevertheless, genetic trend for stayability may be negative (9), and phenotypic trends are negative for most breeds (12). Many dairy producers are concerned that the cows most able to yield large volumes of milk may not survive very long. Breeders could select more directly for longevity and monitor the progress or decline in genetic merit for this trait if evaluations were routinely provided.

Goals of this research were 1) to define a measure of longevity appropriate for national genetic evaluations, 2) to develop factors to predict eventual longevity of living cows, and 3) to determine whether a mixture of projected and completed longevity records (analogous to data for yield traits) could improve both the timeliness and accuracy of genetic evaluations.

MATERIALS AND METHODS

Total months in milk by 84 mo of age (**MIM84**) was investigated as a measure of length of useful life. Figure 1 demonstrates calculation of MIM84 for an example cow. Number of months in milk from each lactation were summed except for two restrictions. Each lactation received a maximum credit of 10 mo because records >305 d currently are not stored. Cows with short rather than long calving intervals accumulate credit faster and can have higher MIM84. The limit of 84 mo of age made the distribution somewhat more normal and made complete data available without a delay until the last cow died.

An alternative limit of 72 mo was tested in a preliminary analysis of Ayrshire data but was discarded because of slightly lower heritability. A limit on months of age instead of months from first calving tends to favor cows that live long but have their first calf early. Number of lactations initiated by the cow by 84 mo of age was included as a simpler trait by comparison. The binary trait stayability at 48 mo also was included, primarily for comparison with predictions of MIM84 made at 48 mo.

If a cow changed herds, MIM84 was summed across herds, but the cow was compared only with others from her first herd. If a cow's last record was coded as sold for dairy

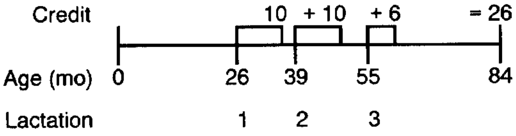

Figure 1. Calculation of months in milk by 84 mo of age for an example cow.

purposes, her completed MIM84 was unknown. She may have been sold to a herd not on official test or exported. In this study, a cow received no credit for months of milk in herds not on official test. In routine genetic evaluations, records of cows sold for dairy purposes could be extended, as for longevity records in progress. For such cows, a predicted MIM84 could be computed, expanded, and given less weight, as for yield records in progress (20).

Predictions of MIM84 were made by a linear model that included herd-year-season and the following variables to indicate each cow's status at a given age: cumulative months in milk, age at first calving, lactation status (0 = milking ≤305 d; 1 = dry or milking >305 d), current months in milk, and current months dry (including months in milk >305 d). These variables describe the cow more fully than binary (9) or even nonlinear models (8, 18). For example, a recently freshened cow usually milks several more months, but a cow in late lactation may be culled soon. Standardized (21) first lactation milk yield (SM1) was tested as another potential variable at 36 mo. Interactions and squared terms were not included in regressions because preliminary tests showed very small gains in R^2.

No predictions are required for dead cows because their MIM84 is already known. Because disposal codes after 305 d are not stored, cows with >305 d in one lactation but that have not yet started the next lactation could be either alive or dead. About 23% of all cows had unknown status at 36 mo; at later ages, fewer cows had unknown status. Such cows were considered to be dry if a next lactation was present but were considered to be dead if the next lactation was absent. Thus, data for the study were more accurate than would occur in practice because information about the next lactation was available. Whether a cow is dead or alive could be made known by collection of disposal codes for cows between lactations.

Regressions of MIM84 on indicator variables at each of six ages were computed using PROC GLM of SAS (16). Ages included were 36, 42, 48, 54, 60, and 72 mo. For ages <36 mo, low percentages of cows culled would result in less information and more serious violations of normality. Effects of herd-year-season were absorbed. Year and season refer to birth; there were three 4-mo seasons per year. Management and culling policies change across time, and cows change herds, but each cow belongs to only one herd-year-season group. The analysis of Ducrocq et al. (8) was more flexible because it included different culling groups across time. Herd-year-seasons in which at least 25% of cows were coded as sold for dairy were excluded for lack of complete data.

