

Genetic Evaluation for Herd Life in Canada

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Abstract

Methods for genetic evaluation of herd life of Canadian Holsteins sires were developed. Official evaluations were released first in January 1996. Herd life evaluations are adjusted for production in first lactation to remove the effect of culling for production. Resulting evaluations reflect the ability of a sire's daughters to survive for reasons other than production. Both direct (HL-DIR) and indirect (HL-IND) information was used to arrive at published HL evaluations. HL-DIR evaluations were obtained by combining evaluations for survival in each of the first three lactations, which were obtained through a multiple trait evaluation of survival (0/1) within lactations 1, 2, and 3. HL-IND evaluations were based on an index of the composite conformation traits mammary system, feet and legs, rump, and capacity. A multiple trait sire model based on Multiple Across Country Evaluation (MACE) methodology was used to combine HL-DIR and HL-IND evaluations. Resulting multiple trait HL-DIR and HL-IND evaluations were then combined into a single value for HL, which was published for all sires with an official evaluation for conformation. HL evaluations were normally distributed and represented a range of about one lactation, which implies that daughters of extreme sires are expected to differ by one lactation in functional herd life.

Objectives

Objectives of this study were to develop a national genetic evaluation system for herd life for Canadian Holstein sires, including information on survival and conformation traits.

Materials and methods

Methods that were developed for genetic evaluation of sires for herd life (HL) consist of three parts:

- I. Genetic evaluation of sires for HL based on survival data (HL-DIR)
- II. Genetic evaluation of sires for HL based on conformation traits (HL-IND)

- III. Combining genetic evaluations for HL-DIR and HL-IND into an overall genetic evaluation for HL (HL-PUB).

I. Genetic Evaluations for HL-DIR

Genetic evaluations for HL-DIR were based on survival (0/1) of cows in lactations 1, 2, and 3, conditional upon initiation of that lactation. Survival data were obtained from the data used for genetic evaluation for production and were based on the presence or absence of a subsequent lactation record in the data set. Survival data from a given lactation was not included until 2 years past calving, to allow sufficient time for inclusion of a subsequent lactation record in the data set used for genetic evaluation for production. Cows sold for dairy purposes were assumed

to have survived in that lactation. Calvings prior to July 1980 were excluded. A first lactation survival record was required on all animals. The edited data set contained survival records on 1,275,852 cows.

Lactational survival data were analyzed using a multiple trait animal model, in which survival in each lactation was considered a separate trait. The model used for each lactational survival trait was:

$$y_{ijkl} = hq_{il} + rhs_{jl} + (age_{k1})_l + (prot_{k1} * rhs_{jl})_{jl} \\ + (prot_{k1})_l + (fat_{k1})_l + animal_{kl} + e_{ijkl}$$

where

y_{ijkl} is the observation for survival (0/1) in lactation l ($l=1, 2$, or 3) on cow k that calved in herd-quota-year i

hq_{il} is the fixed effect of herd-quota-year i for lactation l

rhs_{jl} is the fixed effect of subclass j for registry status * herd size change * season of calving for lactation l

$(age_{k1})_l$ represents linear and quadratic regressions of survival in lactation l on age at first calving

$(prot_{k1} * rhs_{jl})_{jl}$ is the linear regression of survival in lactation l on $prot_{k1}$ by rhs_{jl} subclasses, where $prot_{k1}$ is the cow's normal rank for mature equivalent 305-day protein yield in first lactation within herd quota-year of first calving

$(prot_{k1})_l$ and $(fat_{k1})_l$ represent linear, quadratic, and cubic regressions of survival in lactation l on the cow's normal ranks for protein and fat yield in lactation 1 within herd-quota-year of first calving

$animal_{kl}$ is the random additive genetic effect of animal k for survival in lactation l ; and

e_{ijkl} is a random residual.

Registry status was defined in four classes: cows in herds with over 90% registered cows, cows in herds with less than 10% registered herds, registered cows in mixed herds (herds with between 10 and 90% registered cows), and non-registered cows in mixed herds.

