

# Genetic Evaluation for Longevity in Hungary

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## Abstract

A routine genetic evaluation for longevity for Holstein and Fleckvieh in Hungary was developed. The genetic evaluation was carried out using survival analysis (Survival Kit). The heritability of longevity for Holstein was 0.04. Hungary participated in the Interbull testrun of March 2006 for longevity. Correlations with other countries (with at least 1000 bulls in the evaluation) ranged from 0.32 to 0.83 and were 0.59 on average (0.68 between all countries). The routine genetic evaluation will be implemented in Hungary in August 2006, participation in the Interbull evaluation will be from November 2006 onwards.

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## 1. Introduction

Hungary has planned to participate in the Interbull longevity evaluation from November 2006 onwards, as first country from Eastern Europe. The implementation of the genetic evaluation for longevity in Hungary will be in August 2006.

The development of the genetic evaluation in Hungary was carried out using the “Survival Kit”, version 5.1 (SK, Ducrocq and Sölkner, 1998, Ducrocq, 2002). The development was carried out by NRS, in order of OMMI, and included the development and validation of the model, estimation of parameters and creating software to provide proofs for bulls. The development was carried out for two breeds: Holstein and Fleckvieh. In this paper results for Holstein will be presented.

The objectives of this paper are:

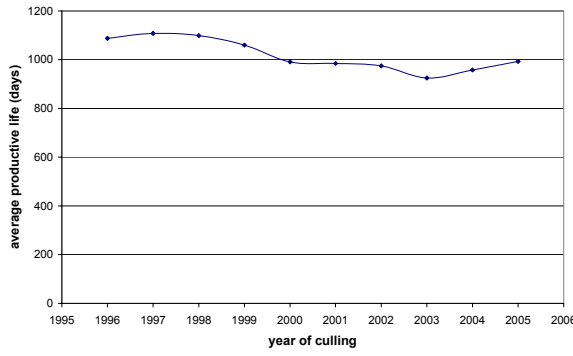
1. To describe the results of the development and validation of the model for the genetic evaluation of longevity for Holstein in Hungary.
2. To describe the results of the Hungarian genetic evaluation model for longevity for Holstein.

## 2. Material and Methods

### 2.1. Data

All daughters of Holstein bulls (at least 50% Holstein) with at least 15 daughters or granddaughters (regardless breed) were included for both the development of the model and the genetic evaluation. Age at first calving had to be between 640 days and 1200 days for cows to be included. Cows without test day after January 1, 1988 were excluded. Data included 1,403,747 cow-herd combinations. The cows were offspring of 5,664 bulls.

The analysed longevity trait was length of productive life of the cow defined as the number of days between the first calving and the last test day in parity 10. If the cow was still alive after the last test day in parity 10, the record of the cow was made censored. Data after parity 10 was not used due to potential problems with estimating parity effects for parity 10+. The length of productive life of cows culled between 1996 and 2005 is in Figure 1.



**Figure 1.** Average length of productive life per year of culling for Holstein cows.

## 2.2. Methods

From the raw data a non-parametric hazard function was estimated. The hazard function on day  $t$  ( $\hat{H}(t)$ ) was estimated within lactation as

$$\hat{H}(t) = \frac{n_{t-1} - n_t}{n_t} \quad [1]$$

where  $n_t$  is the number of cows alive at day  $t$  and  $n_{t-1}$  is the number of cows alive at day  $t-1$ .

Stages of lactation were defined based on the estimated hazard function per day in lactation. A mixed model was applied with piecewise Weibull hazard functions per stage of lactation per parity. Genetic parameters were estimated and used for the estimation of breeding values (EBVs). The heritability ( $h^2$ ) of longevity on the original scale was calculated as:

$$h_{orig}^2 = \frac{4 \cdot \sigma_{sire}^2}{(\sigma_{sire}^2 + \sigma_{hys}^2 + 1)} \quad [2]$$

where  $\sigma_{sire}^2$  is the sire variance and  $\sigma_{hys}^2$  is the herd-year-season variance.

