

# Using a Piecewise Weibull Mixed Model in the Genetic Evaluation for Longevity

*C. van der Linde, G. de Jong and A. Harbers*  
NRS, P.O. Box 454, 6800 AL Arnhem, The Netherlands  
E-mail: [Linde.R@cr-delta.nl](mailto:Linde.R@cr-delta.nl)

## Introduction

As of August 1999, functional longevity is genetically evaluated in the Netherlands using the Survival Kit (SK) version 3.0 (V3.0) (Ducrocq and Soelkner, 1998).

The SK describes the hazard  $h(t)$  of a cow of being culled at time  $t$  given that she is alive just before  $t$ . The culling hazard  $h(t)$  of a cow is the product of the baseline hazard function and cow specific culling risk variables.

One of these culling risk variables is stage of lactation \* parity of the cow. This variable accounts for the changing risk for a dairy cow of being culled during her lactation. In the old Dutch genetic evaluation, the stage of lactation effect has been modelled as a time dependent fixed effect with 8 classes within each lactation, changing at 30, 60, 180, 250, 270, 290 and 330 days after calving.

Ducrocq (2002) described results from a piecewise Weibull mixed model and found that the current French evaluation model, which is comparable to the old Dutch model, overestimated the culling risk in early lactation (before 270 days) and at the end of very long lactations (>380 days). Ducrocq suggested that the overestimation of culling risk in early lactation may be one of the reasons for the frequent increase of estimated breeding values (EBVs) of proven sires after the inclusion of a large number of young second crop daughters observed in France. In version V5.1 of the SK, a piecewise Weibull baseline hazard function can be included, which may remove the described biases. In this model a different hazard line is estimated for each parity \* lactation stage.

The objectives of this study were:

1. To implement the SK V5.1 with a piecewise Weibull hazard function.
2. To describe the changes in the Dutch genetic evaluation model for longevity.
3. To compare the results obtained by SK V5.1 and the new model with the results obtained by SK V3.0 and the old model.

## Material and Methods

### Data

Daughters of 14,137 bulls with at least 50 daughters or granddaughters, including all breeds, were included for both the variance components estimation and the genetic evaluation. Data included 7,271,790 cows. Cows with their first calving before the age of 640 days and cows without a test day production record after January 1, 1988 were excluded. The analysed longevity trait was the productive life span of the cow defined as the number of days between the first calving and the last test day.

### Old model genetic evaluation longevity

The old model for the genetic evaluation of longevity included a baseline Weibull hazard function, time-dependent fixed effects for year-season, parity-stage of lactation, herd size change, intra-herd lactation value of the current and the previous lactation, a time-independent fixed effect for age at calving and random effects for herd-year-season, sire and maternal grandsire. Genetic groups, based on breed and year of birth replaced unknown ancestors of bulls. Maternal granddams of cows were replaced by 115 genetic groups, based on breed and year of birth, to adjust for selection in the cow population. More details about this model can be found in Vollema *et al.* (2000). Slight modifications to the model

were made afterwards. The parameters currently used for the genetic evaluation of longevity are in Table 1.

**Table 1.** Parameters currently used for the genetic evaluation of longevity.

Parameter	Value
Rho ( $\rho$ ) <sup>1</sup>	1.49
Sire variance	0.020
Gamma ( $\gamma$ ) <sup>2</sup>	4.19
Herd-year-season (hys)-variance	0.269
Heritability (original scale)	0.066

<sup>1</sup>Parameter of baseline hazard function

<sup>2</sup>Parameter of hys-variance

### *New model genetic evaluation longevity*

The next changes to the model for the genetic evaluation of longevity were made:

