Genetic Analysis of Longevity in Dutch Dairy Cattle using Random Regression

M.L. van Pelt*† and R.F. Veerkamp*


ABSTRACT: Records for monthly survival up to 72 months in productive life were used to estimate genetic parameters for longevity in dairy cattle with a random regression sire-maternal grandsire model using Legendre polynomials. Heritabilities for monthly survival were below 0.011, but the heritability for lifespan across the entire period of 72 months was 0.146. Genetically survival was more similar between months close together and survival was a different trait when months were further apart with genetic correlations ranging from 0.16 to 0.99. The genetic correlations suggest that in the current genetic evaluation, heritabilities are overestimated when only information of early productive life is available, survival in first six months predicts entire lifespan with a maximum reliability of 0.64. This low reliability might explain the observed changes in estimated breeding values despite the apparent high accuracy coming from the current model assuming genetic correlations of unity.

Keywords: dairy cattle; survival; genetics

Introduction

Longevity of dairy cattle is an important trait for dairy cattle breeding, both from an economic as from an welfare perspective. Reducing involuntary culling will improve farm profit and animal welfare. Longevity or lifespan is the number of days between first calving and last milk recording date, but is only known after an animal is culled, whereas selection and breeding decisions are made earlier in life. Therefore methods for genetic evaluations are likely to rely to a large extent on censored data. To accommodate the use of censored records several different models have been introduced for genetic evaluations (Forabosco et al. (2009)). Neither of the models currently used cover all required statistical properties, and for example one of the major differences between the applied models is whether or not longevity is assumed to be genetically the same trait during the entire life of a cow (Veerkamp et al. (2001)). Studies using linear multi-trait models showed genetic correlations between parities significantly differ from unity, on average 0.77 with a range from 0.33 to 0.96 where correlations decrease with increasing distance between parities (Boettcher et al. (1999); Brotherstone et al. (1997); Holtsmark et al. (2009); Sewalem et al. (2007); Veerkamp et al. (2001); Visscher and Goddard (1995)). In the current genetic evaluation in The Netherlands it is assumed that longevity is genetically the same trait during the total lifespan of a cow, and the question is if this is justified or not. The objective of this study was to estimate genetic parameters for survival across the entire life of a cow in order to aid proper decision making on the model selection for genetic evaluation.

Materials and Methods

Data. Data were available from the Dutch/Flemish cattle breeding cooperative CRV (CRV, Arnhem, The Netherlands). Records for survival were constructed for each month a cow was present in a herd since the first calving and was recorded for milk production; if the cow survived to month i+1, the cow was assigned alive (score 100) for month i; and if the cow was culled in month i, the cow was assigned dead (score 0) for month i. A cow which was culled in month j has j-1 records with score 100 and record j with score 0. After culling monthly records were treated as missing. Records after 72 months in productive life were discarded as well as animals that had left-censored records. Cows had to be at least 87.5% black and white genes, i.e. Holstein Friesian or Dutch Friesian, and had the first calving between 21 and 40 months old. Maximum lactation length was 48 months and only lactations with the last testdate after 1 January 1988 were included. Several data edits at the herd and animal level were applied to eliminate erroneous data and to reduce the size of the dataset. The resulting dataset consisted of 26,995 cows with 950,616 monthly observations for survival from 1988 to 2012 originating from 42 herds and 650 (maternal grand)sires. Pedigree information of these sires was traced back 6 generations resulting in a pedigree file with 977 (maternal grand)sires.

Model. Genetic parameters were estimated with a random regression sire-maternal grandsire model. Fixed effects included year-season, parity-stage of lactation, parity-year-season and a second order Legendre polynomial on age at first calving. Random effects included additive genetic effect for sire using third order Legendre polynomials, herd curve effect using third order Legendre polynomials for every herd 5-year combination, permanent environment effect and an error effect for every three months in productive life. Variance components were estimated with ASReml (Gilmour et al. (2009)). Estimates of the (co)variance components of the random regression were used, together with the Legendre polynomials coefficients to calculate parameters for each month. A first order Taylor series expansion was used to estimate variance components for cumulative survival to a certain endpoint conditional on the previous months, and this method is a refinement of the method used by Brotherstone et al. (1997) and Visscher et al. (1994), where all periods are assumed to be genetically the same trait with equal variances.
Results and Discussion

Monthly survival rate of cows up to 72 months in productive life is shown in Figure 1 for the national data set and the data set used for the genetic analysis. Most animals that start a month also appear in the next month, resulting in survival rates close to 100%. The monthly survival rate decreased with increased number of months in productive life. For young cows, that were in the first 12 months of productive life, the monthly survival rate was on average 99 percent and for older cows, that were in the months 61 to 72 of productive life, the average monthly survival rate decreased to 96 percent. Moreover, after 24 months in productive life monthly survival rate cycles with intervals of approximately one year or one lactation. The lowest survival rate was at months 24, 36, 48, 60 and 72 and the highest survival rate was in the middle of each cycle at months 30 and 31, 42, 54 and 66. The decrease within a cycle from maximum to minimum survival is on average 0.8 percent for the third to the sixth year of productive life.

