

# GENETICS AND BREEDING

## Genetic Analysis of Cow Survival in the Israeli Dairy Cattle Population

P. SETTAR<sup>1</sup> and J. I. WELLER<sup>2</sup>

Institute of Animal Sciences, Agricultural Research Organization,  
The Volcani Center, Bet Dagan 50250, Israel

### ABSTRACT

The linear model method of VanRaden and Klaaskate for analyzing herd life was expanded. Information on conception and protein yield was included in the estimation of predicted herd life of Israeli Holsteins. Variance components were estimated by a multitrait animal model. Heritability was slightly higher for herd life than for number of parities, but genetic correlations were close to unity. Animal model heritability estimates of herd life were higher than were sire model estimates. The expected herd life of pregnant cows was 420 d greater than for open cows. Each kilogram of increase in protein yield increased expected herd life by 9.5 d. Heritability of expected herd life increased from 0.11 for cows 6 mo after first calving to 0.14 for cows 3 yr from first calving. The genetic correlation of expected and actual herd life increased from 0.87 for records cut after 6 mo to 0.99 for records cut 3 yr after first calving. Phenotypic correlations increased from 0.61 to 0.94. Sire genetic evaluations based on predicted herd life of live cows were strongly biased if all records were weighted equally, and evaluations derived by weighting incomplete records to account for the effects of current herd life on variance components were nearly unbiased.

**(Key words:** genetic analysis, cow survival, Israeli Holsteins, animal model)

**Abbreviation key:** ANP = adjusted number of parities, CHL = current herd life, DD = days dry, DO = days open, EHL = expected herd life, EHLX = expected herd life times predicted value of the ratio of the square root of the genetic covariance between herd life and expected herd life, HL = herd life, HYS = herd-year season, NP = number of parities, PHL = predicted herd life, PRG = predicted value of the ratio of the square root of the genetic covariance between herd life and expected herd life, RG = ratio of the square root of the genetic covari-

ance between herd life and expected herd life, RHL = remaining herd life.

### INTRODUCTION

Longevity, or herd life (**HL**), is of major economic importance in dairy cattle (13). In the past, direct selection for cow survival has been limited. First, actual measurement of longevity is only possible after the cow has been culled, and most selection decisions, especially with respect to bulls, are made long before the last of their daughters are culled. Second, although there is disagreement as to the optimal measure of cow survival, all measures have relatively low heritability (15), and unlike milk yield traits, there is only one record per cow.

Two approaches have been suggested to include longevity in a breeding program: inclusion of a direct measure of longevity in the selection index (13) or selection for other traits, which are correlated with longevity but have higher heritability and are expressed earlier (16). Numerous studies (3, 15, 16) have considered using conformation traits to indirectly select for longevity.

Three basic strategies have been suggested to evaluate longevity for live cows. In the first, cow survival to a specific age can be analyzed as a binary trait by either linear or threshold models (1, 4, 5, 17). In the second strategy, VanRaden and Klaaskate (11) proposed estimating life expectancy of live cows and including these records in a linear model analysis. Estimates based on incomplete data are regressed toward the mean, and therefore have lower heritability and variance than do complete records (7, 14, 19). By use of the method first proposed by Weller (19), incomplete records were multiplied by a factor to bring all records to an equal genetic variance. Because the incomplete records have lower heritability, this strategy results in greater residual variance for the incomplete records. The records are then weighted in the mixed model equations according to their residual variances. Both adjustment factors are computed as functions of current herd life (**CHL**). The third method is survival analysis or consideration of cows still alive as censored records (1, 3, 17, 18). The dependent variable is the hazard function, which is the instantaneous probability of cow being culled at time *t*, provided that she was alive prior to *t*. Although the

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<sup>1</sup>Permanent address: Biometry and Genetics Department, Ege University, Izmir, Turkey.

<sup>2</sup>To whom correspondence and reprint requests should be addressed.

previous methods could be applied to either animal or sire models, survival analysis can only be applied to sire models, and evaluations will be biased if the number of daughters per sire with complete records is low (18).

