

Longevity Evaluation in Finland: Stability of Evaluations and Estimation of Genetic Parameters

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Abstract

In Finland, national genetic evaluation for functional longevity in dairy cattle has been done since 2003 using a Weibull proportional hazard model. Genetic parameters used in the national genetic evaluation have not been estimated from the Finnish dairy cattle population. The aim of this study was to test stability of estimated breeding values (EBV) in national genetic evaluation and to estimate variance components for functional longevity in Finnish Ayrshire. Stability of the EBVs of sires was tested by calculating correlations between EBVs based on full (recent) data and reduced (previous) data. Also the linear regression of EBVs from full data on EBVs from reduced data was calculated to detect possible bias in prediction. Correlations between EBVs within birth year groups were close to 1.0 for sires born in 1985-1990. The correlations decreased along the five youngest birth year groups and was 0.76 in year 1995. Regression coefficient of recent EBVs on previous EBVs was 0.865. Genetic parameters for Finnish Ayrshire were calculated from a subsample of the data. The heritability estimate for functional longevity was 0.05. Current heritability estimate used in the Finnish national genetic evaluation is 0.09. The regression coefficient of recent EBVs on previous EBVs might indicate that heritability estimate used in national genetic evaluation is too high.

1. Introduction

Dairy cow longevity can be expected to have a large impact on dairy farm profitability. Finland uses survival analysis in genetic longevity evaluation for dairy cattle (Nielsen *et al.*, 2003). Length of productive life was defined as the number of days from first calving to culling or censoring. Longevity was adjusted by milk, protein and fat production level to describe a cow's ability to stay in a herd regardless to its production level. Cows who were alive at the time of evaluation or sold to other herd were censored.

Genetic and Weibull-parameters used in Finnish national genetic evaluation are based on the literature (Pedersen and Nielsen, 2002). Population parameters for longevity are essential to get reliable EBVs and to calculate selection response if selection is on survival. In Finland longevity has been incorporated to the breeding goal indirectly through health, fertility and conformation traits.

The objective of this study was to test stability of EBVs over time and to estimate the genetic parameters for functional longevity in Finnish Ayrshire using survival analysis.

2. Materials and Methods

2.1. Data

Two datasets were used to estimate breeding values for functional longevity in Finnish Ayrshire. 1) full data, 1,103,632 cows (7,235 sires) calving for the first time between 1988 and 2006. The proportion of censored records was 13.11%. 2) reduced data, 904,679 cows (5,634 sires) calving for the first time between 1988 and 2000. The censoring percentage was 20%. Mean length of productive life for culled cows in the full data was 968 days and in the reduced data it was 966 days.

Data to estimate genetic parameters was collected from a subsample of the full data. It contained 129,453 cows (2,138 sires) calving for the first time between 1995 and 2005 in 1,500 different herds. The censoring percentage was 23.85%. Mean length of productive life in the data used for genetic parameter estimation was 859 days.

2.2. Model

The trait definition $\lambda(t)$ was a cow's risk to be culled t days after its first calving, given that a cow was alive at the time of t . In genetic evaluation the following Weibull mixed model for functional longevity was used,

$$\lambda(t) = \lambda_0(t) * \exp\{\text{year} \times \text{season}_i + \text{age}_j + \text{calv}_k(t') + \text{milk}_l + \text{fat}_m + \text{prot}_n + \text{lact} \times \text{stage}_o(t') + \text{herd} \times \text{year}_p(\tau) + \text{sire}_g + 0.5 \times \text{mgs}_r\},$$

where $\lambda_0(t)$ was the Weibull baseline risk function $\lambda_0(t) = \rho^{-1} t^{\rho-1}$ (with $\rho = 1.27$) and the exponential terms included:

- year \times season $_i$ was a fixed year times season effect (four seasons) at the time of first calving.
- age $_j$ was fixed age at first calving (20-36 months).
- calv $_k(t')$ was a fixed time-dependent lactation number effect (1,...6, 7+), t' days after first calving.
- milk $_l$, fat $_m$, prot $_n$ were yield potential classes divided by the time periods of first calving: 1988-1995, 1996-1999 and 2000-2006. The cows were classified into ten different classes by the cow's yield deviation for milk, fat and protein.
- lact \times stage $_o(t')$ was a fixed time-dependent effect for lactation number times stage of lactation class: days in milk 0-60, 61-180, 181-305 and >305, t' days from previous calving.
- herd \times year $_p(\tau)$ was a random effect where year was a time-dependent effect and assumed to follow a log-gamma distribution (with log-gamma = 6.12).
- sire $_g$ and $0.5 \times \text{mgs}_r$ were random effects assumed to follow the multivariate normal distribution MVA $(0, A\sigma_s^2)$ (with $\sigma_s^2 = 0.03$).

2.3. Stability

EBVs were estimated from both datasets using Survival Kit 3.12 software (Ducrocq and Sölkner, 1998). National genetic evaluation for functional longevity was calculated using heritability estimate of 0.09. Stability of the EBVs was tested by comparing genetic trends and by calculating correlations between EBVs from full and reduced data to test whether EBVs stay stable while sires get more daughter observations. Correlation between EBVs in full data and reduced data were calculated for sires who had daughter observations in both data.

In addition, a linear regression of EBVs from full data on EBVs from reduced data was calculated whose expectation is 1.0 (Reverter *et al.*, 1994). The regression coefficient was calculated in condition that a sire had more than 100 culled daughters in the both data. Also sires had more culled daughters in full data compared to the reduced data.

2.4. Estimation of genetic parameters

Genetic parameters were estimated using the same sire maternal grandsire model as in national evaluation with one exception; the time-dependent lactation number effect was only represented in the model by the joint lactation number \times stage of lactation effect.