Several mixed models were applied to the data and validated. Validation was based on results of Interbull test 2. Interbull test 2 was applied to test whether the non-genetic time trend was estimated correctly (Boichard *et al.*, 1995). Therefore Daughter Yield Deviations (DYD) were weighted with a weight factor that was calculated by the SK. The weight factor was dependent on the amount of information available for the animal. All data were included in the analysis. The model with the

trend estimate most close to zero was chosen for the final analysis of the data.

The genetic trend was estimated by calculating the average breeding values per year of birth of the bulls. Years with at least 50 bulls with a breeding value for longevity with a reliability of at least 35% were included.

Genetic correlations between countries of the Interbull testrun for longevity of March 2006 were analysed to compare correlations of Hungary with correlations of other countries.

## 2.3. Model genetic evaluation longevity

Effects included in the model were herd-year-season, parity-stage of lactation, parity-year-2 months, herd size change, age at first calving, relative production class in the current and previous lactation, heterosis, recombination, genetic effect (sire-maternal grandsire model) and genetic groups of the maternal granddam. Genetic groups, based on breed and year of birth replaced unknown ancestors of bulls

Description of some factors in the model:

1. Hazard functions per parity-stages of lactation classes were estimated within three lactations where parity 3 and higher were merged.
2. Age at first calving was included as classes of 15 or 30 days, depending on the number of animals per class. The total number of classes was 30. The last class (30) contained only animals with unknown age at first calving.
3. Relative production classes (RPCs) were based on the average and the standard deviation of the 305-day lactation yield (adjusted to age at calving of 27 months) per year of calving in one herd. The relative production was divided into 20 classes per trait. RPCs were included in the model for milk, fat and protein yield in the current and the previous lactation. The RPCs changed with each calving and were calculated as:

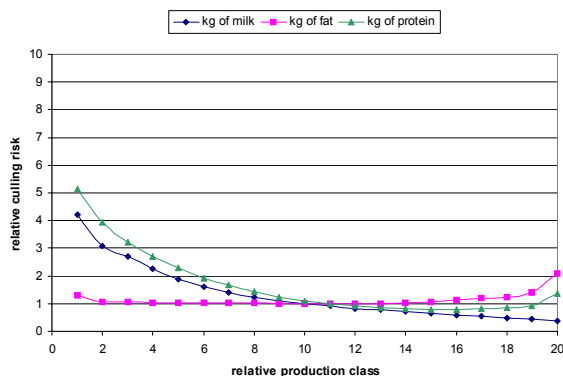
$$RPC = \frac{\text{lactation yield} - \text{herd average}}{\text{standard deviation of herd}} * 3.5 + 10.5$$

4. Heterosis and recombination were included in the model as covariables of the percentages heterosis and recombination.
5. Maternal granddams were replaced by 124 genetic groups, based on breed and year of birth, to adjust for selection in the cow population. Groups were created per year of birth for Holstein and per 5 years of birth for other breeds.

### 3. Results and Discussion

#### 3.1. Fixed effects

The culling risk for relative production classes of kg fat in the current lactation was relatively flat (Figure 2). For kg of milk and protein the relative culling risk decreased for increasing production classes, except a small increase for the highest fat and protein classes. The cows with the lowest milk and protein production in the herd (class 1) had a four to five times higher culling risk than the cows with a herd average production. These results show that the production level of the cow in the current lactation is taken into account in selection decisions of Hungarian farmers.