Numerous suggestions for a definition of the longevity trait have been based chiefly either on the number of parities or the actual length of HL (15). VanRaden and Klaaskate (11) evaluated months in milk up to a maximum of 84 mo but counted only a maximum of 10 mo per lactation because records >305 d are not stored. Genetic differences for milk yield will have a major effect on direct measures of survival because low milk yield is a major cause of cow culling. Thus, many studies have proposed analyzing functional HL, which is generally computed as longevity adjusted for milk yield (1, 2, 3, 5, 10, 15, 17). This trait accounts only for culling that is due to causes other than milk yield. The problem of double counting of production in a selection index that includes both milk yield and uncorrected longevity correlated with yield can also be handled by computing appropriate economic values for these traits (13). Analyzing HL adjusted for yield is complicated because selection goals change over time. Until 1980, milk yield was the primary selection objective of most breeding programs. Now protein yield is the chief goal, and many countries put a negative economic weight on milk yield (6).

VanRaden and Klaaskate (11) used cumulative months in milk, current months in milk, age at first calving, current months dry for dry cows, first parity milk yield, and lactation status (dry or milking) to predict the HL of live cows. Although their evaluations for HL were based on an animal model, they used a sire model to compute variance component adjustment factors. Optimally, the same model should be used for both.

In addition to low yield, the main causes of cow culling are mastitis and nonconception. In Israel, all milk-recorded cows are checked for pregnancy 60 d after insemination unless the cow is reinseminated prior to 60 d (20). Thus, the pregnancy status of all cows is known in real time, and this information can be used to increase the accuracy of HL predictions.

Objectives of this study were to compare three measures of longevity for Israeli Holsteins; to study the effect of incorporating data on pregnancy, days open (DO), and protein yields in the computation of expected HL; to compute adjustment factors for live cows; and to determine the effects of the adjustment procedure for incomplete records on genetic evaluations. Adjustment factors were derived from variance components for complete and incomplete HL records estimated by a multitrait animal model analysis; records of different lengths were considered as correlated traits.

TABLE 1. Number of levels of effects included in the three data sets that were analyzed.

Effects	Data set			
	1	2	3	4
Cows	130,025	85,965	75,825	370,406
Records	82,196	51,888	45,300	284,541
Sires	422	393	379	965
Herd-year seasons	4509	3319	3074	16,816
Genetic groups	2	2	25	42

## MATERIALS AND METHODS

### Estimation of Variance Components for Survival Traits

Three measures of longevity were compared on a preliminary data set consisting of 335,832 first through seventh parities of Israeli Holsteins with first calvings between 1984 and 1988. The measures were HL, which was computed as the number of days from first calving to the cow's exit date; the number of parities per cow up to seventh (NP); and the adjusted number of parities (ANP), which was computed as the number of completed parities up to the seventh plus the days in milk at last parity divided by 305. If days in milk was >305, then ANP was set to NP. For cows still in the herd after completing seven lactations, HL was computed as the number of days from first calving to seventh calving plus 400 d. Because only cows that first calved prior to 1989 were included in the analysis, all cows could have completed at least seven lactations by the date of the analysis, June 1998. Cows were deleted from the analysis if the first parity record was missing; age at first calving was <570 or >1000 d; any calving intervals were <250 d; mean calving interval was >550 d; last recorded parity was <7, and exit day was missing for that parity; parity was >1 with valid exit date; or protein yield was <50 or >600 kg for the last valid parity record.

After edits, the number of cows, records, sire, and herd-year seasons (HYS) included in this data set (data set 1) are given in Table 1. The means for the three traits analyzed and the number of cows by year of first calving are given in Table 2. No clear trends were evident, although the means for all three traits were lowest for cows with first calving in 1986.

Genetic and environmental variance and covariance components were estimated using an animal model by multitrait REML (8). The analysis model was

$$LT_{ijkl} = HYS_{ik} + A_{ij} + G_{il} + e_{ijkl} \quad [1]$$

where  $LT_{ijkl}$  = longevity record for trait  $i$  (HL, NP, or ANP) of cow  $j$ , from HYS  $k$ ;  $HYS_{ik}$  = fixed effect of HYS  $k$  on trait  $i$ ;  $A_{ij}$  = random additive genetic effect of cow

TABLE 2. Means of the three longevity traits analyzed by year of first calving.

Year of first calving	Cows	Means		
		Parities <sup>1</sup>	Herd life <sup>2</sup>	Adjusted number of parities <sup>3</sup>
	(no.)		(d)	
1984	8120	3.07	1045	2.79
1985	13,250	3.03	1026	2.75
1986	19,310	2.93	990	2.64
1987	20,350	2.96	1002	2.67
1988	20,320	2.95	1012	2.68
Total	81,620	2.97	1010	2.69

<sup>1</sup>To a maximum of seven.