Herd size change was determined based on the % change in herd size from one quota year to the next and was grouped into 5 classes: <-25%, -25 to -10%, -10 to +10%, +10 to +25%, and >+25%. Registry status and herd size were determined by quota year based on all cows calving in the herd. Three seasons of calving were defined relative to timing of the quota year: July to October, November to February, and March to June.

Genetic and residual (co)variances used in genetic evaluation analysis were estimated in a separate study using multi-trait DFREML. Parameters used in the evaluation are given in Table 1. Records in owner-sampler herds received 40% less weight than survival in herds on official recording to account for lower heritability of survival traits in such herds.

Complete pedigree information was included in the analysis. Phantom parents were assigned on the basis of origin of animal (Canada/Foreign), year of birth, and the four selection pathways.

The multiple trait animal model yields sire estimated breeding values (EBV) for survival in each lactation, which were combined into an overall EBV for HL-DIR based weights which were derived from economic values for survival in each lactation along with genetic parameters. Approximately equal emphasis on each trait resulted. Overall evaluations for HL-DIR were, therefore, calculated as a simple average of EBV for survival in lactations 1, 2, and 3.

Reliabilities for HL-DIR were approximated by first computing an approximate single trait reliability for EBV for survival in each lactation based on the method of Meyer (1989). Single trait reliabilities for the three survival traits were then combined into an approximate reliability for HL-DIR based on selection index procedures.

II. Genetic Evaluation for HL-IND

Sire evaluation for HL can be predicted indirectly based on evaluations for conformation traits based on genetic correlations between type traits and herd life. Table 2 shows recent estimates of genetic

correlations between composite type traits and herd life for cows that are classified for type. Correlations are shown for herd life with or without adjustment for production.

Estimates from Table 2 were used to develop the following indirect prediction of sire EBV for functional HL based on selection index theory and upon consultation with the industry.

$$\text{HL-IND} = 1 \text{ ETA}_{\text{capacity}} + 1 \text{ ETA}_{\text{rump}} + 4 \text{ ETA}_{\text{feet \& legs}} + 8 \text{ ETA}_{\text{mammary system}}$$

The combination of traits in this index explained approximately 36% of genetic variation for HL, which was only slightly less than an optimum index derived based on the genetic parameters in Table 2.

Reliabilities for HL-IND were approximated by 0.36 times the reliability of the sire's ETA for Conformation, where 0.36 is the squared genetic correlation between HL and the type index.

III. Combining sire evaluations for HL-DIR and HL-IND

A multiple trait sire model based on MACE procedures (Schaeffer, 1994) was used to simultaneously analyze and combine sire genetic evaluations for HL-DIR and HL-IND into an overall evaluation for HL (HL-PUB). Multiple trait analysis of HL-DIR and HL-IND involved two steps:

- 1) Deregression of sire evaluations for HL-DIR and HL-IND and estimation of sire variances.
- 2) Multiple trait analysis of deregressed evaluations.

Data included in multiple trait analysis were:

- 1) HL-DIR evaluations for all sires with an official evaluation for conformation and at least 1 daughter with a survival record.
- 2) HL-IND evaluations for all sires with an official evaluation for conformation.

A total of 4546 bulls with HL-DIR and HL-IND EBV were included in the analysis.

The pedigree file included 4969 bulls, including 27 phantom parents that were grouped by year of birth and pathway of inheritance.

Deregression of sire evaluations for HL-DIR and HL-IND was based on the procedures of Banos et al. (1993) and Weigel et al. (1995). Variance ratios used in the deregression procedure were based on a heritability of 0.18 for HL-IND (= approximate heritability of the type index) and a heritability of 0.03 for HL-DIR. Simultaneous to deregression of sire evaluations, genetic variances for HL-DIR and HL-IND were estimated based on single trait iterative approximate EM-REML procedures (Weigel et al., 1995).