Figure 1. Survival rates per month in productive life for Dutch dairy cows with observations in the period 1988-2012 for the total national dataset and the dataset for the genetic analysis.

Over the entire observed period of 72 months for survival, heritabilities for monthly survival ranged from 0.002 to 0.011 and the highest values correspond with the later periods in productive life (Table 1). Although heritabilities on a monthly base appear very low, they were significantly different from zero, and the cumulative heritability of survival over the entire period of 72 months gradually increased to 0.146. Heritabilities used in national genetic evaluations were in the range of 0.016 to 0.181 (Forabosco et al. (2009)) and in the review of Sasaki (2013) the range was 0.003 to 0.197. The linear increase in the cumulative heritability up to 36 months in productive life is similar to the results reported by Ducrocq (2005). On a monthly scale genetic and phenotypic standard deviations ranged from 0.005 to 0.021 months and 0.09 to 0.20 months, respectively. Over the entire period of 72 months genetic and phenotypic standard deviations accumulated to 7.81 and 20.47 months, respectively. The genetic standard deviation of 7.81 illustrate that considerable genetic variation exist for total lifespan.

<table>
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<th>month</th>
<th>$\sigma^2_G$</th>
<th>$\sigma^2_P$</th>
<th>$h^2$</th>
<th>$\text{cum. } h^2$</th>
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<td>0.003</td>
<td>0.003</td>
</tr>
<tr>
<td>6</td>
<td>0.21</td>
<td>89.70</td>
<td>0.002</td>
<td>0.006</td>
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<td>0.004</td>
</tr>
<tr>
<td>18</td>
<td>0.42</td>
<td>136.77</td>
<td>0.003</td>
<td>0.006</td>
</tr>
<tr>
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<td>0.003</td>
<td>0.005</td>
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<tr>
<td>60</td>
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<td>0.017</td>
</tr>
<tr>
<td>72</td>
<td>4.48</td>
<td>412.76</td>
<td>0.011</td>
<td>0.041</td>
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</table>

The current genetic evaluation for longevity in The Netherlands is a piecewise Weibull model using Survival Kit software (Van der Linde et al. (2007)). The applied heritability is 0.12 and the genetic standard deviation is 270 days and in this study the total heritability over the entire period of 72 months was 0.146 and the genetic standard deviation was 7.81 months or 238 days. Compared to the Dutch genetic evaluation the genetic standard deviation in this study was comparable but a bit lower, because data was restricted up to 72 months in productive life, whereas in the current genetic evaluation no restriction was applied to the length of productive life. The assumption that longevity is genetically the same trait over the total lifespan seems less appropriate, as genetic correlations were not unity between individual months. Based on data from the first six months in productive life, breeding values estimated with the Survival Kit can have reliabilities up to 99% when bulls have very large progeny groups, whereas with results from this study, where the genetic correlations between survival up to 6 months and lifespan over the entire period of 72
months is 0.80 (Figure 2), the maximum reliability would only be 64%. In the current genetic evaluation, the genetic correlation is assumed unity, and therefore, reliabilities are overestimated. This might explain why more changes in the breeding value for the entire period of 72 months are observed than expected from the reliability, when adding extra information after 6 months in productive life. When the same estimated variances are used whilst assuming genetic correlations of unity across all months, the total heritability over the entire period of 72 months was 0.175 and the genetic standard deviation was 259 days. Also, illustrating that the variation in bulls and accuracy is slightly overestimated with the current model. Applying a genetic model that can treat longevity as different traits during lifespan could improve the genetic evaluation.

**Conclusion**

Results suggest survival is genetically not the same trait during the entire life, because genetic correlations differ from unity between different months in life especially when months are further apart. Heritabilities for monthly survival were low. However, the heritability for lifespan across the entire period of 72 months was higher. In the current genetic evaluation it is assumed longevity is genetically the same trait over the total lifespan. Based on the results of this study, a better model for genetic evaluation should treat survival as different traits during the entire lifespan to avoid overestimated reliabilities and changes in breeding values for lifespan.

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**Literature Cited**


**Figure 2. Genetic correlations between entire lifespan (up to month 72) and cumulative survival up to months 1 till 72.**