<sup>2</sup>Number of days from first calving to the exit date of the cow.

<sup>3</sup>Number of completed parities up to seventh plus days in milk at last lactation divided by 305.

$j$  on trait  $i$ ;  $G_{il}$  = fixed effect of genetic group  $l$  on trait  $i$ ; and  $e_{ijkl}$  = random residual for trait  $i$ . The HYS was defined relative to the first parity calving date. Two seasons, beginning in April and October, were defined for each herd year. Pedigree information from all known parents and grandparents of cows with records was included in the analysis. Two phantom parent groups were defined for unknown parents by sex of parent (21). The total number of animals in the analysis is also given in Table 1. The initial estimate of the ratio of the residual to additive genetic variance was 12.

For comparison, heritability estimates were also derived by REML using a multitrait sire model (12). The model was the same as Equation [1], except that the additive genetic effect was replaced with a sire effect. Sires were assumed to be unrelated in the analysis. Heritability was estimated as four times the sire variance component divided by the sum of the sire and residual variance components.

### Estimation of Expected HL for Live Cows and Estimation of Variance Components

Data set 2, including 559,035 Israeli Holstein lactation records with first calving dates from 1984 through 1989, was generated to predict HL for live cows. Lactation records were discarded for the reasons given previously or if days in milk were >500 or if a cow was scored pregnant but days open = 0. After edits, 51,888 valid cow records were in this data set.

A linear model was used to estimate HL from incomplete records. Multiple records were derived for each cow by cutting the records at 6-mo intervals beginning 6 mo after first calving until 4 yr after first calving and then cutting records at yearly intervals until 6 yr after first calving. At each cut date, a record was generated only

TABLE 3. Number and percentage of cows at each level of current herd life.

First calving to cut date	Number of cows	%
(yr)		
0.5	44,728	19.3
1.0	38,573	16.7
1.5	32,787	14.2
2.0	27,261	11.8
2.5	23,169	10.0
3.0	19,902	8.6
3.5	16,699	7.2
4.0	14,021	6.1
5.0	9398	4.1
6.0	4920	2.1
Total	231,458	100

for cows that survived until that cut date. Thus, up to 10 records were generated per cow. Number and percentage of cow records cut at each 6 mo interval are in Table 3. This data set included 231,458 cow records.

The dependent variable was remaining HL (**RHL**), computed as days from the cut date to the exit date. The independent variables were **CHL**, defined as days from first calving to cut date; last parity prior to cut; expected protein yield of the last parity prior to cut; pregnancy status, where 1 = pregnant, and 0 = not pregnant; **DO** of the last lactation for cows pregnant by the cut date or days in milk for cows not pregnant at the cut date, days pregnant (**DP**) at cut date for pregnant cows; and days dry (**DD**) at the cut date if the record was cut during the dry period. Days pregnant = 0 for cows not pregnant at the cut date. The expected protein yield was computed as described previously (19). The HYS were defined as described previously, and were absorbed. Last parity prior to cut, pregnancy status, and HYS were analyzed as discrete effects; all other effects were analyzed as continuous variables. Means, standard deviations, minimums, and maximums for the continuous variables included in the model and HL are in Table 4. The original

TABLE 4. Basic statistics of the continuous variables used to estimate expected herd life.

Variable <sup>1</sup>	$\bar{X}$	SD	Minimum	Maximum
CHL	747	479	184	2190
DO	112	70	1	495
DD	6	16	0	208
EPY	287	39	106	506
DP	83	83	0	321
HL	1530	642	185	3017

<sup>1</sup>CHL = current herd life, computed as number of days from first calving to cut day; DO = days open of the last lactation or days in milk if the cow was not pregnant at the cut date; DD = days dry if the cow record was cut during the dry period; EPY = expected kilograms of protein yield of the last parity prior to cut; DP = days pregnant at cut date; and HL = actual herd life in days.

model included linear, quadratic, and cubic effects for all the continuous variables and all two-way interactions. All nonsignificant effects ( $P < 0.05$ ) were deleted from the final analysis model.

The final model was used to estimate predicted RHL for each record. If predicted RHL was  $<0$ , then predicted RHL was set to zero. Estimated HL (**EHL**) was computed as HL for cow records that were culled prior to the cut and as the sum of predicted RHL and CHL for records cut after the cut date. Genetic and environmental variance components among HL and EHL computed for the 10 cut dates were estimated by multitrait REML (8) using the analysis model of Equation [1] for these 11 traits. As in the previous analysis, pedigree information from all known parents and grandparents of cows with records were included, and two phantom parent groups were defined. The total number of cattle in this analysis (data set 2) is also given in Table 1.