Survival Kit 3.12 (Ducrocq and Sölkner, 1998) was used to estimate genetic parameters for functional longevity in Finnish Ayrshire. Parameters were estimated one parameter at the time. The heritability estimate was calculated using the formula

$$h^2 = 4 * \sigma_s^2 / (\sigma_s^2 + \sigma_{\text{herd} \times \text{year}}^2 + 1/p)$$

where p was the proportion of uncensored cows. The formula does not depend on the Weibull-parameters and was suggested as an equivalent heritability to linear models heritability (Yazdi *et al.*, 2002).

3. Results and Discussion

Correlations for EBVs between full data and reduced data were high (> 0.97) for sires born before 1990. Thenceforth correlation started to decrease and was 0.76 for the youngest sire group born in 1995 (Table 1).

Standardized means of EBVs for all sires by year of birth from both full and reduced data are shown in the Figure 1. EBVs were standardized to a mean of 100 (for bulls born in 1990) and standard deviation of 10.

A higher EBV indicates better longevity. The genetic trend was quite flat. The trends followed well each other except in year 1995

for which the mean of EBVs for all sires in full data was 99.31 (230 sires) and 97.73 (102 sires) in reduced data.

Regression coefficient of EBVs of full data on EBVs of reduced data was 0.865 when 1,177 sires, having at least 100 culled daughters, were included to the analysis. The estimate differed significantly ($p < 0.0001$) from the expectation of 1.0. The result might indicate that the used heritability estimate in the national genetic evaluation for functional longevity is too high. This is supported by the obtained heritability estimate from the Finnish data. It is also possible that there are uncounted environmental effects as suggested by Nielsen *et al.* (2003).

Table 1. Correlations and number of observations in reduced and full data.

Birth year of sires	Number of sires	Number of culled daughters per sire		Correlations between EBVs in reduced and full data
		Reduced data	Full data	
1990	172	176	262	0.97
1991	176	171	371	0.96
1992	185	144	369	0.92
1993	122	121	298	0.87
1994	110	100	465	0.82
1995	102	31	297	0.76

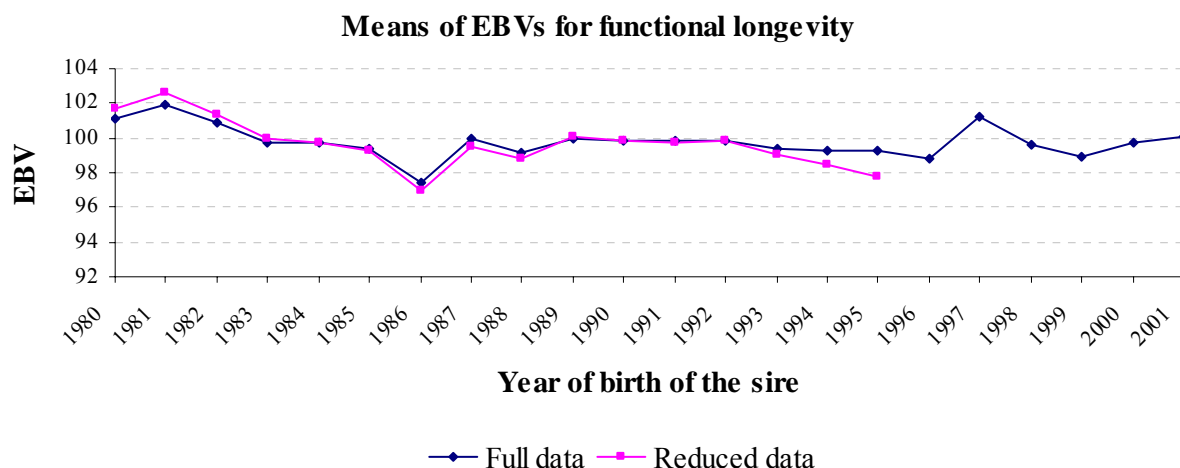


Figure 1. Means of EBVs for longevity for Ayrshire sires born in 1980-1995 (reduced data) and 1980-2001(full data).

The heritability estimate for Finnish Ayrshire was 0.05 which is lower than the current one. Estimated parameters are presented in the Table 2. The estimated Weibull-parameter ρ was 1.88, thus the risk to be culled increase with the time.

Table 2. Estimated parameters and comparison with ones currently used.

	Ayrshire estimates	National evaluation
P	1.88	1.27
Log-gamma (γ)	16.05	6.12
$\sigma^2_{\text{herd} \times \text{year}} = \Psi(\gamma)$	0.064	0.18
σ^2_s	0.016	0.03
Prop. of uncens. records	0.76	0.87
$h^2 = 4 * \sigma^2_s / (\sigma^2_s + \sigma^2_{\text{hv}} + 1/p)$	0.05	0.09

The sire variance was close to the sire variance estimate of 0.013 for Hungarian Holstein (Van der Linde *et al.*, 2006). Otherwise estimated sire and herd \times year variances were lower than in the other studies. The heritability estimate was close to Roxström and Strandberg (2002) and Sewalem *et al.* (2005) studies for red breeds who reported heritability estimates of 0.10 (0.06) and 0.09 (0.03) respectively. Values in parentheses are equivalent heritability estimates, converted from the variance and censoring information in the cited studies.

4. Conclusions

According to the correlations, EBVs stayed quite stable from one evaluation to other except the youngest sire groups. Regression coefficient of EBVs of full data on EBVs of reduced data was below 1.0. That might indicate that the current heritability estimate used in national genetic evaluation is too high. The heritability of 0.05 was estimated for functional longevity in Finnish Ayrshire, which is lower than the currently used heritability estimate of 0.09. Further research should focus on applying the piecewise Weibull hazard model.

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