TABLE 1. Numbers and percentages of live Holstein cows at various ages and mean months in milk at 84 mo of age (MIM84).

Age	Live cows		MIM84
(mo.)	(no.)	(%)	(mo.)
All cows	2,575,134	100	24.3
36	2,190,533	85	27.2
42	1,893,591	74	30.0
48	1,626,284	63	32.4
54	1,359,296	53	35.1
60	1,131,874	44	37.4
72	743,848	29	41.2
84	452,451	18	42.8

A total of 2,575,134 Holsteins born from 1979 to 1983 and with lactation records in the USDA-DHIA genetic evaluation system contributed to the analysis. All cows had a first lactation record and an opportunity to reach 84 mo of age. The number and percentage of cows remaining alive at each age and their mean MIM84 are in Table 1. Only 18% of cows were still alive at 84 mo. Those cows had accumulated 42.8 mo in milk compared with an overall mean MIM84 of 24.3 mo. Cows were not grouped by registry status for this study but would be for actual evaluations.

A final data file combined MIM84 from dead cows with predictions of MIM84 for living cows. Predictions included a mean herd-year-season effect, which was obtained as mean MIM84 for live cows minus the means of all variables except herd-year-season effects times their respective regression coefficients. Multiple-trait REML estimates of variances and covariances were obtained from a sire model including records of 1,984,038 cows. These cows were daughters of 1911 sires; each sire had at least 70 daughters. Data from another 169 bulls were added to provide relationship ties.

Completed records often have more phenotypic and genetic variation than do projected records. Both types of records can be included

TABLE 2. Regression coefficients for variables included in predicting months in milk at 84 mo of age (MIM84) at earlier ages and R^2 within herd-year-season for actual MIM84 with MIM84 predicted from combined projected and completed records.

	Regression coefficient for						
Age	Cumulative months in milk	Current months in milk	Age at first calving	Current months dry	Lactation status[1]	SM1[2]	R^2
(mo)							
36							
SM1 Included	1.053	–.345	–.049	–.067	–.704	.000766	.08
SM1 Not included	1.246	–.329	.069	.024	–.615	. . .	.05
42	1.276	–.397	.118	.170	–1.214	. . .	.05
48	1.253	–.392	.101	.151	–1.016	. . .	.10
54	1.239	–.397	.123	.192	–1.283	. . .	.14
60	1.172	–.392	.081	.194	–1.117	. . .	.21
72	1.080	–.289	.047	.183	–.662	. . .	.59
84[3]	1.000	.000	.000	.000	.000	. . .	1.00

[1] Dry or milking (dry = 1 and milking = 0).

[2] First lactation milk yield standardized to mature equivalent, twice daily milking, 305-d basis (21).

[3] Complete data.

in the same analysis by expansion of deviations of the projected records and reduced weighting of these records (20). Actual expansion factors were calculated as the ratio of genetic standard deviations for completed and projected records. Two types of theoretical expansion factors (20) also were calculated: 1) ratio of phenotypic variances for complete and projected records and 2) reciprocal of the squared phenotypic correlation. Weighting factors were calculated as $(1 - h^2)/(x - h^2)$, where h^2 is heritability of completed records, and x is the expansion factor. In the corresponding formula for milk yields (20), repeatability of records replaced heritability because permanent environmental effects were included in the model.

RESULTS AND DISCUSSION

Regression coefficients to predict MIM84 from variables available at 36, 42, 48, 54, 60, and 72 mo of age and R^2 of predicted MIM84 with actual MIM84 within herd-year-season are in Table 2. Inclusion of SM1 in the model at 36 mo increased R^2 from .05 to .08. The R^2 were higher for older ages (up to .59 at 72 mo).

Regression coefficients were similar across the ages studied. Calculation of additional regression coefficients between the ages reported was considered to be unnecessary. Interpolation between those ages should yield useful predictions for cows at any age between 36 and 84 mo. The alternative approach, shifting the cow's status back to the most recently computed age, would lose some information. Regression coefficients for cumulative months in milk were slightly >1.0, which indicated that cows with high early totals end with even larger advantages. Cows at the end of lactation received predicted values 3 or 4 mo less than cows that had just freshened.

