A New Model for the Genetic Evaluation for Longevity in German Holsteins

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Abstract

The genetic evaluation for longevity in German Holsteins was based on a proportional hazards model (PHM) for about 20 years. A new evaluation was developed based on a linear multiple trait model. In this model the first three lactations are separated into 3 stages each, days in milk 0 - 49, 50- 249 and 250 – consecutive calving. Therefore, 9 genetically correlated survival traits are modelled. Survival of each stage is coded as 1 (survived) or 0 (disposed). Breeding values of the 9 stages are combined to an index breeding value of total survival.

Advantages of the new model are, among others, consideration of information on survival in early lactations and a better comparison of daughter survival within lactation and stage of lactation. Accuracies of early predictors and stability of EBVs in the new model are clearly better than with the current PHM. Overestimation of young bulls' proofs, as observed in the PHM, cannot be seen from the linear model.

Key words: Longevity, Estimation of breeding values

Introduction

Longevity of dairy cows plays an important role in international breeding programs and has a high weight in total merit indexes in several countries (Miglior *et al.*, 2005). It is an economically important trait for farmers (Allaire and Gibson, 1992) and has gained in importance as a global indicator for animal welfare (Thomson and Houe, 2006; Pritchard *et al.*, 2013). Longevity is defined as survival at successive time periods. It is genetically often defined as the same trait over the complete life of a cow (Ducrocq, 1994; Caraveillo *et al.*, 2004; González-Recio and Alenda, 2007; Pritchard *et al.*, 2013). However, several studies suggest that survival is a genetically different trait in different parities, even in different stages of a lactation. (Visscher and Goddard, 1995; Dematawewa and Berger, 1998; Jairath *et al.*, 1998; Boettcher *et al.*, 1999; Veerkamp *et al.*, 2001; Sewalem *et al.*, 2007; Holtsmark *et al.*, 2009), Different diseases (Beaudeau *et al.*, 1994; Gröhn *et al.*, 1998; Rajala-Schultz and Gröhn, 1999a), reproduction traits (Rajala-Schultz and Gröhn, 1999b; Bicalho *et al.*, 2007) and their influence on culling during the lactation underline that the genetic background of survival of different periods within the same lactation may differ (Ducrocq, 1999). Disposal reasons which reflect the subjective decision-making of the farmer on culling support this hypothesis as well as involuntary reasons. Their distribution patterns depend on the parity and the stage of lactation (Seegers *et al.*, 1998; Pinedo *et al.*, 2010). Further, Roxström and Strandberg (2002) found culling for different reasons to be genetically different and Ducrocq (2002) found strong indications that survival late in lactation is genetically distinct to survival early in lactation regardless of lactation number.

A new model was developed by vit in order to adopt the different genetic structures in first, second and third parity for the genetic evaluation of longevity for dairy cows in Germany.

Trait definition

Traits are defined as survival of different periods of the first three parities. The first period is from day 1 to day 49, the second from day 50 until day 249 and the third period is defined as time between das 250 and the next calving. In this case the third period is variable of length, allowing for different lactation lengths. This assures the comparison of cows within period that are truly in the same lactation

stage and therefore face similar culling reasons. Each record contains 9 measured survival traits, 3 periods within each of the first three lactations. When a cow survives a period, it is denoted as '1', if she is culled within a period, this is recorded as '0', unknown performances are treated as 'missing'. In case of complete survival to the 4th calving, the cow will record 9 times '1'. The definition of the phenotypic data is shown in table 1.

Table 1. Definition of periods.

Periods (d)		Lactation		
Start	**End**	**1**	**2**	**3**
0	49	L1.1	L2.1	L3.1
50	249	L1.2	L2.2	L3.2
250	Consecutive calving	L1.3	L2.3	L3.3

Model for genetic analysis

The following model is fitted to the data:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{e}$$

where **y** is a vector of survival (0/1) observations for different periods as defined in Table 1, **X** is an incidence matrix, linking observations to fixed effects, **b** is the vector of fixed effects, **Z** is the incidence matrix of random animal effects, **a** is the vector of random animal effects. Fixed effects in the model are an effect for herd × year × season of the day of entrance into each period, an effect for region, and an effect of milk yield relative to the herd mean, measured from the previous period × 5-year period for periods L1.2 to L3.3.