1. Stages of lactation classes were made, based on estimated non-parametric hazard functions.
2. Weibull hazard functions were estimated per parity (1, 2 and 3+) \* stage of lactation classes.
3. The parity \* stage of lactation effect was removed as fixed effect from the model because these effects were estimated using Weibull hazard functions.
4. Parity was added as a fixed effect to the model where parity 1 to 3 were merged into one parity class because Weibull hazard functions were estimated for these parities. Parity 10 and higher were merged.
5. Classes for current Lactation Value (LVC) were merged in periods of three years counting back from the last test day of the most recent data file. Classes for previous Lactation Value (LVP) were determined in the same way starting one year earlier than the LVC-classes. LVC and LVP higher than 129 were merged in five point classes. If the oldest class contained less than 3 years of data, the class is merged with the next class in time. In the old model, classes for LVC and LVP were merged over the whole time period.
6. Heterosis was added to the model as fixed effect with 10 classes. Class 1 included cows without heterosis, class 2 cows with 0.1 to 12.4 % heterosis, class 9 cows with 87.5 to 99.9 % heterosis and class 10 cows with 100 % heterosis.

7. Recombination was added to the model as fixed effect with 10 classes. Class 1 included cows without recombination, class 2 cows with 0.01 to 6.24 % recombination, class 9 cows with 43.8 to 49.9 percent recombination and class 10 cows with 50 % recombination.

Changes 5 to 7 were additional changes to the model, beside the change to a piecewise Weibull model.

### *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:

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

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. Firstly, parameters ( $\rho$ ,  $\gamma$  and sire variance) were estimated with the new model and secondly EBVs were estimated with the new parameters. 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.

The estimated parameters and EBVs were compared to genetic parameters and EBVs estimated with the old model.

Interbull test 2 was applied to test whether the non-genetic time trend was estimated correctly (Boichard *et al.*, 1995).

The genetic trend was estimated as the coefficient of the regression of EBVs on year of birth of the bulls. Years with at least 300 Holstein bulls with a reliability of at least 35% were included. Finally, differences in the

average per year of birth were calculated between the old and the new model.

## Results and Discussion

### Fixed effects

The culling risk per parity is in Table 2. The estimated risk ratios (RR) are relative to the average RR of the first three parities.

**Table 2.** Culling Risk Ratio (RR) estimated per parity.

Parity	RR	Parity	RR
1-3	1.00	7	1.62
4	1.16	8	1.79
5	1.31	9	1.77
6	1.43	10	1.52

Parity 8 has the highest RR compared to parity 1 to 3 with 1.79. The RR per parity is increasing from parity 1 to 8 and decreasing after parity 8. This might be the effect of farmers giving old cows more credits because of emotional reasons or to enable the cow to achieve a certain milestone. It might be considered to make the records of cows with parity > 8 censored, because additional lifetime might not only be the result of fitness of the cow.

The maximum estimated heterosis effect was a change in RR from 1 to 0.94 for class 9 (87.5 to 99.9% heterosis), which is equal to 20% of the genetic standard deviation. For 305-day milk production the estimated heterosis effect in the Dutch genetic evaluation is about 148 kg of milk, which is equal to 21% of the genetic standard deviation.

The maximum estimated recombination effect was a change in RR of 1 to 1.03 for class 10 (50% recombination), which is equal to 10 % of the genetic standard deviation. For 305-day milk production the estimated recombination effect in the Dutch genetic evaluation is about -62 kg of milk, which is equal to 9% of the genetic standard deviation.

Figure 1 contains the RR for LVC. The RR estimated per 3-year period for cows with LVC equal to 80 (i.e. producing 20% below the herd average) ranged from 2.4 to 3.2 times higher than cows with LVC equal to 100, increasing

over the last 4 periods of 3 years. The RR for cows with LVC equal to 120 ranged from 0.51 to 0.58 times the RR of cows with LVC equal to 100 and was quite constant over 3-year periods. In the old model, the RR for LVC equal to 80 was estimated on 2.27 and for LVC equal to 120 on 0.57. The RR for LVC equal to 80 was estimated higher with the new model than with the old model, the differences in RR for LVC equal to 120 are comparable between the old and the new model. The RR estimated per 3-year period for LVP equal to 80 ranged from 0.94 to 1.16 times higher than LVP equal to 100, decreasing over the last 4 periods of 3 years. The RR for LVP equal to 120 ranged from 1.05 to 1.30 times the RR for LVP equal to 100 and was increasing over the last 4 periods of 3 years. In the old model, the RR for LVP equal to 80 was estimated on 1.07 and for LVP equal to 120 on 1.13. The RR for LVP equal to 80 and 120 in the old model are about the average of the solutions of the 3-year periods in the new model.