#### Estimation of Adjustment Factors for Genetic Evaluations of Incomplete Records

The EHL records as a function of CHL were first adjusted so that the genetic covariance between EHL and actual HL records would equal the genetic variance of the actual records. This adjustment was slightly different from the model of VanRaden and Klaaskate (11), who adjusted records to equal genetic variances. Multiplicative adjustment factors were estimated with PROC NLIN of SAS (9) based on the following nonlinear function of CHL:

$$RG_i = b_0 + (b_1/CHL_i) + e_i \quad [2]$$

where  $RG_i$  = ratio of the square root of the genetic covariance between HL and  $EHL_i$ , EHL at cut date  $i$ ;  $b_0$  and  $b_1$  = regression constants; and  $e_i$  = residual. This model was based on the results of VanRaden and Klaaskate (11), who found that  $RG$  is large for small values of CHL and tends toward unity for large values of CHL. With this formula, as CHL increases, the term  $b_1/CHL$  becomes negligible with respect to  $b_0$ , and  $b_0$  should be approximately equal to unity. The EHL records were then multiplied by the predicted values of  $RG$  from Equation [2],  $PRG$ , which also increased the mean. The following nonlinear model was used to adjust for the increase in the mean as a function of CHL based on data set 3:

$$EHLX_j = b_2 + b_3/CHL_j + e_j \quad [3]$$

where  $EHLX_j$  =  $EHL \times PRG$  for cow  $j$ ,  $b_2$  and  $b_3$  = regression constants, and the other terms are as described previously. Predicted HL (**PHL**) was then com-

puted as  $EHLX - b_3/CHL$ ;  $b_2$  was not subtracted because, as a constant, it would have the same effect on all records.

In the animal model analysis, the PHL records were weighted by the inverse of the ratio of the residual variances of PHL and HL as a function of CHL. Weighting factors for the square root of the residual variances of PHL were computed using the model of Equation [2]. If this model is appropriate, then  $b_0$  should be approximately equal to the residual standard deviation of HL.

#### Genetic Evaluation for Longevity

Data set 3 was generated for computation of animal model genetic evaluations for HL and PHL. Edits were the same for lactation records, except that cows with first calvings in 1989 were also included. The HL was computed for each cow as described previously, except that if HL was  $>2557$  d (7 yr), then HL was set to equal 2557 d. The CHL was computed as days from first calving to January 1, 1990. Cows with CHL  $<35$  d were deleted, leaving 45,300 cow records.

The analysis model of Equation [1] was used to compute genetic evaluations for HL, PHL with equal weights for all records, and PHL weighted as described previously. Pedigree information from all known parents and grandparents was included. The pedigree file included a total of 379 sires. Twenty-five phantom parent groups were defined by year of birth and sex of parent (21). Number of cows, records, sire, and HYS included in data set 3 are also given in Table 1. The two methods for analyzing PHL were compared by correlations of the sires' EBV for these methods and the EBV for HL and by the regression of the HL sire EBV on the PHL EBV.

Genetic evaluations for HL based on the method developed were also computed on the complete Israeli-Holstein dairy cattle population in September 1998, including 284,541 cows with first calving dates since January 1, 1985 and at least 35 DIM at the date of evaluation. Other edits were the same as for data set 3, and all known parents and grandparents of cows with records were included in the analysis. The numbers of cows, records, bulls, HYS, and genetic groups for this data set (data set 4) are also given in Table 1. Genetic trends were computed as the regression of the EBV of cows on their birth dates, including all cows born since 1981. Phenotypic trends were computed as the regression of the cows HL on their birth dates but including only cows with valid HL records. For live cows EHL was used instead of HL to calculate the phenotypic trend. Correlations were computed between bull EBV for HL with milk and protein production for bulls with reliability  $>0.5$  for all three traits. Bull EBV for milk and protein were computed by a standard animal model (20).

TABLE 5. Heritability (on the diagonal), genetic correlations (above diagonal) and phenotypic correlations (below diagonal) for three cow survival traits.

	Number of parities	Herd life	Adjusted number of parities
Number of parities <sup>1</sup>	0.11	0.98	1.00
Herd life <sup>2</sup>	0.97	0.12	0.99
Adjusted number of parities <sup>3</sup>	0.99	0.98	0.11

<sup>1</sup>To a maximum of seven.

