Original scientific paper

**Estimation of genetic parameters for longevity in Slovenian dairy cattle populations**

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**Abstract**

Genetic parameters for longevity in Slovenian Holstein (H), Simmental (S) and Brown Swiss (B) cattle were estimated with sire-mgs (maternal grandsire) model using survival analysis, applying a proportional hazard function following a Weibull distribution. Longevity was described as length of productive life (LPL), that is as number of days from first calving to the culling or to the moment of data collection (completed – uncensored and censored records). Truncation date was January 1, 1991 while August 1, 2008 was date of data collection. Estimated sire variances were 0.050 (H), 0.021 (S) and 0.034 (B). Herd variances were 0.191 (H), 0.299 (S) and 0.318 (B). Heritabilities estimates were 0.161 (H), 0.064 (S) and 0.101 (B).

Keywords: longevity, genetic parameters, proportional hazards model, dairy cattle.

**Introduction**

Longevity or length of productive life (LPL), as a trait with a great impact on dairy production economy has become a trait of considerable selection importance (Charffeddine et al., 1996; Strandberg and Sölkner, 1996). Length of productive life can be measured only after culling of cows, meaning that the information on the longevity of daughters of sires becomes available with increasing sire age. Low heritability value for longevity (Short and Lawlor., 1992; Volema and Groen, 1996) induces unreliable estimation of breeding values (BV) based on information of parents or grandparents. More reliable estimation of BV for longevity implies longer generation interval.

Alternatives are: usage of stayability traits (binominal traits that measure cows survival to the certain time) which contains less information than LPL; usage of correlated traits (conformation traits, measuring are performed early in life) with limited reliability of BVs estimation (Burnside et al., 1984), or usage of survival analysis for BV estimation (Ducrocq et al., 1988a; 1988b). Survival analysis differ from BV estimation using traditional mixed model analysis in posibilities of: analysing censored (records for cows that have not been culled at the moment of data collection) and completed (uncensored) records as well as modeling effects as time-dependent or time-independent. In the last ten years several countries induces longevity in routine genetic evaluation, and most of them use proportional hazard (PH) models (INTERBULL-centre, 2008).

The objectives of this study were to estimate and compare genetic parameters for longevity of Slovenian dairy cattle populations with a maternal grandsire model (sire-mgs model)
using survival analysis, applying a proportional hazard function following a Weibull distribution.

Materials and methods
Data on culling and production of Slovenian dairy cattle were provided by the Agricultural Institute of Slovenia. Complete lactations of Slovenian Holstein, Simmental and Brown Swiss cows were used in the analysis. As truncation date January 1, 1991 was taken, while August 1, 2008 was date of data collection. Longevity was described as length of productive life (LPL) that is as number of days from 1st calving to the culling or to the moment of data collection (completed (uncensored) and censored records).

Distributions of analysed variable (completed and censored records) with projected Normal and Weibull distribution curve separately for each cattle breed are shown in Graph 1.

Graph 1. Distribution of analysed variable (completed – UC and censored – C records) by breeds (Holstein, Simmental, Brown Swiss).

Better fit to the analysed data set of the Weibull distribution curve in comparison to the Normal distribution, both for completed and censored records for each cattle breed is visible on the Figure 1. Better fit of Weibull distribution was one of the reasons for...
electing Survival Kit (Ducrocq and Solkner, 1998) for the estimation of genetic parameters for longevity.

The number of used data according to cattle breed is presented in Table 1.

**Table 1 Data description according to cattle breed**

<table>
<thead>
<tr>
<th>Data</th>
<th>Holstein</th>
<th>Simmental</th>
<th>Brown Swiss</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lactations, no.</td>
<td>282,711</td>
<td>350,920</td>
<td>172,651</td>
</tr>
<tr>
<td>Cows, no.</td>
<td>93,048</td>
<td>100,730</td>
<td>46,543</td>
</tr>
<tr>
<td>Sires, no.</td>
<td>453</td>
<td>658</td>
<td>446</td>
</tr>
<tr>
<td>Pedigree, no.</td>
<td>2,052</td>
<td>1,748</td>
<td>1,078</td>
</tr>
<tr>
<td>Censored records, %</td>
<td>32.56</td>
<td>29.04</td>
<td>26.01</td>
</tr>
<tr>
<td>Average productive life, day</td>
<td>1,228.46</td>
<td>1,426.21</td>
<td>1,541.02</td>
</tr>
<tr>
<td>Average censoring time, day</td>
<td>891.93</td>
<td>1,000.66</td>
<td>1,157.64</td>
</tr>
</tbody>
</table>

The following Weibull proportional hazards sire-mgs model was used for analysis of length of productive life:

\[
h(t) = h_0(t) \exp \left\{ l_{\mu}(t) + \sum_k f_k(t) + s_{sire} + 0.5s_{mgs} \right\}
\]

where:
- \( h(t) \) – hazard function (current probability of culling) for a given cow at time \( t \);
- \( h_0(t) \) – Weibull baseline hazard function;
- \( t \) – time from 1st calving to the culling or to the moment of data collection (days);
- \( l_{\mu}(t) \) – time-dependent fixed effect of lactation stage within parity (according to lactation stage five classes were formed: I. – 1st to 60th day; II. – 61st to 150th day; III. – 151st to 270th day; IV. – 271st day till drying; V. – dry period.
- \( f_k(t) \) – represents other fixed and random effects:
  - herd – time-dependent random effect assumed to follow a log-gamma distribution,
  - year – time-dependent fixed effect (1990 – 2008),
  - age at first calving (months) – time-independent fixed effect (19 – 50),
  - milk class – time-dependent fixed effect representing deviation of milk yield within herd per calving year (7 classes: I. [min, -70%]; II. [-70%, -40%]; III. [-40%, -10%]; IV. [-10%, 10%]; V. [10%, 40%]; VI. [40%, 70%]; VII. [70%, max]),
  - herd size class – time-dependent fixed effect representing deviation in herd size across years (7 classes: I. [min, -70%]; II. [-70%, -40%]; III. [-40%, -10%]; IV. [-10%, 10%]; V. [10%, 40%]; VI. [40%, 70%]; VII. [70%, max]).
- \( s_{sire} \) – time-independent random genetic effect assumed to follow a multivariate normal distribution. Maternal grandsire relationship (sire-mgs model) was used for estimation of genetic parameters.