### Parameters

Based on the estimated non-parametric hazard functions within parity (parity 1 to 3 are in Figure 2) 6 stages of lactation were defined, 0-30, 31-190, 191-250, 251-330, after 330 days and the dry period. Parity 3 and higher were merged because differences in shape of the hazard function were constant within the lactation between these parities, therefore a fixed effect for parity was added to the model. The estimated  $\rho$  parameters of the Weibull distribution per stage of lactation for parity 1 to 3 are in Table 3.

**Table 3.** Estimated parameter  $\rho$  of the Weibull distribution per stage of lactation within parity 1 to 3.

Parity	1	2	3
Days in lactation	$\rho$		
0-30	1.49	1.43	1.35
31-190	1.08	1.42	1.40
191-250	0.94	1.07	1.13
251-330	1.18	1.24	1.26
>330	1.79	1.60	1.37
Dry period	0.00	0.00	0.00

The  $\rho$ 's estimated for the first five stages of lactation are equal or lower than the  $\rho$  estimated with the baseline hazard function,

except the  $\rho$ 's estimated for lactations in parity 1 and 2 with more than 330 days. The  $\rho$ 's estimated for the dry period are 0.00 because no cows were culled during their dry period, they were only assigned to the dry period if they also had a next calving with at least one test day in that lactation. These results mean that for cows with a lactation length between 300 and 350 days the risk of being culled is estimated lower with the piecewise Weibull hazard model than with a baseline Weibull hazard model. The estimated parameters with the new model are presented in Table 4.

**Table 4.** Estimated parameters from the survival analyses with the new model.

Parameter	Value
Sire variance	0.030
$\Gamma$	3.31
HYS-variance	0.352
Heritability (original scale)	0.086

The estimated parameters changed quite much using the new model compared to the old model. The sire variance increased from 0.020 to 0.030. The HYS-variance increased from 0.269 to 0.352. The heritability increased from 0.066 to 0.086.

### Genetic trend

The estimated genetic trend was validated by applying Interbull test 2. The estimated regression coefficient of the DYDs on the relative year of calving of the daughters of a bull was  $-0.01$  and the estimated standard error on this regression factor was 0.006. The regression factor was  $-2.9\%$  of the genetic standard deviation. Taking a 95% confidence interval, the regression factor did not significantly deviate from 0.

The estimated genetic trend with the old and the new model is plotted in Figure 3. The regression factor of the average EBV per year of birth of bulls was 4.2% of the genetic standard deviation for the current model and 5.3% for the new model. The genetic trend was estimated slightly higher with the new model than with the current model. The average EBV of the youngest bulls (1996-1998) were lower with the new model, compared to the old model, whereas for older bulls (1987-1995) the average EBV was higher in the new model.

## Conclusions

The risk of being culled was estimated lower with the piecewise Weibull model than with the baseline Weibull model in the first 330 days of the lactation.

The estimated effects of heterosis and recombination on longevity and milk production were quite comparable, when expressed in genetic standard deviations.

The culling risk for cows producing below the herd average was estimated higher with the new model compared to the old model. The culling risk for cows producing above the herd average was comparable for the old and the new model.

The culling hazard per parity increased for parity 1 to 8 and decreased after parity 8.

