

ALTERNATIVE METHODS FOR GENETIC EVALUATION OF SIRES FOR SURVIVAL OF THEIR DAUGHTERS IN THE FIRST THREE LACTATIONS

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SUMMARY

Canadian Holstein sires were evaluated for survival of their daughters in lactations 1 to 3. Results from three methods of analysis were compared: 1) a linear model, 2) a threshold model, and 3) a survival analysis with a Weibull model. Records from up to 700,000 cows were available. Explanatory factors in the three models were as similar as possible and were chosen based on the factors included in the official genetic evaluation of herd life in Canada. Genetic parameters for the linear and threshold models were estimated from the data. Heritabilities for survival were approximately 0.04 and 0.07 from the linear and threshold models, respectively. Correlations between estimated breeding values for sires from the three analyses were approximately 0.80 within the same lactation.

Keywords: herd life, survival analysis, genetic evaluation.

INTRODUCTION

For dairy cattle, herd life or the ability to survive involuntary culling is a trait of considerable economic importance. When herd life is increased, costs associated with raising or purchasing replacement females are decreased. Average production of the herd is increased because a greater proportion of culling can be based on production and because the proportion of mature cows, which produce more milk than young cows, is increased.

Because the economic importance of herd life is so great and because measures of longevity can be derived from milk recording data, several countries are now performing genetic evaluations for herd life (Interbull 1996). Longevity can be measured in a variety of ways and genetic evaluations are not standardized across countries. Some countries (Ducrocq and Sölkner 1998) use survival analysis to evaluate days of productive life. Other countries (e.g. VanRaden and Klaaskate 1993) evaluate longevity with a standard linear model. In Australia and Canada, survival in each of the first three lactations is recorded as a binomial trait and evaluated with a linear model (Madgwick and Goddard 1989, Jairath et al. 1997). Despite their differences, all of methods of evaluation are designed to help select for the same aggregate genotype of lifetime profitability. The objective of this research was to compare estimates of genetic parameters and breeding values obtained from a variety of analyses of survival.

MATERIALS AND METHODS

Data. The original data available were 1,334,404 records used for the February 1997 genetic evaluation of survival for Canadian Holsteins. To decrease the data to a more manageable size, edits required age at first calving between 20 and 32 months, inclusive, and year of first calving between 1986 and 1992, inclusive. An additional step of editing kept only records from animals in herds that had at least 12 animals in at least one herd-quota-year of first calving. This step was designed to ensure that contemporary group sizes were relatively large. Following these edits, 699,722 records from 7,678 herds remained. Further edits were made when necessary for each of the various analyses.

Models. The explanatory factors in the various analyses were chosen to be as similar as possible to those used in the national evaluation of survival (Jairath *et al.* 1997). In their method, survival is modelled as a separate trait for each of the first 3 lactations. Fixed effects in the model included herd-quota year of calving; age at first calving; the interaction of herd registry status, change in herd size, and season of calving with protein deviation; and linear, quadratic, and cubic regressions on deviated production of fat and protein in first lactation. Random effects were animal and residual.

For the linear model, variance components were estimated using MTDFREML (Boldman and Van Vleck 1991) and a sire model. Estimates were obtained for five samples of data, each containing approximately 60,000 records from daughters of 1100 sires, and results were averaged across the five samples. Single-trait sire and animal models were then used to obtain BLUP breeding values for survival in each of the three lactations. An overall EBV was obtained by calculating the simple average of EBV from each lactation. Numbers of records and animals in the data and relationship files are given in Table 1 for each lactation.

