Evaluation of Functional Traits in Different Regions of Dairy Cattle Data in Turkey

Serhat Arslan Hamit Mirtaghizadeh
University of Yuzuncu Yil, Faculty of Agriculture, Department of Animal Science,
65080 Van-Turkey

Abstract: The objective of this study was to evaluate for functional herd life (FHL) of Turkish Holstein in sires and cows using with repeatability model. Repeated records were collected from 1990 to 1996 and consisted about 6368 lactation records from Holstein cattle in different lactation. FHL, direct herd life (DHL) based on survival of sires of daughters, indirect herd life (IHL) based on an index of EBV for conformation traits, and combined herd life (CHL) were investigated for traits on survival. Survival data were analyzed using a multiple-trait repeatability animal model and Hazard functions. The multiple-trait animal model for solution and evaluation of three survival traits were reached after 1000 iterations. Results of estimating parameters for functional herd life of Holsteins were lower than results of literature. Heritabilities in three lactations are also different then literature. For survival analysis, all effects in the model were highly significant for data from different herds. The estimates for parameters of transmitting abilities (TED) were 1.43, 1.44, 1.58, and 1.23 for four state farms. Estimates of ρ between TED indicated that a baseline hazard function that increases over of birth had a slightly lower change of being culled, even if corrected for parity. Heritability estimates for FHL were 0.083, 0.069, 0.058, and 0.093 for herds, respectively. Estimates of Heritability Using hazards functions were with 0.018, 0.019, 0.023, and 0.033 lower than linear model. In conclusion, the difference between linear mixed model and survival analysis were mainly the difference in data that can be analyzed. EBV prediction for longevity should be based on survival analysis to use information from censored records as well, thus yielding higher accuracies.

Key words: Survival, culling, animal model

Introduction

Longevity traits have very important effects on economical performance. When longevity or lifespan is increase, economic benefits are also increase. However, total herd life or length of productive life (LPL) can only be measured after animals have been culled. This is seriously obstacle to determine for effective selection criteria based on LPL traits. Generally, heritability of LPL traits was reported as low (Blanchard *et al.*, 1983 and Burnside *et al.*, 1984). LPL have been quantified in the literature (Blanchard *et al.*, 1983; Jairath *et al.*, 1998; Ducrocq, 1994; Ducrocq *et al.*, 1988). Vollema & Groen (1996) demonstrated that use of satiability traits, the binomial traits which measure whether a cow has survived to a certain time. However, they are containing less information than traits that measure the entire lifespan of a cow. Survival analysis to estimate breeding values is another alternative approaches for longevity. Ducrocq *et al.* (1988) and Ducrocq (1994) used failure time analysis models that treated records on cows in the herd as censored observations. Another application to survival within lactations was demonstrated by Grignola & Schaeffer (2000) using survival analysis were estimated for herd lives, each a new cows enters or culling from the herd, new herd effects must have been estimated. Dekkers (1993) indicated that longevity corrected for production, or functional longevity, is a better measure of involuntary culling. Van Arendonk (1985) showed culling decisions are always taken on a within herd basis, which indicates that correction has been done using the production in the first lactation compared with that of herd mates, but, in other studies (Burnside *et al.*, 1984 and Jairath *et al.*, 1998), the production in the last lactation was used. Using survival analysis, production can be implemented as a time dependent effect in the model, which should result in a better model than one that uses first or last lactation alone. With those methods, survival was considered to be the same trait throughout the life time of an animal. But, genetic correlations were each of the first three lactations (Deckers, 1993). These results supported that a multiple traits procedure must be used for genetic evaluation of functional herd life (FHL) or life span traits.

Estimating genetic component of FHL is determined and helps to decisions of culling for the dairy producer. Management strategies that have an impact on her life differ among herds, among years. Survival analysis (Vollema and Groen, 1996) and survival analysis within each of the lactation allow for the time dependent systematic environmental effects in models for genetic evaluation of herd life.

The objective of this study was to develop a national genetic evaluation system for FHL of Turkish Holstein sires and cows that includes information a survival and conformation traits.

Materials and Methods

Data were collected from the different state Farm recording systems and were selected to herds. Herds were limited to have only Black and White cows (Frisian, Holstein-Frisian or both). Data were collected from 1990 to 1996 and cows were obtained from the lactation records for production. Data consisted of 6368 lactation records on Black and White cows. Productive life was calculated from milk recording as number of days between first calving and the last known milk recording test day. The last test day was assumed to be the culling date because culling dates and reasons were not systematically recorded. Survival records were coded as 0 if the cow was culled throughout that lactation and as 1 missing or undefined if the cow had not had an opportunity to start or complete that lactation. The latter group consisted later lactations for cows that were culled and current and later lactations for cows that were still in the herd.