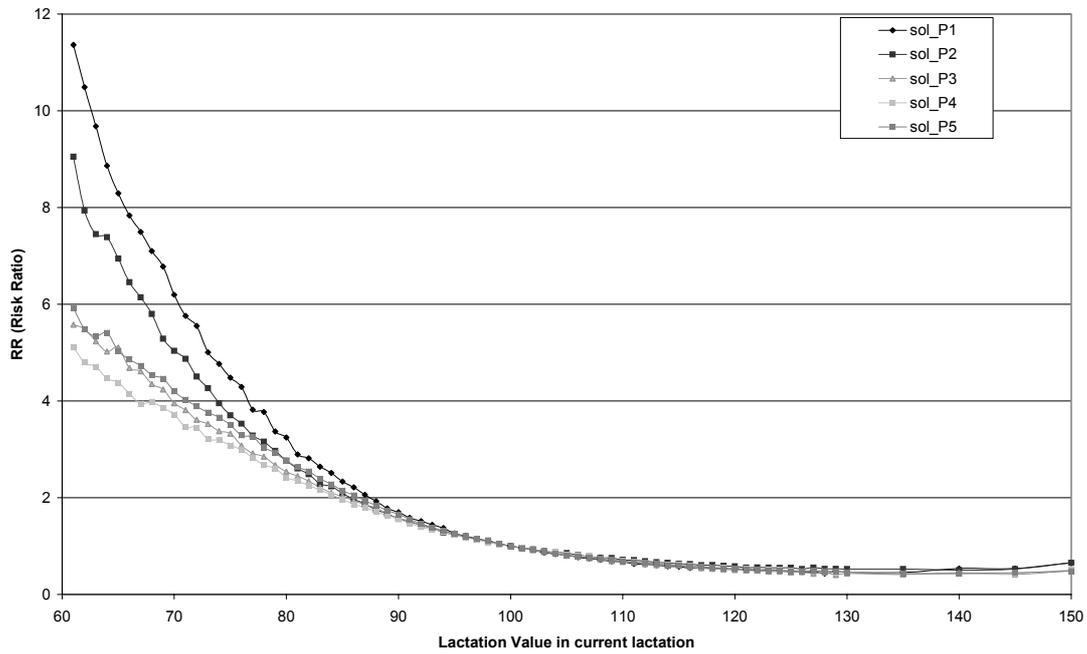
The estimated genetic trend was slightly higher for the new model compared to the current model. However, the average EBV of the youngest bulls decreased.

