

## Genetic Evaluation of Survival Traits in German Holstein Dairy Cattle Using a Six-Trait Linear Model

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**ABSTRACT:** Data of 11.106.125 German dairy cows were used for genetic evaluation of survival in the first three lactations. The lactations were split into two periods before or after 150 days from calving. Survival was defined as the recurrence in the next period. Culling risks ranged between 0.05 and 0.24 for different periods and increased over lactations. Heritability estimates were between 0.020 and 0.055. Most genetic correlations were below 0.90, indicating that the genetics for survival are not the same over the different periods. Correlations between corresponding periods of different lactations were in most cases higher than between periods within the same lactation. Correlations between traits of the second and third lactation were higher than between the first and later lactations.

**Keywords:** dairy cattle; survival; longevity; linear model

### Introduction

Longevity of dairy cattle is not only part of the public discussion about animal welfare and sustainability but also an economically important trait and has hence been in the focus of geneticists from all over the world for decades. The German genetic routine evaluation exists since 1996 and is conducted with the Survival Kit (Ducrocq (2005)). The productive life of a cow ends with her culling which is reasoned in the subjective decision of the farmer and nature. Important traits that are related to culling are performance traits (e.g. Hadley et al. (2006)), fertility traits (e.g. Sewalem et al. (2008)), and diseases (e.g. Gröhn et al. (1998)). The knowledge of culling reasons can help to understand the decision making on culling (Allaire et al. (1977); Seegers et al. (1998)). A preliminary assessment of culling reasons in the data used for this study showed that frequencies of culling reasons (including “low performance”, “fertility”, “claw and limb diseases” and “mastitis”) change over and within lactations, suggesting that the genetics of survival in different periods could be different.

Holtmark et al. (2009) compared the predictability for 365 d survival of a multiple-trait linear model (survival in the first three lactations as correlated traits) to a threshold and a Weibull frailty model and found that the linear model performed slightly better. The authors inferred from the genetic correlations among the traits that survival in first lactation is a distinct trait from later lactations. Boettcher et al. (1999) came to a similar appraisal from a linear three-trait model for the first three lactations.

Previous studies using linear multiple-trait models to analyze survival in different production periods mostly defined different lactations to be different traits, sometimes splitting the first lactation into several periods (Sewalem et

al. (2007)). To understand the genetics of survival, the objective of this study was the investigation of genetic parameters between corresponding stages of the first three lactations, which were split into two periods each and analyzed with a six-trait linear model. This knowledge is important to improve the existing national genetic evaluation system to achieve more stable sire breeding values when the number of direct observations of culled daughters increases.

### Materials and Methods

**Data.** Data of 11.106.125 German Holstein cows used in the national evaluation were analyzed. Birth and culling dates and reasons for culling were recorded as well as the date and herd of each calving. Records of cows with first calving between 1998 and 2008 were used, so that cows had the opportunity to finish at least three lactations. Only cows with valid dates for birth, calving and, if present, culling, age of first calving between 500 and 1500 days and complete records from their first to last calving were included in the following analysis.

**Statistical analyzes.** Survival in periods up to the third lactation was analyzed using a linear six-trait random sire model with herd\*year of calving as fixed effect, where year meant the milk quota year (from April to March). The first three lactations were cut into two periods each at 150 days from calving (L1.1 - L3.2). For the binary definition of the response variable (later referred to as BR), survival for a certain period was coded 1, if the cow reached the following period and 0, if the cow was culled during this period. Another definition of the response variable following Snell (1964) (SR) was compared to BR. The binary response was replaced by the mean z-value on an underlying scale within defined strata. Strata were defined within herd\*year, merging neighbouring classes if there were less than 200 observations within a stratum. Cows with no date of culling were considered to be censored at the date of the data cut (25 June 2013) or, if the last observation was before 29 September 2010, at the date of her last observation. Periods with no information due to censoring or after culling were treated missing.

Due to computational requirements, estimation of genetic parameters was conducted on samples. To maximize the number of daughters per sire, sampling was conducted over herds within regions which are associated to breeding associations. Differences in management and culling patterns are assumed to be present between regions with large herd sizes and regions with lower herd sizes. Therefore two regions were chosen, the one having an average herd size in calving year 2008 of 77 cows (referred to

as SHR), the other one having an average herd size of 269 cows (LHR). Four scenarios, consisting of 10 samples each, were compared: SHR vs. LHR and BR vs. SR. Each sample contained 250 (150) herds in SHR (LHR). This resulted in an average of 61.956 (153.232) cows and 2.660 (5.349) sires per sample. Different numbers of herds were intended to increase the number of cows in the SHR dataset. Each herd\*year class of a herd had to comprise at least 15 observations. VCE (Groeneveld et al. (2010)) was used for estimation of variance components within each sample. Estimated heritability was compared to approximate heritability on the underlying scale suggested by Dempster and Lerner (1950) for binomial response variables. Results from samples within a region using the same definition of the response variable were summarized by computing means and standard deviations for the sample estimates of heritability, genetic correlations and survival frequencies.