Table 1. Sizes of the data and relationship files for the linear and threshold model analyses

Lactation	Linear model		Threshold model	
	Records	Animals	Records	Sires
1	699,722	1,276,344	674,404	4785
2	477,130	946,717	466,192	5564
3	274,963	616,066	267,619	4515

The use of the threshold model required several specific edits and modifications to the model. Most notably, sire models were used for all analyses. Animal models were used initially, but results were poorly behaved. Also, a specific step of editing was done to ensure that all contemporary groups included both surviving and culled cows. This was accomplished by clustering some groups from the same herd but across two consecutive years. Some small herds reported no culled cows and these herds were removed from the data. Similarly, contemporary groups were considered as random effects to improve the stability of estimates of variances. Sires were required to have 10, 5, and 4 daughters in first, second, and third lactations, respectively. The numbers of records and sires used for each of the three lactations are in Table 1. Variance components and breeding values were estimated in single-trait

analyses using a modified version the *g2* software of Janss *et al.* (1995), which used Gibbs sampling to marginalize densities. Two independent chains of 10,500 rounds were generated for the first lactation data. Four independent chains of 10,500 rounds were generated for second and third lactations. The first 500 rounds of each chain was used as a "burn-in" period. These strategies yielded approximately 200 independent observations of sire variance of the respective posterior distributions. As with the linear model, an overall EBV was obtained as the average of EBV from each lactation.

A single trait, days of life though the end of third lactation, was analyzed with survival analysis models. Each cow was allowed a maximum of 305 days per lactation. Cows that initiated a subsequent lactation were given 60 more days for the dry period. Records from cows that completed one lactation, but were not reported to have terminated (by culling or drying off) a subsequent lactation were considered censored. Approximately 40% of the cows had censored records. Herd-year of calving and the interaction of season, herd registry status, change in herd size were modeled as time dependent effects, changing for each parity. Effects of herd-years were random. Days of life were assumed to follow a Weibull distribution and were analyzed by using a sire model and the "Survival Kit" software of Ducrocq and Sölkner (1994). A heritability of approximately 8% was used for the evaluation, based on results of Ducrocq and Sölkner (1998). The data and relationship files included 674,827 records and 4785 sires, respectively.

RESULTS

Estimates of the heritability of survival in the first three lactations are in Table 2 for both the linear and threshold model. Estimates are similar to those found in literature for functional herd life (e.g. Lawlor and Short 1992). As expected, estimates of heritabilities were greater on the underlying scale (threshold model). For both models, heritabilities were similar for all lactations. Genetic correlations between lactations, based on the linear model, were 0.85, 0.84, and 0.91 between first and second, first and third, and second and third lactations, respectively.

Table 2. Estimates from linear and threshold models of heritabilities for survival in first, second, third lactations

Lactation	Linear model ^A	Threshold model ^B
1	0.039	0.073
2	0.046	0.069
3	0.037	0.068

^AEmpirical standard errors of mean heritabilities ranged from 0.001 to 0.003.

^BStandard deviation of the posterior distribution of heritability was 0.005.

Correlations between EBV from the various analyses are in Table 3. Results indicated that ranking of sires varied considerably when different models were used for the analysis of survival. When data from all lactations were used, the overall correlation between the threshold model and linear animal model was only 0.86. Most of this difference was the result of using an animal model for the linear analysis and sire model for the threshold analysis.

When a linear sire model was implemented, the overall correlation of EBV from the linear model with those from the threshold model was 0.98. Correlations of EBV from the survival model were 0.75, 0.88, and 0.83 with the linear animal model, linear sire model, and threshold sire model, respectively. Between lactations within the same analysis, correlations of EBV were generally around 0.50 and were greater between second and third lactations than between first and either second or third lactations.

Table 3. Correlations between estimated breeding values from different analyses.

Threshold Model	Linear models				Survival Model
	Animal		Sire		
	Same lactation	Overall	Same lactation	Overall	
Lactation 1	0.82	0.64	0.97	0.77	0.70
Lactation 2	0.85	0.74	0.97	0.83	0.70
Lactation 3	0.84	0.71	0.98	0.78	0.60
Overall	...	0.86	...	0.98	0.83
Survival	...	0.75	...	0.88	1.00

CONCLUSIONS

Considerable reranking of sires was observed when EBV for survival were calculated with linear models, threshold models, or Weibull survival analyses (sire models). Correlations among EBV across analyses were approximately 0.80. For the linear and threshold model, most of the reranking was associated with differences between using an animal model versus a sire model. Additional research is required to determine which analysis yields the EBV that are most highly correlated with actual herd life as it contributes to lifetime profitability.

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