## Acknowledgements

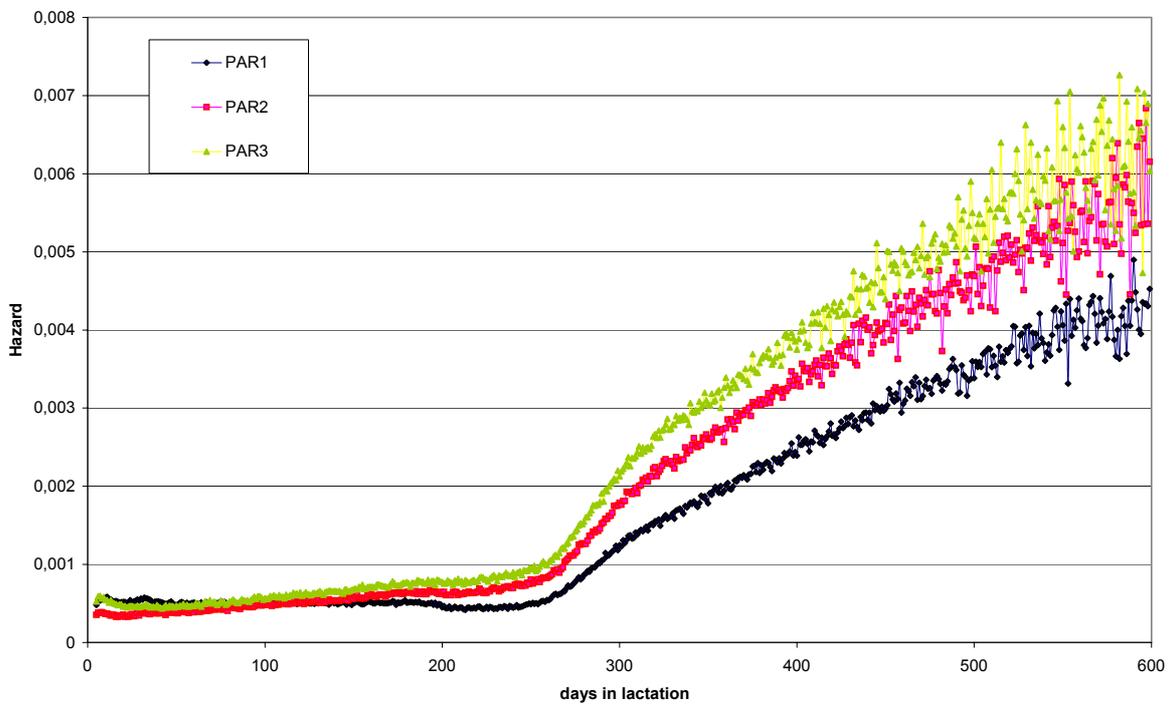
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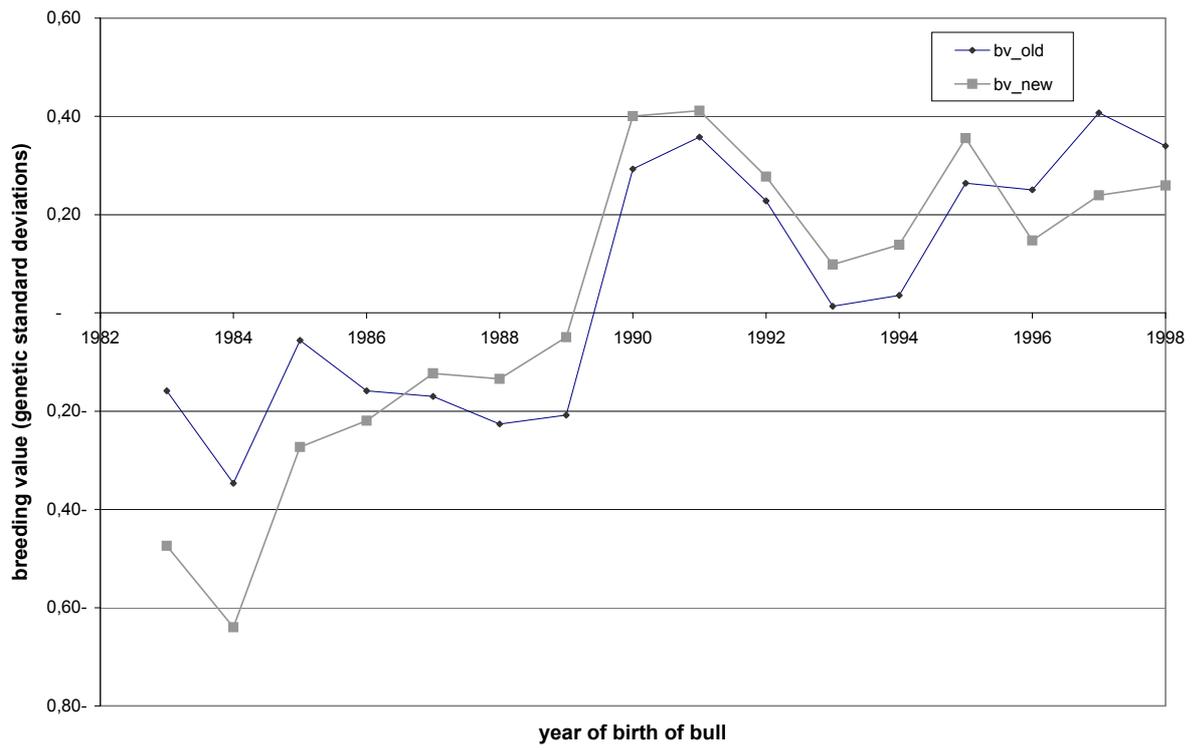
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**Figure 1.** Solutions for LVC per 3-year period (P1 is the most recent 3-year period).



**Figure 2.** Estimated non-parametric hazard function of the first three lactations.



**Figure 3.** Genetic trend in EBVs for longevity with the current and new model.