The data were processed by SAS software package (SAS Institute, 2000), while Survival Kit version 3.10 (Ducrocq and Solkner, 1998) was used for the estimation of genetic parameters in Weibull proportional hazards sire-mgs model.
For calculation of heritability following formula was used (Yazdi et al., 2002):

\[ h^2 = \frac{4\sigma^2_i}{\sigma^2_i + \psi^{(1)}(\gamma) + 1} \]

where:

\( \gamma \) – parameter of log-gamma distribution for herd effect;

\( \psi^{(1)}(x) = \frac{\partial^2}{\partial x^2} \ln \Gamma(x) \) – trigamma function.

### Results and discussion

The main objective of this study was to estimate genetic parameters for longevity of Slovenian Holstein, Simmental and Brown Swiss breed. Estimated sire variances ranged from 0.021 to 0.050, while the range for herd variance was from 0.191 to 0.318 (table 2). Lowest sire variance was estimated in Simmental breed, while lowest herd variance was observed in Holstein cattle breed. The highest value of average productive life length was observed in Browns Swiss, while the lowest was in Holstein breed (table 1). The longest length of productive life was obtained in Simmental breed (graph 1) what could be explained by larger population comparing to Brown Swiss. Comparing the determined phenotypic and genetic variability of analyzed breeds (graph 1 and table 2) it could be observed that phenotypic variability is higher in Simmental and Brown Swiss than in Holstein, while genetic variability is the highest in Holstein breed. It could be concluded that Simmental and Brown Swiss sires are more long-lived or that have higher longevity, while Holstein sires have higher variability of analyzed trait.

### Table 2 Estimated genetic parameters for longevity according to cattle breed

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Breed</th>
<th>Holstein</th>
<th>Simmental</th>
<th>Brown Swiss</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sire (variance), day</td>
<td></td>
<td>0.050</td>
<td>0.021</td>
<td>0.034</td>
</tr>
<tr>
<td>Herd (gamma parameter)</td>
<td></td>
<td>5.727</td>
<td>3.820</td>
<td>3.618</td>
</tr>
<tr>
<td>Herd (trigamma parameter – variance)</td>
<td></td>
<td>0.191</td>
<td>0.299</td>
<td>0.318</td>
</tr>
<tr>
<td>Heritability</td>
<td></td>
<td>0.161</td>
<td>0.064</td>
<td>0.101</td>
</tr>
</tbody>
</table>

Heritabilities estimated from the used model ranged from 0.064 in Simmental to 0.161 in Holstein breed (table 2). Almost all countries, members of INTERBULL, for estimation of breeding values in recent international evaluation for longevity use survival analysis and proportional hazards sire-mgs model (INTERBULL-centre, 2008). Heritability estimates for Holstein breed in those countries ranged from 0.05 (Hungary) to 0.18 (Austria), while for Simmental and Brown Swiss cattle lower heritability values comparing to Holstein breed were determined (0.12 : 0.18 in Austria and 0.11 : 0.14 in Switzerland). Heritability values estimated in this research for Holstein breed was similar to values estimated in Austria (0.18) and Germany (0.16) and relatively high comparing with other countries estimates. For Simmental breed, this study estimate was rather low, while for Brown Swiss estimate was similar to estimates of other countries.

Heritability estimates of countries that use multi-trait animal or multi-trait sire model for estimation of breeding value for longevity were rather low (0.005 in New Zealand; 0.016 in Ireland; 0.08 in Sweden and USA), implicating usage of proportional hazards sire-mgs
model. Estimated genetic parameters, beside population variability, also depends on the data preparation as well as on statistical model. In results comparison of analysed breeds this should be taken into consideration. In this research, data preparation and election of adequate statistical model were based on currently applied knowledge in other countries that are members of INTERBULL (Interbull-centre, 2008) as well as on structure of data supplied by the Agricultural institute of Slovenia. In supplied data base, small proportion of animals had correct data on culling cause. In a case of having correct culling causes data on most of the analysed animals, named effect could be taken into account in statistical model which could lead to more accurate estimation of breeding values.

Conclusions
In estimation of breeding value for longevity, considering the structure of analysed data, application of Weibull distribution was proper. Applying proportional hazard function, corresponding the Weibull distribution in sire-mgs model for Slovenian dairy cattle breeds following genetic parameters were estimated:

- sire variances – ranged from 0.021 (S) to 0.050 (H);
- herd variance – ranged from 0.191 (H) to 0.318 (B);
- heritabilities – ranged from 0.064 (S) to 0.161 (H).

The statistical model used in this research is suitable for routine work. More accurate estimation of breeding values for longevity could be achieved by taking into account the effect of culling causes in statistical model. Furthermore, the possibility of indirect breeding value estimation for longevity should be examined.

References