### Results and Discussion

The risk of a cow to be culled during a period, conditional on her survival up to this period, differed between LHR and SHR (table 1). For the second period within a lactation (150 d up to the next lactation) the ratio between the risks of LHR and SHR was about 1.1, while it ranged between 1.75 and 1.84 for the first periods.

**Table 1. Risk of culling in different periods for different regions in Germany**

Period	LHR	SHR	Ratio
L1.1	.09	.05	1.84
L1.2	.15	.13	1.12
L2.1	.12	.07	1.76
L2.2	.20	.18	1.10
L3.1	.19	.11	1.75
L3.2	.24	.22	1.08

Heritability in LHR increased over lactations from 0.026 (L1.2) to 0.046 (L3.1) while there was hardly a difference within lactations (table 2). Heritability estimates in SHR showed a slightly different pattern (table 3): For the first periods of all lactations it was approx. 0.013 lower than for second periods. Also the increase from the first lactation to the third was lower. The heritability estimates were close to those reported by Boettcher et al. (1999), Sewalem et al. (2007) and Holtsmark et al. (2009). Approximate heritability estimates on the underlying scale are shown in table 4. For SHR data they ranged between 0.073 (L2.1) and 0.107 (L3.2) and were more stable over the traits than estimated heritability. For LHR, approximate estimates for the second period of a lactation were by 0.009 to 0.024 lower than for first periods. However, heritability estimates for the first periods of the lactations in LHR compared to the second periods were higher than in SHR, no matter if considered as direct estimates or as approximation on the underlying scale. The reason could be that farmers of smaller herds give cows with a problem at the beginning of a lactation a special treatment to avoid culling which is not given to cows in LHR. Therefore cows in small herds show less of their genetic potential.

**Table 2. Mean of heritability and genetic correlations over 10 samples in the large herd region (LHR)**

Period	L1.1	L1.2	L2.1	L2.2	L3.1	L3.2
L1.1	.027 (.003)	.77 (.10)	.82 (.04)	.66 (.13)	.75 (.04)	.59 (.11)
L1.2		.026 (.003)	.72 (.09)	.91 (.05)	.64 (.06)	.82 (.04)
L2.1			.032 (.007)	.75 (.05)	.96 (.02)	.72 (.09)
L2.2				.035 (.008)	.71 (.06)	.95 (.02)
L3.1					.046 (.008)	.73 (.07)
L3.2						.039 (.010)

Heritability on the diagonal, genetic correlations above; SE of results from 10 samples in parenthesis

**Table 3. Mean of heritability and genetic correlations over 10 samples in the small herd region (SHR)**

Period	L1.1	L1.2	L2.1	L2.2	L3.1	L3.2
L1.1	.020 (.010)	.77 (.12)	.75 (.12)	.71 (.12)	.66 (.22)	.68 (.15)
L1.2		.034 (.006)	.73 (.12)	.92 (.03)	.59 (.13)	.88 (.06)
L2.1			.020 (.006)	.86 (.07)	.91 (.09)	.85 (.06)
L2.2				.043 (.004)	.77 (.10)	.96 (.04)
L3.1					.034 (.009)	.78 (.10)
L3.2						.055 (.009)

Heritability on the diagonal, genetic correlations above; SE of results from 10 samples in parenthesis

**Table 4. Approximate heritability on the underlying scale following Dempster and Lerner (1950)**

Period	LHR	SE	SHR	SE
L1.1	.086	.011	.088	.041
L1.2	.062	.007	.084	.016
L2.1	.082	.017	.072	.019
L2.2	.073	.015	.093	.010
L3.1	.096	.017	.094	.023
L3.2	.073	.019	.107	.017

Results of 10 samples

Most correlations between traits L1.1 - L3.2 were clearly below .90, indicating that the traits are genetically distinct. Correlations between traits of the first lactation and traits from second and third lactation tended to be lower than between second and third lactation. This matches the findings of Holtsmark et al. (2009). Correlations between corresponding periods of consecutive lactations tended to be higher than correlations of periods which belonged to the same lactation. This tendency was strongest between second and third lactation, where e.g.  $r_{L2.1,L2.2}$  and  $r_{L2.1,L3.1}$  in LHR were 0.75 and 0.96, respectively. The only period for which this pattern did not hold was L1.1 in SHR. This could be for similar reasons as already mentioned for the differences in heritability.

Results from SR are not shown, because they were close to those from BR. This is in accordance to results from Abdel-Azim and Berger (1999) reported for simulated

data. The distribution of the transformed response was highly bimodal and in most cases a threshold could be chosen so that the binomial variable could be retrieved with no deviance from the initial value.

### **Conclusion**

The study shows that survival probability at different stages in the life of a cow is not only genetically different over lactations but also within lactations. It is necessary that a model for a routine genetic evaluation accounts for this issue. Despite some statistical inadequacies, a linear model has the advantages of being easy to apply and having relatively low computational requirements compared to other methods, mainly in large populations. This study achieved plausible results for genetic parameter estimates. Further research will be necessary to find the most useful model for the national genetic evaluation.

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