<sup>2</sup>Number of days from first calving to the exit date of the cow.

<sup>3</sup>Number of completed parities up to seventh plus days in milk at last lactation divided by 305.

### RESULTS AND DISCUSSION

Heritability, genetic, and phenotypic correlations derived from the animal model analysis are given in Table 5 for NP, HL, and ANP using data set 1. All genetic correlations were >0.98, and phenotypic correlations were >0.97. The animal model heritability estimates of 0.11 to 0.12 were higher than were the sire model estimates of 0.07, 0.08, and 0.075 for NP, HL, and ANP computed from data set 1 (data not shown). The sire model estimates were similar to estimates for the corresponding traits obtained in previous analyses (11, 15). Heritability for HL was slightly higher than for the other two traits in both models. Vollema and Groen (15) also found higher heritability for HL than for NP. All previous estimates of genetic correlations among longevity traits were always higher than 0.90; genetic correlation estimates are generally slightly lower than phenotypic correlation estimates (15). Because of the slightly higher heritability for HL and the nearly complete genetic correlations among all three traits, the remaining analyses were performed only for HL.

The RHL was estimated from data set 2 as described previously. After removing nonsignificant effects from the analysis, the final equation for estimating RHL from the incomplete records was

$$\begin{aligned}
 \text{RHL} = & \text{PPC} - 908 + (0.131) \text{CHL} + (-0.00029) \text{CHL}^2 \\
 & + (-0.872) \text{DP} + (-5.218) \text{DO} + (0.0169) \text{DO}^2 \\
 & + (-0.0000313) \text{DO}^3 + (0.00126) \text{CHL} (\text{DO}) \\
 & + (-0.536) \text{DD} + (9.532) \text{EPY} \\
 & + (-0.011) \text{EPY}^2 \quad [4]
 \end{aligned}$$

where PPC = last parity prior to cut, DP = days pregnant, and EPY = expected protein yield; all other terms are as defined previously.

All effects included in the final model were significant at  $P < 0.0001$ . The coefficient of determination was 0.33. The largest coefficients were for DO and EPY, although the sum of the type I sum of squares for EPY and EPY<sup>2</sup>

TABLE 6. Estimated effects for levels of the class effects on remaining days of herd life.

Effect	Level	Effect (d)
Parity	1	62
	2	-56
	3	-108
	4	-123
	5	-51
	6	0
Pregnancy status	Open	0
	Pregnant	420

explained only 3% of the total variance when entered last in the model. Pregnancy status had the largest type III sum of squares. The discrete parity and pregnancy status effects are given in Table 6. Parity effects showed no discernible trend because this effect was highly confounded with CHL, which was also included in the model. Pregnancy at the cut date increased RHL by 420 d, but the effect of DP was negative.

Heritability of HL and EHL and genetic and phenotypic correlations between HL and EHL are given in Table 7. Genetic correlations increased from 0.87 for records cut after 6 mo to 0.99 for records cut after 3 yr. The phenotypic correlation was 0.61 for records cut after 6 mo and increased to 0.94 for records cut after 3 yr. The genetic and phenotypic correlation estimates between complete and incomplete HL records were higher than were those reported by VanRaden and Klaaskate (11), but they did not include data on pregnancy status.

Heritability increased from 0.11 for records cut at 6 mo to 0.14 for records cut after 3 yr and then remained constant. The heritability obtained in this data set for complete records was slightly higher than was the estimate derived from data set 1 in Table 5. VanRaden and Klaaskate (11), using a sire model, reported that heritability of cut records increased from 0.03 to 0.08.

TABLE 7. Heritabilities of expected herd life computed from cut records and genetic and phenotypic correlations between actual herd life and expected herd life.

Years from first calving to cut date	Heritability	Correlations	
		Genetic	Phenotypic
0.5	0.11	0.87	0.61
1.0	0.11	0.92	0.70
1.5	0.12	0.98	0.82
2.0	0.13	0.98	0.87
2.5	0.13	0.99	0.92
3.0	0.14	0.99	0.94
3.5	0.14	1.00	0.96
4.0	0.15	1.00	0.98
5.0	0.14	1.00	0.99
6.0	0.14	1.00	1.00
Actual herd life	0.14	...	...