Multiple trait analysis of deregressed proofs was based on the following model (Schaeffer, 1994; Weigel et al., 1995) for each trait i (i = HL-DIR or HL-IND):

$$Y_i = c_i \mathbf{1} + Z_i Q g_i + Z_i s_i + e_i$$

where

- Y_i is the vector of deregressed proofs for trait i
 c_i is the overall mean for trait i (unknown)
 Z_i is an incidence matrix
 Q is an incidence matrix that relates sires to phantom groups
 g_i is a vector of genetic group effects of phantom parents for trait i
 s_i is a vector of random sire effects for trait i (to be estimated)
 e_i is a vector of random residual effects

(Co)variance matrices assumed for random genetic effects were:

$$\text{Var} \begin{bmatrix} s_{ind} \\ s_{dir} \end{bmatrix} = \begin{bmatrix} A G_{ind, ind} & A G_{dir, ind} \\ A G_{dir, ind} & A G_{dir, dir} \end{bmatrix}$$

where

$G_{ind, ind}$ and $G_{dir, dir}$ are the estimated sire variances for HL-DIR and HL-IND, respectively, and

$G_{dir,ind} = r_g G_{dir,dir} G_{ind,ind}$ with r_g set equal to 0.6 (= genetic correlation between the type index and HL)

A is the additive genetic relationship matrix for all bulls based on sire and maternal grand sire relationships.

(Co)variance matrices assumed for random residuals were:

$$Var \begin{bmatrix} e_{ind} \\ e_{dir} \end{bmatrix} = \begin{bmatrix} R_{ind} & E_{ind,ind} & 0 \\ 0 & R_{dir} & E_{dir,dir} \end{bmatrix}$$

where

$E_{dir,dir}$ and $E_{ind,ind}$ are the estimated residual variances for HL-DIR and HL-IND, respectively, and

R_{dir} and R_{ind} are diagonal matrices with elements equal to one over the number of daughters in a bull's evaluation for HL-DIR and HL-IND, respectively.

Residual covariances were assumed to be zero to allow use of existing MACE programs. However, in contrast to the use of MACE for international evaluation, residual effects of HL-DIR and HL-IND are not uncorrelated because a daughter can contribute to a sire's EBV for both traits. Assuming residual covariances are zero does not bias results but can reduce the accuracy of ensuing EBV.

The impact of the assumption of zero residual co-variances on accuracy and emphasis on HL-DIR versus HL-IND was investigated using selection index methods. Results showed that ignoring the fact that some or all daughters contribute to both traits increased the weight on HL-IND by up to 12% when the number of daughters was large. At that point, however, the overall weighting put on type is low and a 12% increase has only a limited impact on absolute weights. The weight on HL-DIR increased also, but to a lesser degree. An increase in weights for both HL-DIR and HL-IND resulted in a small increase in the standard deviation of the combined evaluation. The accuracy of the combined evaluation was, however, hardly affected by the assumption

that two independent groups of daughters contribute to HL-IND and HL-DIR. This result justified the assumption of zero off-diagonals in the (co)variance matrix for residuals in the multiple-trait analysis.

Final derivation of published HL evaluations

The multiple trait analysis provides multiple trait evaluations both for HL-DIR (HL-DIR^{MT}) and for HL-IND (HL-IND^{MT}). Official sire ETA for HL (hence called HL-PUB) were computed based on:

$$HL-PUB = b_{IND} HL-IND^{MT} + b_{DIR} HL-DIR^{MT}$$

Because HL-DIR^{MT} and HL-IND^{MT} are multiple trait evaluations, weights b_{IND} and b_{DIR} can be derived based on genetic parameters as:

$$\begin{bmatrix} b_{IND} \\ b_{DIR} \end{bmatrix} = \begin{bmatrix} G_{ind,ind} & G_{dir,ind} \\ G_{dir,ind} & G_{dir,dir} \end{bmatrix}^{-1} \begin{bmatrix} G_{ind,pub} \\ G_{dir,pub} \end{bmatrix}$$

With other parameters as defined previously, $G_{ind,pub}$ and $G_{dir,pub}$ are genetic covariances of HL-IND and HL-DIR with HL-PUB, which can be derived based on (assumed) genetic correlations. Genetic correlations were set equal to 0.6 for HL-IND and HL-PUB (0.6 is the estimated genetic correlation between the type index and HL) and equal to 0.9 for HL-DIR and HL-PUB. Use of 0.9 instead of 1 for the correlation between HL-DIR and HL-PUB accounts for potential inaccuracies in the survival data that are used for HL-DIR and for potential benefits of conformation traits beyond their observed relationship with HL.