Genetic parameters for the described model were estimated similarly. A detailed description of the derivation of the model and its parameters can be found in Heise *et al.* (2016).

Estimated heritabilities are given in table 2. The heritability of the combined relative index (RZN)is 0.088.

Table 2. Phenotypic frequencies, estimates of heritability (three periods per parity) on the observed scale.

Trait	phenotypic frequency	h^2
L1.1	.95	.025
L1.2	.92	.016
L1.3	.87	.023
L2.1	.96	.019
L2.2	.90	.025
L2.3	.85	.029
L3.1	.93	.027
L3.2	.88	.030
L3.3	.82	.035

Genetic correlations between the 9 periods are given in table 3. For the 9-trait animal model a full variance-covariance matrix is available which can be derived from the given genetic parameters. The estimated genetic correlations show a specific pattern. Values between different periods within same lactation are regularly lower than values between equal periods but in different lactations. This underlines the given assumption that different periods within the same lactation have a different genetic background.

Table 3. Genetic correlation estimates of the 9-trait model.

Trait	L1.2	L1.3	L2.1	L2.2	L2.3	L3.1	L3.2	L3.3
L1.1	0.82	0.47	0.83	0.69	0.47	0.69	0.62	0.53
L1.2		0.57	0.72	0.87	0.64	0.67	0.76	0.69
L1.3			0.50	0.54	0.95	0.41	0.66	0.65
L2.1				0.69	0.58	0.89	0.66	0.65
L2.2					0.67	0.64	0.91	0.72
L2.3						0.50	0.68	0.98
L3.1							0.63	0.50
L3.2								0.71

Construction of the index breeding value

Solving the above described model results in nine estimated breeding values (**EBVs**) on the risk-level for each animal in the pedigree. At the end, the goal is to publish only one EBV for functional longevity. To combine such EBVs from multi-trait linear models, a non-linear method is applied, using approximation of the area under the survival curve (Sewalem *et al.*, 2007). Reliabilities are approximated following Liu *et al.* (2004) with weights derived from the linear method as seen from Table 4.

Table 4. Relative weights from index combination for EBVs on the risk-level and lengths of different periods in days.

Period	Relative weights	Length
L1.1	0.228	50
L1.2	0.201	200
L1.3	0.162	160
L2.1	0.128	50
L2.2	0.108	200
L2.3	0.076	160
L3.1	0.053	50
L3.2	0.035	200
L3.3	0.010	160

Validation of the new model

As a first step in order to validate the new model for the genetic evaluation of longevity the estimated breeding values were used to perform the Interbull validation method III (Interbull, 2017). This validation compares the genetic trend of EBVs estimated four years ago with current values, supposing an increase of daughter information per sire within this period. The validation is passed, if the genetic trend does not exceed 2% of the underlying genetic standard deviation. The new model shows an estimated genetic trend of less than 0.9% of the genetic standard deviation, performing better than compared to the high value in the current model.

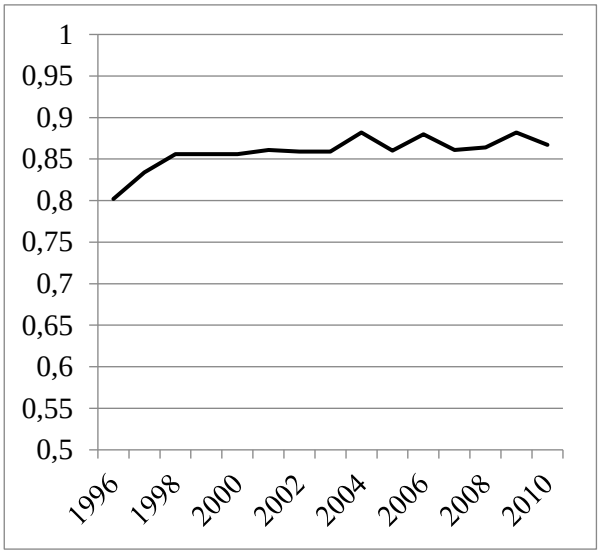

Figure 1. Correlation of the relative (index) breeding value for longevity between the current and new model, shown per birth year.