TABLE 8. Regression coefficients, coefficients of determination and correlations between actual and predicted function of variance components based on the nonlinear analysis model.

Dependent variable <sup>1</sup>	Coefficients <sup>2</sup>		R <sup>2</sup>	Correlation
	b0	b1		
RG	0.95	293	0.93	0.96
EHLX	1081	224,010	0.98	0.99
Square root of residual variance of PHL	656	45,256	0.86	0.93

<sup>1</sup>RG = ratio of the square root of the genetic covariance between herd life and expected herd life; EHLX = expected herd life times predicted value of the ratio of the square root of the genetic covariance between herd life and expected herd life.

<sup>2</sup>The analysis model was  $y = b_0 + (b_1/CHL_i) + e$ ; where  $y$  = dependent variable, and  $CHL$  = days from first calving to cut date.

The genetic covariances between the complete records and incomplete records were then used to compute genetic adjustment factors based on Equation [2]. The coefficients are given in Table 8. The RG and PRG, based on Equation [2] as functions of CHL, are plotted in Figure 1. As expected, the intercept is close to unity. Thus, as the length of the incomplete record tended toward infinity, PRG tended toward unity. Predicted EHLX was then computed based on Equation [3]. The coefficient values are also given in Table 8. Actual EHLX and predicted EHLX as functions of CHL are plotted in Figure 2. Residual variance weighting factors for PHL were then computed as described. The coefficients are given in Table 8. The constant coefficient was equal to 656, and the square root of the residual variance of HL was 666. For convenience, the residual weighting factors

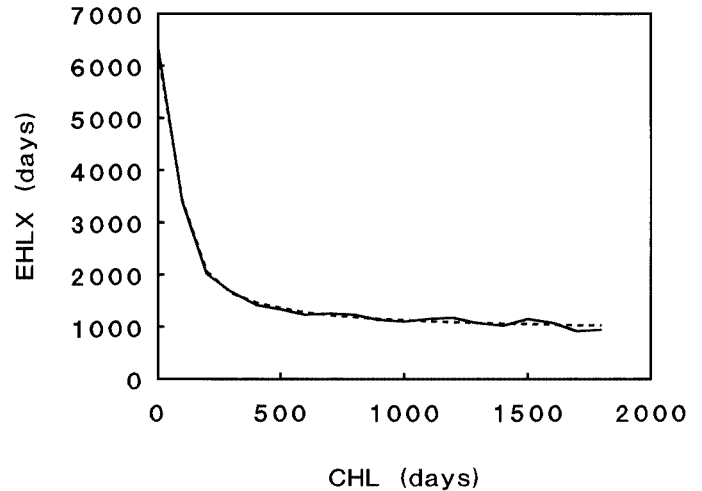


Figure 2. The means of estimated herd life from cut records after adjustment to equal genetic covariance (EHLX) as a function of current herd life computed as days from first calving to cut date (CHL). Predicted EHLX (---); actual EHLX (—).

were then computed as  $656/(656+45256/CHL)$ . The square root of the residual variance of PHL as a function of CHL and the predicted values based on Equation [2] are plotted in Figure 3. Although both the genetic covariances and the environmental variances were monotonic functions of CHL, the residual variances are no longer monotonic after adjustment to equal genetic covariances. The coefficients of determination for all three nonlinear models are also given in Table 8. The coefficient of determination was lowest for the residual variance of PHL, but all values were >0.8.

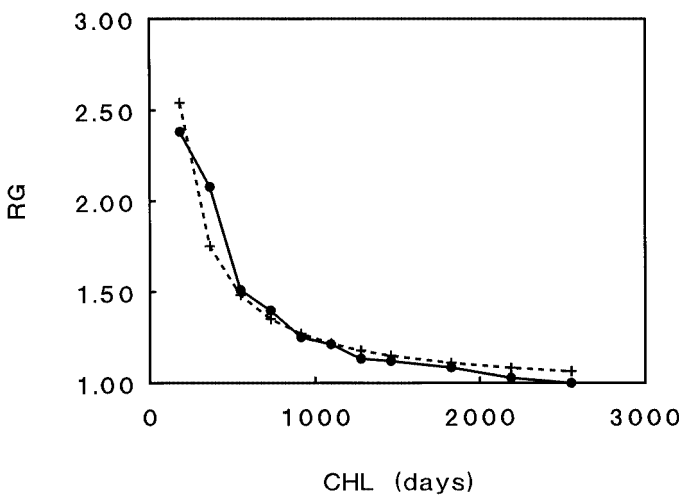


Figure 1. Ratio of the square root of the genetic covariance between herd life and estimated herd life from cut records to the genetic variance of herd life (RG) as a function of current herd life computed as days from first calving to cut date (CHL). Predicted RG (+); actual RG (●).