Investigating traits on survival were genetic evaluations for FHL, direct herd life (DHL) based on survival of sire of daughters, indirect herd life (IHL) based on an index of EBV for conformation traits, and combined herd life (CHL). CHL were combined genetic evaluations for DHL and IHL in an overall genetic evaluation for FHL.

Genetic evaluation for DHL of lactation survival data were analyzed using a multiple-trait animal model in which survival in each of the lactations was considered as a separate trait. The model used for each lactation survival trait was

$$Y_{ijkl} = hy_{il} + rhs_{jl} + (age_k)_l + animal_{kl} + e_{ijkl} \qquad (1)$$

where Y_{ijkl} is observation for survival (0 or 1) in lactation l (1, 2 or 3) on cow k that calved in herd year i; hy_{il}, fixed effect of herd year i for lactation l; rhs_{jl}, fixed effects of subclass j for change x season of calving for lactation l; $(age_k)_l$, linear and quadratic regressions of survival in lactation l on age at first calving. Three calving season were defined relative to timing of the year such as spring, summer, and autumn. The multiple-trait animal model can be described as;

$$Y_i = Xb + Za + e, \qquad (2)$$

where, y: vector of observations on survival traits for different lactation; b: vector of fixed effects, including regressions, a, vector of animal additive genetic effects for the three survival effects, e: vector of residual effects. X and Z is incidence matrices assigning observations to respective effects. Expectations and variances are also:

$$E\begin{vmatrix} Y \\ a \\ e \end{vmatrix} = \begin{vmatrix} Xb \\ 0 \\ 0 \end{vmatrix} \text{ and } E\begin{vmatrix} a \\ e \end{vmatrix} = \begin{vmatrix} G & 0 \\ 0 & R \end{vmatrix} \qquad (3)$$

where $G = A \otimes G$, where A is a matrix of additive genetic relationships, G = 3x3 matrix with genetic (co)variances between residual effects for the three traits. Genetic and residual (co)variances used in the genetic evaluation analysis were estimated by Jairath et al. (1998) using a similar multiple-trait animal model.

Solutions to the mixed model equations (MME) arising from the multiple-trait animal model procedure were computed based on Gauss-Seidel iteration on data (Groeneveld, 1995; Ducrocq & Casella, 1996). The criterion for convergence was defined as the relative difference between solutions for breeding values in consecutive rounds of iteration (Ducrocq & Sölkner, 1994).

The following Weibull model was used to estimate the bulls EBV for longevity described by Samone et al. (2003):

$$\lambda(t) = \lambda_0(t) \exp\{i(\tau) + m_j(\xi) + p_k(\xi) + f_i(\xi) + a_m + z_\eta(t') + l_0(t') + h_q(t') + s_r\} \qquad (4)$$

where $\lambda(f)$ is the hazards of a cow, t days after calving $\lambda O(f) = (\lambda \rho(\lambda f)^{\rho-1})$ is the Weibull baseline hazards function, with scale parameter λ, and shape parameter ρ.li(T) the time dependent effect of stage of lactation by lactation number i.

Results and Discussion

The multiple-trait animal model for solution and evaluation of the three survival traits required high processing unit. So convergence was reached after 1000 iterations. Standard deviations of EBV for functional survival in lactations first, second and other for sires and with at least one daughter with survival data and correlations among EBV traits showed in Table 1.

Generally, results of estimating parameters for functional herd life of Holsteins are lower than results of Jairath et al. (1998). Heritabilities are on the diagonal in Table 1. Heritabilities in different lactations are also higher than their

Table 1: Parameters of functional lactation survival for functional herd life of Holsteins

Lactation	Lactation		
	1	2	3
1	0.08	-0.43	-0.18
2	0.58	0.06	-0.20
3	0.45	0.78	0.05
Genetic variance(x10^{-3})	8.58	7.08	9.07

Table 2: Standard deviations of and correlations among multiple-trait EBV for functional survival in the first three lactations and direct herd life (DHL)

Lactation	Lactation		
	1	2	3
2	0.73	1.00	
3	0.71	0.90	1.00
Dairy Herd Life	0.83	0.88	0.87
SD	0.038	0.030	0.031

results. Phenotypic correlations for FHL are similar to results with literature.