Comparison to the current model

Whenever the model of a genetic evaluation system changes as in this case, effects on EBVs and sire rankings are to be expected. A comparison of both models is shown in fig. 1, where the correlation of EBVs in the current and new genetic evaluation per year of birth is displayed.

The overall correlation between current and new EBVs is 0.86. The value remains equal for all birth years, only in early stages the differences in the data structure is causing slightly lower correlations. The correlation of 0.86 indicates that the trait definition is significantly different between the new and the old system.

One problem of the current model is the overestimation of young bulls with incomplete (censored) daughter information. Developing a new model should perform better in the estimation of sires with early daughter information in respect to their EBV estimated with high amount of information. The model was explicitly chosen, because early survival and culling is taken into account. In order to

investigate this assumption, the two data sets used for the Interbull validation were chosen in order to compare early and late EBVs with different amount of underlying phenotypic information. Figure 2 shows the correlation between current EBVs and EBVs estimate four years ago, grouped by birth year.

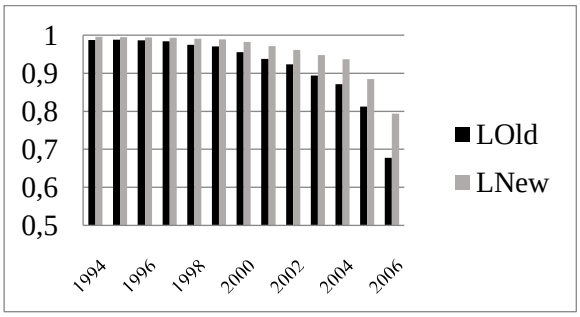

Figure 2. Correlation between EBVs estimated in 2012 and 2016, using the current model (LOld) and the new model (LNew), grouped by birth year of bulls.

In figure 2 is illustrated, that EBVs in 2012 and 2016 are very high correlated, when estimated for older bulls with final information on total longevity. The current and the new model show only small differences with a favorable trend for the new model. For younger bulls, that have incomplete information on total longevity in the 2012 data set, the situation is different. In the current model (LOld), the correlation between the 2012 vs. 2016 estimates are clearly lower than in the new model (LNew), showing how the early EBVs predicted better full informative longevity the 9-trait linear model.

Long term stability has been investigated, but also stability over consecutive estimation runs needs to be analyzed in order to validate the new model. Six consecutive estimations, three from 2015 and three from 2016 were simulated in order to analyze the development of EBVs. It has been found that estimates from all estimation runs keep stable, either grouped by reliability or by birth year (results not shown).

Estimates of the new model as predictors for true longevity as time trait

The new model uses survival in the first three lactations, up to the information of a fourth calving of a cow. Information on differences in the true longevity of cows survived the 4th calving is not taken into account in the new model. In principle this should be a disadvantage predicting true longevity as time trait compared to models using true longevity as time trait. The new model has been analyzed, how good the estimated breeding values can predict distinctions in mean phenotypic overall longevity of daughters. Bulls were classified in top and bottom 10% in terms of relative breeding values. Only bulls with complete information on first crop daughters were analyzed, i.e. bulls born 2002 - 2005. The results of this comparison are shown in figure 3 and figure 4, for the current and the new model resp.