Reliabilities of HL-PUB were approximated based on reliabilities of HL-DIR and HL-IND, using selection index procedures.

Expression of sire genetic evaluations

Sire evaluations for HL were expressed as estimated transmitting abilities (ETA) in

number of lactations and represent expected daughter differences in functional HL. The average ETA of bulls with daughters calving in the last 3 years was set equal to 3. For example, daughters of a bull with an ETA of +3.25 are expected to last a quarter of a lactation longer than daughters of an average bull (set equal to 3 lactations), given the same level of production.

Results

Figure 1 shows the frequency distribution of sire ETA for HL-PUB. With an average of 3, ETA for HL-PUB ranged from 2.36 to 3.46 lactations. This indicates that daughters of extreme sires are expected to differ by 1 lactation in length of functional herd life. The standard deviation of ETA for HL-PUB (based on all bulls included in the MACE analysis) was 0.145. The average reliability was 0.77.

Table 3 shows correlations of HL-PUB with HL-DIR, HL-IND (prior to MACE analysis), and ETA for conformation, protein yield, and somatic cell score. Only bulls born past 1983 and with an official evaluation for conformation were included in the analysis.

HL-DIR and HL-IND had moderately high and approximately equal correlations with HL-PUB (0.77) (Table 3). Correlations of HL-DIR with ETA for HL-IND and conformation traits were lower. Correlations of ETA for HL were uncorrelated with protein yield. Correlations of both HL-DIR and HL-COMB with SCS were low and negative (desirable).

Although ETA for HL-DIR and HL-IND had approximately equal correlations with ETA for HL-PUB (Table 3), the emphasis on HL-DIR versus HL-IND differs for individual

bulls, depending on the amount of information available for HL-DIR and HL-IND. Figure 1 shows the approximate weights put on HL-DIR and HL-IND in HL-PUB, depending on the reliability of HL-DIR. Results in Figure 1 were approximated using selection index procedures. The figure shows that the emphasis on HL-IND decreases with increasing reliability of HL-DIR but does not asymptote to zero because of the use of a genetic correlation of 0.9 between HL-DIR and HL-PUB.

Figure 2 shows genetic trends in the male population for HL-DIR, HL-IND (prior to MACE), and HL-PUB. Genetic trends were based on mean ETA by year of birth. Genetic trends were similar for all three traits and positive, which is likely the result of selection for type traits.

References

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Table 1. Parameters of functional lactational survival used in national genetic evaluation for functional HL of Canadian Holsteins (h^2 on diagonal, genetic correlations below diagonal and phenotypic correlations above diagonal)

	Lactation 1	Lactation 2	Lactation 3
Lactation 1	.03	-.29	-.10
Lactation 2	.62	.03	-.14
Lactation 3	.57	.75	.03

Table 2. Estimates of genetic correlations of composite conformation traits with herd life, with (functional) or without (unadjusted) adjustment for production in first lactation

Conformation Trait	Genetic Correlation With	
	Functional HL	Unadjusted HL
Conformation	.59	.45
Capacity	.20	.15
Rump	.19	.12
Feet & Legs	.23	.21
Fore Udder	.56	.33
Rear Udder	.49	.40
Mammary System	.57	.14
Dairy Character	.06	.37

¹⁾ Functional HL is HL adjusted for culling for production.

Table 3. Correlations of published sire ETA for HL (HL-PUB) and sire ETA for HL based on survival data (HL-DIR) with ETA for other traits¹⁾

ETA for	HL-DIR	HL-PUB
HL-IND	0.31	0.78
HL-PUB	0.77	- -
Protein yield	0.03	0.05
Conformation	0.24	0.71
Capacity	0.05	0.27
Rump	0.04	0.23
Feet & Legs	0.21	0.46
Mammary System	0.24	0.71
SCS	-.12	-.17

¹⁾ Based on bulls born past 1983 (2087).