Means, standard deviations within herd-year-season, and heritabilities based on all 2,575,134 cows at each age are in Table 3. Mean MIM84 was 24.3 mo, and heritability was 8.5%. Heritability at 36 mo of age was only 3.1%. Although the number of lactations by 84 mo seems to be genetically almost the same trait as MIM84, the phenotypic correlation was only .94. Stayability at 48 mo had slightly lower heritability and slightly lower phenotypic correlation with MIM84 than did predictions at 48 mo, but genetic correlations with MIM84 were .98 for both traits.

Early data had phenotypic standard deviations much less than MIM84, as expected when one variable predicts another (20). Table 3 also contains phenotypic and genetic correlations of MIM84 with the earlier data, which

TABLE 3. Means, standard deviations within herd-year-season, heritabilities, and correlations with months in milk at 84 mo of age (MIM84) for variables used to predict MIM84.

				Correlation with MIM84	
Variable	$\bar{X}$	SD	h^2	Genetic	Phenotypic
MIM84 (mo) from combined projected and completed records at					
36 mo					
SM1[1] Included	24.2	8.3	.061	.801	.605
SM1 Not included	24.1	7.9	.031	.915	.589
42 mo	24.2	9.9	.044	.960	.741
48 mo	24.2	11.1	.056	.982	.838
54 mo	24.2	12.0	.067	.992	.909
60 mo	24.3	12.5	.072	.997	.952
72 mo	24.3	13.0	.082	1.000	.993
MIM84, mo	24.3	13.1	.085	1.000	1.000
Number of lactations at 84 mo	2.9	1.6	.085	.992	.941
Stayability at 48 mo	.64	.45	.050	.982	.787
SM1, kg	8103	1347	.247	.458	.332
Age at first calving, mo	27.9	2.4	.019	−.110	−.091

[1] First lactation milk yield standardized to a mature equivalent, twice daily milking, 305-d basis (21).

was a mixture of data from both living and dead cows. Phenotypic correlations ranged from .59 at 36 mo of age to .99 at 72 mo. Genetic correlations were higher (all >.92), except that the genetic correlation fell to .80 when SM1 was included in 36-mo predictions. Inclusion of SM1 in models was discontinued based on this low genetic correlation.

Distribution of MIM84 was continuous (Figure 2) but flatter than the normal distribution. Values shown were rounded to the nearest 5 mo. Multiples of 10 were more common because a standard lactation is 10 mo. Figure 3 shows a strongly bimodal distribution for predicted MIM84 at 36 mo of age. Completed data for dead cows are shown (Figure 3, to the left of predicted MIM84 for living cows). Differences between dead and live cows thus contributed most of the variation; exact values of the predicted MIM84 were less important. For ages 42 to 72 mo (not shown), distributions of predicted MIM84 became less bimodal and more similar to the distribution of MIM84 (Figure 2). The coefficient of variation for MIM84 was 54%, much larger than the 17% for milk.

Techniques for inclusion of incomplete milk yield records for evaluation can be

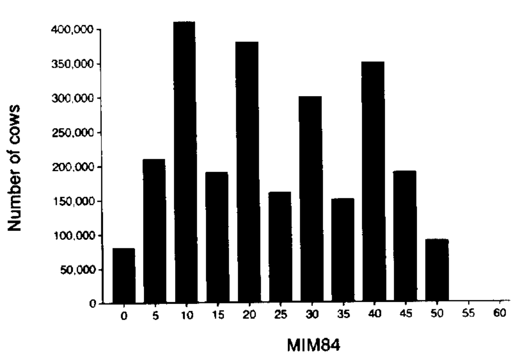

Figure 2. Distribution of months in milk by 84 mo of age (MIM84).