Table 2 shows standard deviations of and correlations among, EBV for functional survival in lactations 1, 2, and 3 for sires born past 1990 and with at least one daughter with survival data.

Correlations among EBV were higher than genetic correlations (Table 1) because of the multiple-trait analysis. These results are similar with results of Jairath et al. (1998). Increasing lactation numbers indicates that cows that are older at first calving have a higher risk of being culled. In studies of Ducrocq (1994) and Ducrocq et al. (1988), the effect of age at first calving was not significant. However, Grignola & Schaeffer, (2000), found that productive life decreased with age at first calving, and Syrstad (1979) showed that survival rates of cows declined dramatically over 34 mo of age at first calving in present study, the maximum age at first calving was 39 month. In the survival analysis, all effects in the model were highly significant for the data from different herds (P< 0.01). The -2 log likelihood of the models containing only the lactation value in the first three lactations as a time dependent effect was 2380079. Thus, the model used in subsequent analyses had lactation value as a time dependent effect.

The estimates for the parameter of transmitting ability (TED) were 1.43, 1.44, 1.58, and 1.23 for four state farms, respectively. To all farms, correlations of TED were found positive value. This ρ indicates a baseline hazard function that increases over time. Results for ρ was similar with (Dekkers, 1993). None of the estimates of the model effects differed substantially between state farms. Cows with a later year and month of birth had a slightly lower change of being culled, even if corrected for parity.

The linear model gave heritability estimates for FHL of 0.083, 0.069, 0.058 and 0.093 for four herds, respectively. The heritability estimates on the hazards (on the log scale) from the survival analysis using all data available were with 0.018, 0.019, 0.023, and 0.033 lower than the linear model. These estimates on the log scale were substantially lower than those from the VCE analysis, but, after transformation to the original scale, the results were comparable with results from VCE analysis: 0.080, 0.068, 0.056 and 0.092, respectively. Heritability of FHL was estimated about 0.06 in the literature (Docrocq et al., 1988; Vollema and Groen, 1996 and Gengler et al., 1997).

The Spearman rank correlations and the Pearson correlations among the phenotypic means of daughters of sire of EBV and the rank correlations of these breeding value predictions between herds were 0.13, 0.14, 0.11, and 0.20, respectively. The corresponding Pearson correlations were 0.14, 0.18, 0.18 and 0.23. Both correlations were in the same range, thus indicating that two important of the information: few or no sires with extreme breeding values and no genetic connection or tie between stage farms. Correction of the Pearson correlation for EBV between herds for the number of daughters per sire by the method of Blanchard et al. (1983) increased its value to 0.48. Based on the information of daughters, the reliability of a selection index of a sire is 0.43 for a trait with a heritability of 0.063. Therefore, it can be concluded that all methods of breeding value prediction were highly comparable between herds.

The standard errors of prediction for sires from the survival analysis decreased when all available records were analyzed instead of only uncensored records. The mean standard errors for prediction of EBV for the 62 sires with more than 230 uncensored records in data files were 0.040, 0.039, 0.023, and 0.018, respectively. Thus, including censored records for the prediction of breeding values increased the accuracy, even for evaluated bulls with a relatively large number of uncensored records compared with young bulls. For young bulls, the advantage

of survival analysis over linear methods would be even larger.

Conclusion

Literature were reported the risk of being culled increased as the year month of birth and age at first calving increased, decreased as the percentage of Holstein Friesian genes increased, and decreased at a relatively low production level compared with that of herd mates. Heritability estimates of the functional herd life differed using a linear model 0.06 or survival analysis 0.02 in the literature

When the heritability from the survival analysis was disappeared, different methods to predict breeding values ranked sires differently. The difference between linear mixed model analysis and survival analysis is mainly the difference in data that can be analyzed. EBV prediction for longevity should be based on survival analysis to use information from censored records as well, thus yielding higher accuracies.

For the Turkish cows, records for survival are not adequately available. For example, in this study, total number of cows in recorded breeding individual cards was 6300, 7890, 8340 and 9130, for herds. Although the recording systems allowed to information of survival, may of the individual cards is empty for this information. So using observation of survival was 264, 240, 236 and 243 for herds, respectively. This is a classical and tragically problems in Turkish animal breeding systems.

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