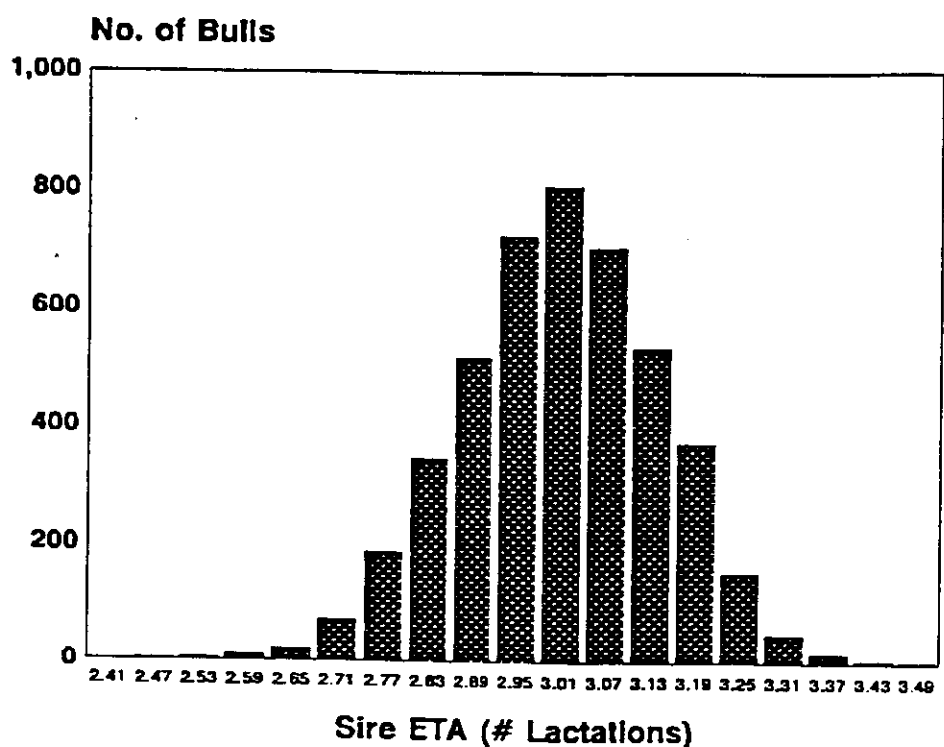


Figure 1. Frequency distribution of HL-PUB evaluations.