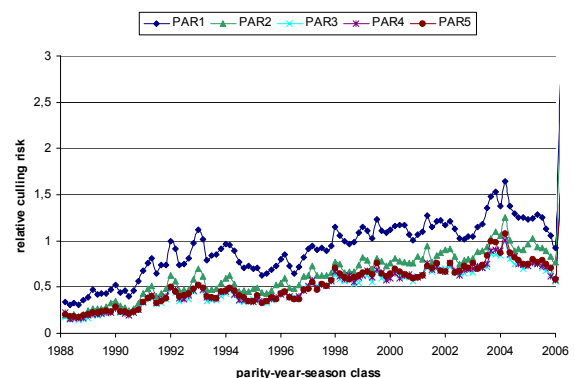


**Figure 2.** Relative culling risk per class of relative production in the current lactation.

The maximum estimated heterosis effect was a change in risk ratio (RR) of 1 to 1.01. The maximum estimated recombination effect was a change in RR of 1 to 0.94. These results did not agree with the expectations that the heterosis effect will effect a lower culling risk

and the recombination effect a higher culling risk. Heterosis effected a lower culling risk and recombination effected a higher culling risk in the Netherlands (van der Linde and de Jong, 2004). Results might be influenced by the absence of purebred animals of non-Holstein breeds in the evaluation.

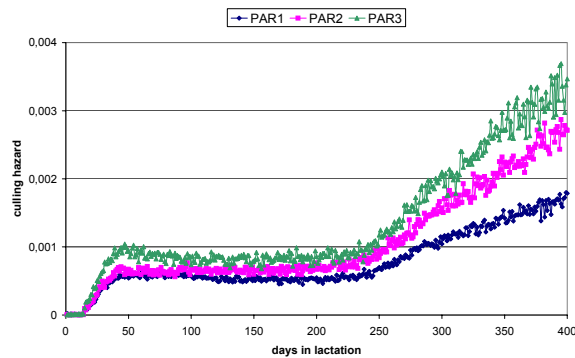
Figure 3 gives the relative culling risk per parity-year-season class. The slope of the relative culling risk increased for all parities with a factor 3 to 4 between 1988 and 2005. In some particular year-seasons the relative culling risk was increasing or decreasing in a short time period (1996 to 1998 and the first year-seasons of 2004). These results might indicate changes in data collection, certain events in dairy farming etc. The levels of the relative culling risk for the different parities are relative to the parity-stage of lactation effect. Therefore the levels per parity can not directly be compared with each other.



**Figure 3.** The relative culling risk per parity-year-season class for the first five parities.

#### 3.2. Parameters

Based on the estimated non-parametric hazard functions (Figure 4) 7 stages of lactation were defined: 0-15, 16-40, 41-140, 141-240, 241-370, after 370 days and the dry period. The estimated  $\rho$  parameters of the Weibull distribution per stage of lactation for parity 1 to 3 were between 1.10 and 3.17 ( $\rho$  for the dry period was 1.00 due to no culling in this period). The highest  $\rho$  were estimated for 16 to 40 days and after day 240 in lactation.



**Figure 4.** Culling hazard for parity 1, 2 and 3 per day in lactation for Holstein cows in Hungary.

Variance components of longevity are in Table 1. The heritability of longevity for Holstein was 0.04. Heritabilities for longevity in other countries estimated with the survival kit ranged from 0.10 (Italy and the Netherlands) to 0.17 in Germany (Interbull, 2006).

**Table 1.** Variance components of longevity.

Parameter	Value
Sire variance	0.0133
Gamma	3.77
HYS-variance	0.304
Heritability (original scale)	0.040

### 3.3. Genetic trend

The model was validated based on results of Interbull test 2. The estimated regression factor of the DYDs on the relative year of calving of the daughters of a bull was  $-1.4 \pm 1.1\%$  of the genetic standard deviation. Taking a 95% confidence interval, the regression factor did not significantly deviate from 0. Development of the model was the most time consuming part of this project. Several changes were made to the model: including the first five lactations, maximum lactation length of 500 days, parity-stage of lactation effect and relative production classes were divided into several time periods. All these changes did not give regression factors for Interbull test 2 closer to zero.