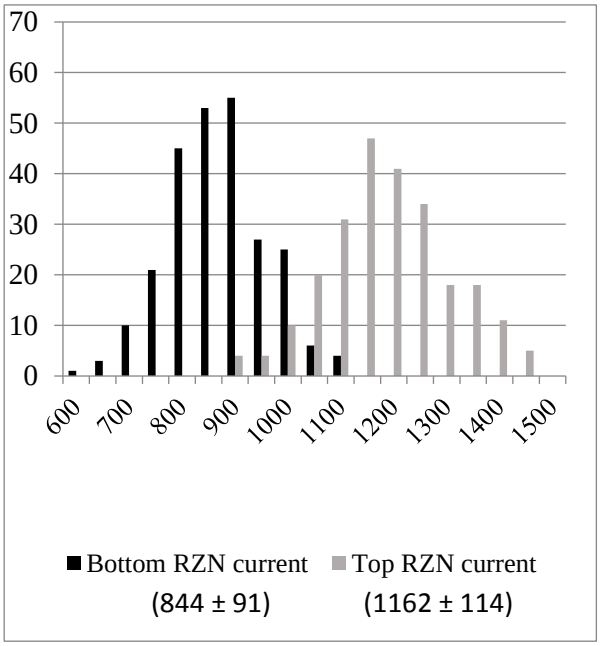

Figure 3. Current model longevity:
Comparison of real phenotypic longevity in days of daughters (mean and SD in brackets) from top 10% vs. bottom 10% sires in EBVs.

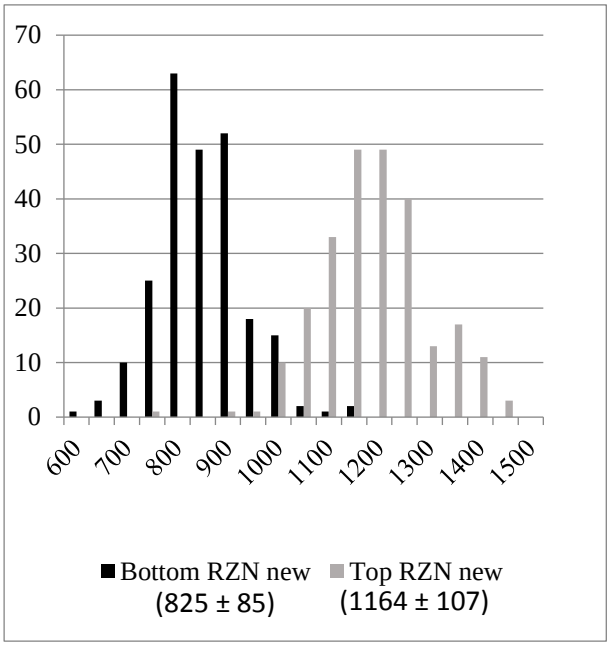

Figure 4. New model longevity:
Comparison of real phenotypic longevity in days of daughters (mean and SD in brackets) from top 10% vs. bottom 10% sires in EBVs.

In figure 3 and 4 the distribution of mean phenotypic survival of daughters from the top and bottom 10% bulls is shown, ranked on relative breeding value (RZN). The current model (fig. 3), which is based on whole life longevity, shows the expected distinction between the phenotypic longevity of daughters from top and bottom bulls. In other words, bulls with a high relative breeding value also have daughters with a high mean phenotypic performance in longevity. This result was to be expected, because the EBVs are estimated based on the overall phenotypic longevity.

In the new model, the phenotypic trait, which is the base of the genetic estimation, is different, because only partial information on true longevity is used. Figure 4 shows how the new model differentiates phenotypic longevity between sires with high and low EBVs. Sires are grouped into top and bottom 10% using the relative breeding value based on three lactations only. Nevertheless the EBVs from the new model predict true overall longevity of their daughters even better (compared to figure 3).

In other words: bulls with a high relative breeding value in the new model also have daughters with a high mean phenotypic performance in overall longevity. This analysis underlines, that the survival rate of the first three lactations predicts true longevity better compared to the current PHM.

Conclusions

For the trait longevity a new model to estimate breeding values has been developed in Germany. The new trait is based on survival of three periods of the first three lactations in the life of a cow. The nine traits in this model are combined to one relative breeding value RZN, representing functional longevity.

The new model has been tested in comparison to the current model and performed better in respect to the estimates of young sires, stability of proofs and prediction of whole life longevity inheritance.

The new model is likely to be introduced in the German routine evaluation of vit for dairy breeds in April 2018.

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