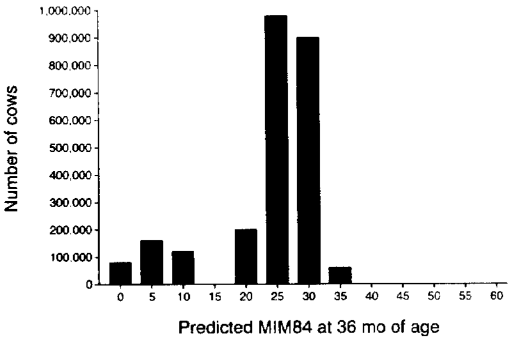

Figure 3. Distribution of predicted months in milk by 84 mo of age (MIM84) from combined projected and completed records at 36 mo of age.

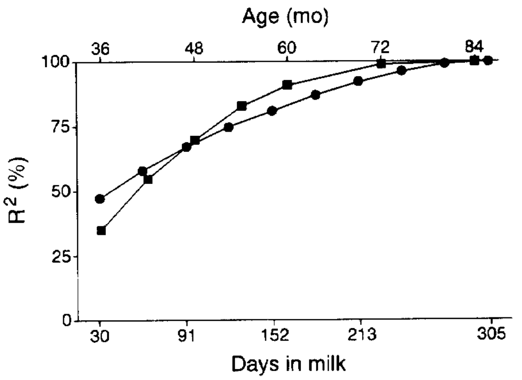

Figure 4. Squared correlations of early with final data for months in milk at 84 mo (●, upper axis) and for standardized (21) first lactation milk (■, lower axis).

adapted to MIM84. Squared correlations of early data with complete data for milk yield and for MIM84 are compared in Figure 4. Squared correlations for longevity showed the same shape of upward increase with age as did those reported (20) for milk yield across the lactation. Heritabilities of longevity across ages were uniformly lower than heritabilities of milk yield (20) from early lactation to 305 d. For both traits, complete data had highest heritabilities.

Early longevity data had genetic variances much less than for complete data. Table 4 gives the expansion factors required to equalize genetic standard deviations. Factors were as high as 2.72 at 36 mo but much closer to 1.00 at older ages. Actual and theoretical expansion factors were all in fairly close agreement. Table 4 also contains the appropriate weights (from .35 to 1.00) for the early data when those data were included in an animal model.

CONCLUSIONS

The measure of longevity MIM84 has intuitive appeal and sufficient heritability (8.5%) to be considered as an additional trait for selection. Early longevity data were a combination of completed MIM84 for dead cows and predicted MIM84 for live cows. Predicted MIM84 was higher for cows that have more accumulated months in milk, are early in lactation, are older at first calving, or have more current months dry. Early longevity variables had high genetic correlations with MIM84 but lower phenotypic correlations and heritabilities. The genetic correlation was much lower if SM1 was included for early prediction, although the phenotypic correlation increased.

Correlations of SM1 with MIM84 were .332 (phenotypic) and .458 (genetic). Although not addressed in this study, the correlated influence of yield could be removed to highlight the health aspects of longevity (1, 3, 8, 11, 15, 17). Further research is needed to determine economic value and timeliness of MIM84 evaluations compared with those of other traits in the selection goal.

This approach should allow genetic evaluations for MIM84 to be computed with programs and procedures already in use for yield

TABLE 4. Genetic standard deviations, actual and theoretical expansion factors, and age weights for predicted months in milk at 84 mo from combined projected and completed records at various ages.

Age	Genetic SD	Expansion factors			Age weights
		Actual	Theoretical 1[1]	Theoretical 2[2]	
(mo.)					
36	1.40	2.72	2.75	2.88	.35
42	2.07	1.84	1.75	1.82	.53
48	2.63	1.45	1.39	1.42	.67
54	3.10	1.23	1.19	1.21	.80
60	3.37	1.13	1.09	1.10	.88
72	3.74	1.02	1.01	1.00	.98
84	3.81	1.00	1.00	1.00	1.00

[1] Factor computed as ratio of phenotypic variances at 84 mo to earlier ages.

[2] Factor computed as reciprocal of squared phenotypic correlation between early and complete records.

traits. Expansion factors analogous to those for yield traits were developed to equalize the unequal genetic variance of early and final longevity data. Early data from both live and dead cows will receive less weight in mixed model equations to offset the higher error variance of expanded early data. This linear model approach should have many of the same advantages claimed for nonlinear analyses (8, 18).

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