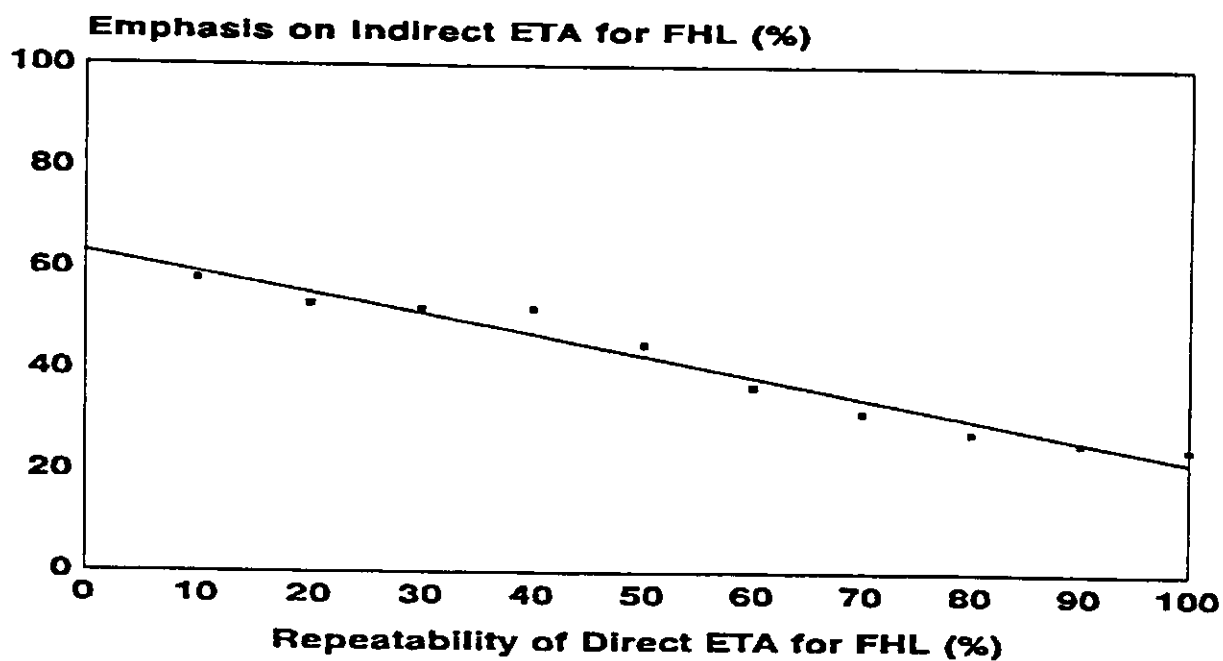


Figure 2. Approximate emphasis on HL-IND in sire ETA for HL-PUB, depending on reliability for HL-DIR.

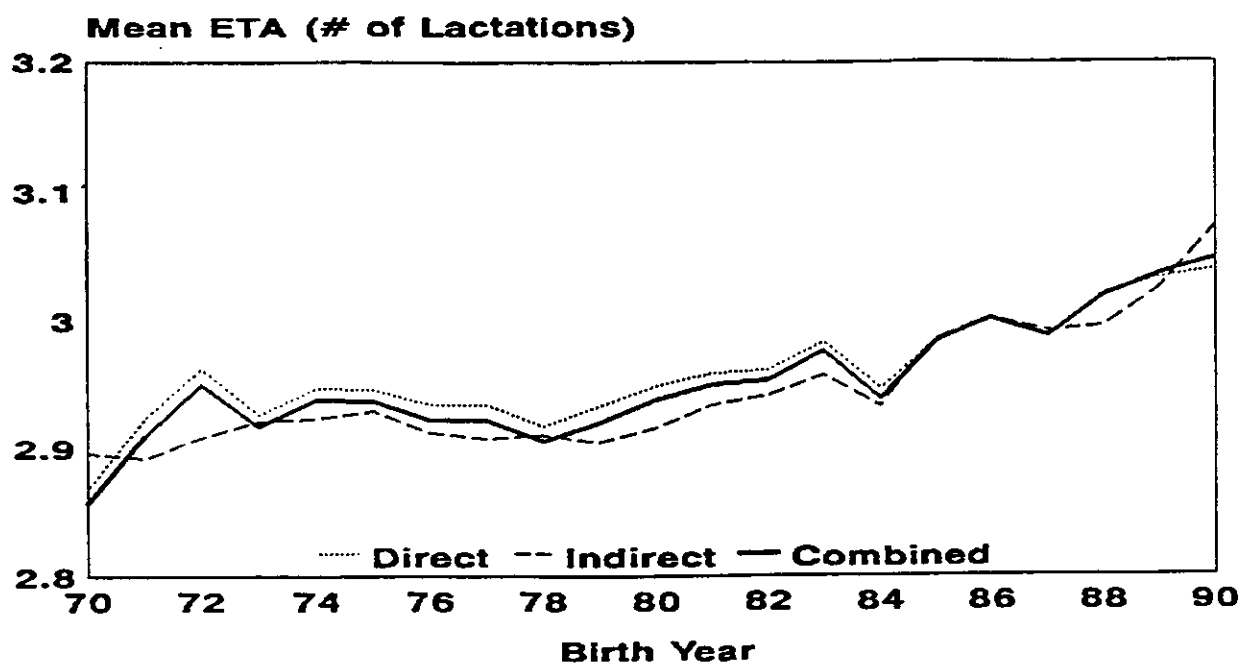


Figure 3. Genetic trend in sire ETA for HL-DIR (Direct), HL-IND (Indirect), and HL-PUB (Combined).