The estimated genetic trend for Holstein is presented in Figure 5. The average breeding value for longevity of bulls was slightly decreasing with 0.5 standard deviation from 0.4 in 1985 to  $-0.1$  in 1992. This drop might be due to using genetics from other countries than

before, resulting in different trends for longevity. Another reason might be the unfavourable trend in phenotypic longevity, mainly from 1997 onwards. One standard deviation of the proofs equalled to 89% of the genetic standard deviation and to 79 days longer lifetime expectancy of the daughters of a bull.

### 3.4. Results Interbull testrun March 2006

Genetic correlations between countries with at least 1000 bulls in the Interbull testrun for longevity of March 2006 were compared. Minimum and maximum correlations and the average correlation with all other countries were calculated. Results for all countries, Hungary and the countries with the lowest (NZL) and the highest (USA) average genetic correlation are in Table 2. The average genetic correlation of longevity for Hungary with other countries is lower than the overall average.

**Table 2.** Genetic correlations for longevity between countries (Interbull testrun, March 2006).

Country	Average	Minimum	Maximum
All	0.68	0.32	0.92
USA	0.78	0.69	0.92
HUN	0.59	0.32	0.83
NZL	0.54	0.34	0.71

## 4. Conclusions

The heritability for longevity in Hungary (0.04) is lower than the heritability in other European countries using the survival kit (0.10 to 0.17).

For the low within-herd producing cows culling risks were estimated 5 times higher than average.

Relative culling risks of parity-year-season estimates were increasing in the course of time with a factor 3 to 4.

The effect of heterosis on longevity was estimated negative and the effect of recombination on longevity was estimated positive.

Genetic trend for bulls shows an undesirable trend before birth year 1992 and a flat trend from 1992 onwards.

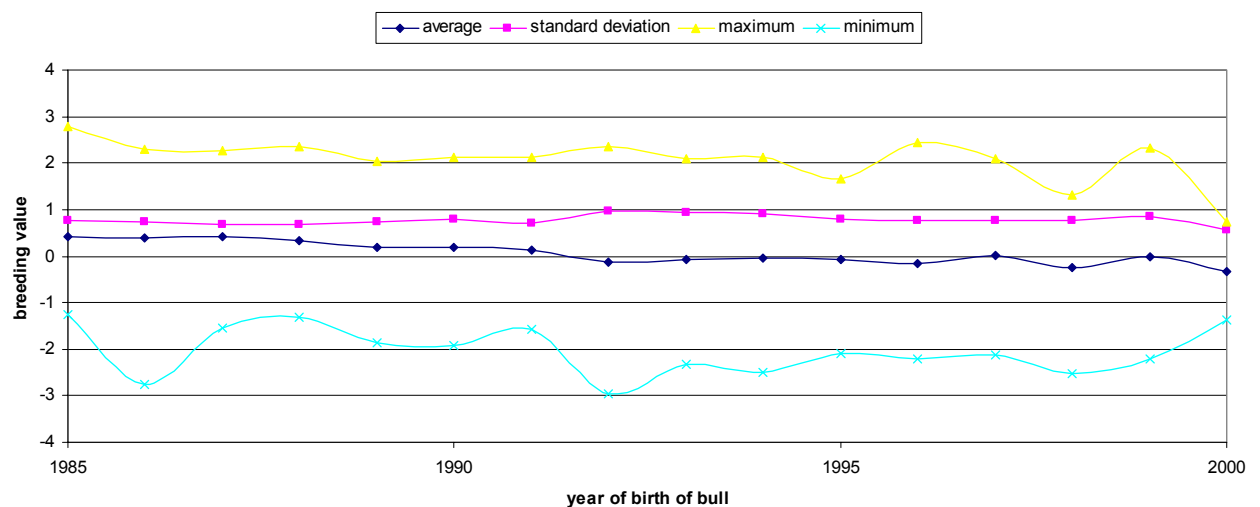
The average genetic correlation of longevity for Hungary with other countries is lower than the average correlation between all countries.

## Acknowledgements

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**Figure 5.** Average, standard deviation, minimum and maximum of breeding values for longevity per year of birth of Holstein bulls.