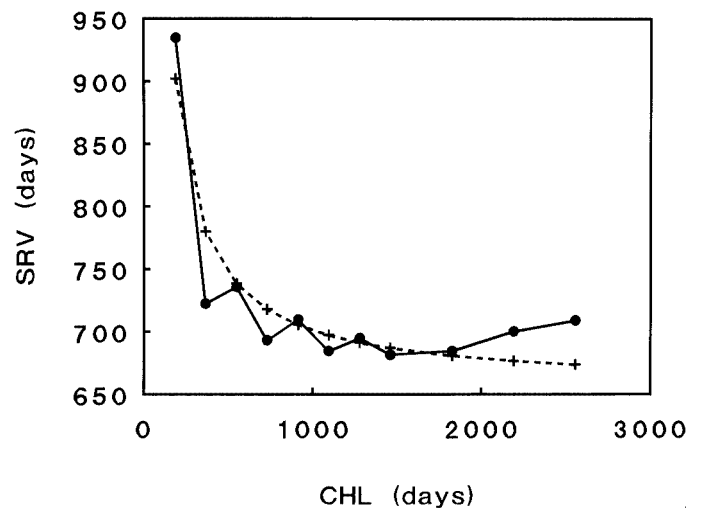


Figure 3. The square root of the residual variance of predicted herd life (SRV) as a function of current herd life computed as days from first calving to cut date (CHL). Predicted SRV (+); actual SRV (●).

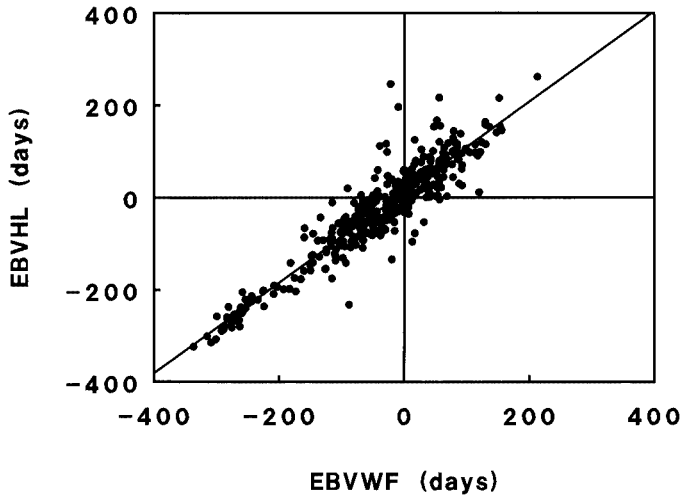


Figure 4. Estimated breeding values of sires for herd life (EBVHL) as a function of estimated breeding values computed from cut records that were weighted (EBVWF).

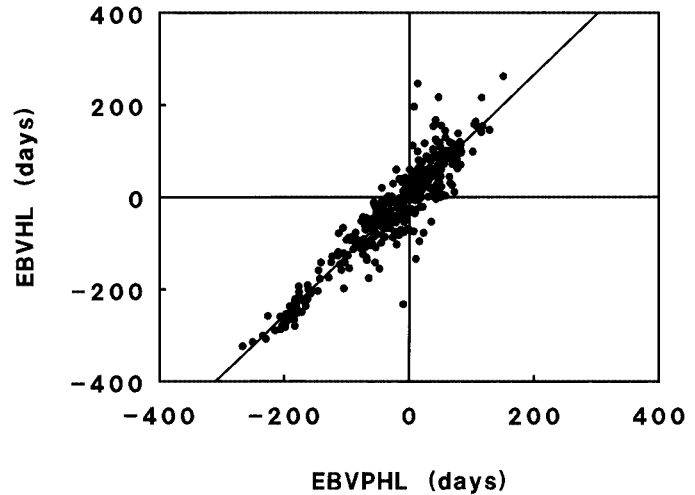


Figure 5. Estimated breeding values of sires for herd life (EBVHL) as a function of estimated breeding values computed from cut records weighted equally (EBVPHL).

The EBV for all animals included in data set 3 were computed for HL and PHL with all records cut at January 1, 1990. Sire EBV for HL is plotted in Figure 4 as a function of PHL with weighting factors and in Figure 5 as a function of PHL without weighting factors. Correlations between sire EBV for HL and PHL with and without weighting factors are given in Table 9 for all sires and for sires with >10 daughters. Because evaluations of young sires should be most affected by incomplete records, correlations were also given for sires born after 1981, 1982, 1983, and 1984. Correlations between HL and PHL computed with and without weighting factors were 0.94 and 0.93, respectively. Correlations were lower if only bulls with >10 daughters were included and were marginally higher for PHL computed with weighting factors. As expected, correlations decreased with decreases in the ages of the bulls. In all cases, differences between correlations for PHL computed with and without weighting factors were no more than 1%.

The regressions of sire EBV for HL on PHL with and without weighting factors are also given in Table 9. Without weighting factors, slopes for all bulls were about 1.3 but were nearly equal to unity for evaluations computed with weighting factors. Thus, nearly unbiased evaluations were derived with weighting factors, and evaluations based on equal weights of all records were biased. For the young sires, without weighting factors, regressions increased up to 1.75 for bulls born after 1984 and were, therefore, highly biased. With weighting factors, regressions decreased slightly with the age of the bull but were still 0.85 for bulls born after 1984. Thus, bias was much smaller with weighting factors.

In the analysis of the complete Israeli Holstein population the phenotypic trend for HL was -15 d/yr, and the genetic trend was 9 d/yr. The genetic correlations between the sire EBV for HL with milk and protein production by birth year of bulls born since 1986 are given in Table 10. The correlations for all bulls born since 1986

TABLE 9. Regression coefficients and correlations between estimated sire breeding values of HL and PHL with and without inclusion of weighting factors.

Weighting factors	Birth year of sires	All bulls				Bulls with >10 daughters			
		Sires (n)	Intercept	Slope	r	Sires (n)	Intercept	Slope	r
With	All	379	12.68	0.98	0.94	212	10.39	0.99	0.87
	>1981	157	9.54	0.99	0.86	145	10.09	0.99	0.87
	>1982	97	12.31	0.95	0.77	86	13.41	0.94	0.76
	>1983	78	14.11	0.95	0.73	68	15.70	0.94	0.72
	>1984	39	3.95	0.85	0.61	31	5.50	0.84	0.61
Without	All	379	4.85	1.31	0.93	212	3.46	1.30	0.86
	>1981	157	0.59	1.30	0.86	145	1.70	1.29	0.86
	>1982	97	-5.01	1.47	0.76	86	-3.87	1.46	0.75
	>1983	78	-5.22	1.55	0.72	68	-3.94	1.54	0.71
	>1984	39	-23.62	1.75	0.63	31	-24.79	1.73	0.62

TABLE 10. Correlations between EBV for herd life with milk and protein production based on genetic evaluation of the complete Israeli Holstein population.

Birth year	Bulls (n)	Correlation with herd life	
		Milk	Protein
1986	40	0.65	0.67
1987	42	0.72	0.65
1988	53	0.43	0.44
1989	33	0.54	0.46
1990	31	0.48	0.64
1991	40	0.59	0.60
1992	42	0.63	0.65
1993	52	0.55	0.68
Total	340	0.53	0.57

are also given. Correlations were lowest in 1988 and 1989, but no clear trends were evident. These correlations were slightly less than the value of 0.77 predicted by Strandberg and Hakansson (10) with 15% voluntary culling based on milk production. In our analysis, HL was not adjusted for milk production, and EPY was used to predict HL for live cows. This method should have increased the similarity between EBV for production and HL, especially for young sires whose daughters were in first lactation. However, the genetic correlations between protein and HL were nearly equal for sires born in 1993 as compared with sires born in 1986.

### CONCLUSIONS

Heritability estimated by an animal model was slightly higher for HL than for number of parities, but genetic correlations were close to unity. Animal model heritability estimates of herd life were higher than were sire model estimates. The expected HL for pregnant cows was 420 d greater than for open cows. Each kilogram of increase in protein yield increased the expected HL by 9.5 d. With inclusion of information on pregnancy and protein yield of the last parity, the genetic correlation of expected and actual herd life was 0.87 for records cut 6 mo after first calving. By weighting incomplete records to account for the effects of current HL on variance components, sire genetic evaluations were nearly unbiased. The genetic trend for HL was 9 d/yr for cows born since 1981.

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