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The genetic structure of longevity in dairy cows

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ABSTRACT

Longevity of dairy cows is determined by culling. Previous studies have shown that culling of dairy cows is not an unambiguous trait but rather the result of several reasons including diseases and selection decisions. The relative importance of these reasons is not stable over time, implying that genetic background of culling may vary over lifetime. Data of 7.6 million German Holstein cows were used to assess the detailed genetic correlation structure among 18 survival traits defined for the first 3 parities. Differences of genetic factors which determine survival of different production periods were found, showing a pattern with 3 genetically distinct periods within each parity: early lactation (calving until d 59), mid lactation (d 60 to 299), and late lactation (d 300 until next calving). Survival in first and later parities were found to be slightly genetically different from each other. The identified patterns were in good accordance with distributions of reasons for disposal, and correlations of estimated breeding values of survival traits for different periods to production and functional traits were generally plausible compared with literature regarding effects on the risk of culling. The study shows that genetic background of survival is variable not only across but also within parities. The results of the study can help developing more accurate models for routine genetic evaluations of longevity that account for nonunity genetic correlations between survival of different periods.

Key words: longevity, culling, dairy, genetics

INTRODUCTION

Longevity of dairy cows is an economically important trait for farmers (Allaire and Gibson, 1992) and has gained in importance as a global indicator for animal welfare (Thomsen and Houe, 2006; Pritchard et al., 2013). In the last decades, numerous studies have shown that longevity is heritable, and routine genetic evaluations for longevity are conducted in all major countries of dairy breeding (Miglior et al., 2005; Interbull, 2015). Longevity results from survival at successive time periods. It is genetically often treated as the same trait over the whole life of a cow (Ducrocq, 1994; Caraviello et al., 2004; González-Recio and Alenda, 2007; Pritchard et al., 2013). However, several studies suggest that survival of different parities is genetically different (Visscher and Goddard, 1995; Boettcher et al., 1999; Veerkamp et al., 2001; Sewalem et al., 2007; Holtsmark et al., 2009). Previous studies further showed that effects of different diseases (Beaudeau et al., 1994; Gröhn et al., 1998; Rajala-Schultz and Gröhn, 1999a) and reproduction traits (Rajala-Schultz and Gröhn, 1999b; Bicalho et al., 2007) on culling are dependent on the parity and also on the stage of lactation. This implies that genetic background of survival of different periods within the same lactation may differ (Ducrocq, 1999). This hypothesis is supported by distributions of disposal reasons reported by dairy farmers, where distribution patterns depend on the parity and the stage of lactation (Seegers et al., 1998; Pinedo et al., 2010). 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. van Pelt et al. (2015) reported the genetic background of survival to be changing over time, using definitions of survival traits based on the overall length of productive life. Lactation-based definitions of monthly survival were only recently examined by Sasaki et al. (2015) in Japanese dairy cattle using a random regression model.

The aim of our study was a systematic investigation of the genetic structure of longevity regarding different periods of first, second, and third parity. Distributions of disposal reasons and correlations of estimated breeding values for the new survival traits to various production and functional traits were used to validate the genetic correlation patterns found. Because survival

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and threshold models are computationally highly demanding and thus not feasible for extensive multivariate genetic analyses on large data sets (Boettcher et al., 1999), a linear multiple trait model was chosen for the refined survival analyses.

MATERIALS AND METHODS

Data

For this study, records of Holstein dairy cows used in the German routine genetic evaluation for longevity were available. Data were restricted to years of first calving between 1998 and 2014, with cutoff date February 10, 2014. Records included dates of birth and calving, the herd code, and in case the cow had left the herd, the reason for and date of disposal. Only records with complete and valid data between first and last observed calving were considered. This means, for example, for a cow that was culled or censored during the third lactation, records of the first and second lactation had to be present in the data set. Records of cows with unknown sires or age of first calving outside the range of 500 to 1,500 d were excluded. Herds had to have at least 15 calvings for each year in the observation period between 1998 and 2013 (data for year 2014 were not complete). After editing, 7,684,455 records remained on the data pool for the analysis of survival.

For parameter estimation, data were further restricted to years of first calving from 1998 to 2008, such that each cow in the data had the opportunity to finish at least 3 lactations. Because estimation of variance components would not have been computationally feasible on the full data set, 10 possibly overlapping samples of 200 herds each were randomly drawn. To avoid sparse category problems, only data of 5 out of the 16 federal states were considered. Each sample consisted of an average of 234,498 records of daughters from 7,103 bulls. Over all samples, a total of 1,495,441 different cow records were used for parameter estimation. Data structure by lactation is shown in Table 1.

Distribution of Disposal Reasons

In Germany, disposal reasons are recorded routinely when a cow exits milk recording. The farmer is requested to report his/her main reason for disposal as one of the predefined disposal reasons: infertility, udder diseases, claw and leg disorders, metabolic diseases, other diseases, poor milk yield, milkability, age, other reasons, or sold for dairy purposes. Only cows being disposed for reasons other than “sold for dairy purposes” were considered. Frequency distributions for disposal reasons were computed by parity and relative to calving by 10-d intervals for days in milk.

Trait Definition

Traits were defined as survival of different periods of the first 3 parities. Genetic analyses were carried out using 2 different period definitions. First, for evaluating the genetic structure of survival in detail, 2-mo periods were defined (A). Second, adjacent periods from A with minimum genetic correlations of 0.9 were joined such that fewer periods (B) were defined to achieve a simpler model for genetic evaluations. Period definitions for A and B are specified in Table 2. In each case, records were coded as 1 if a cow was still alive at the end of the period and 0 if culling occurred during the period. Records of cows which were culled in a previous period or censored during a period were noninformative with regard to survival and therefore not considered. Censoring was assumed when the date of disposal was missing or when the disposal reason was “sold for dairy purposes.” In other words, trait n was defined as survival at the end of period n, given the cow was still alive at the end of the period n − 1.

Model for Genetic Analyses

The basic model equation for all linear multiple trait models was

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Zs} + \mathbf{e},$$

where $\mathbf{y}$ is a vector of survival (0/1) observations, $\mathbf{X}$ is an incidence matrix linking the observations to the fixed effects, $\mathbf{b}$ is the vector of fixed effects (i.e., the effect of herd × year of calving for each period), $\mathbf{Z}$ is the incidence matrix of random sire effects, $\mathbf{s}$ is the vector of random sire effects [$\mathbf{s} \sim N(0,\mathbf{G}_0 \otimes \mathbf{A})$], with the genetic covariance matrix $\mathbf{G}_0$ and the numerator relationship matrix for sires $\mathbf{A}$), and $\mathbf{e}$ is a vector of random residual effects [$\mathbf{e} \sim N(0,\ \mathbf{R}_0 \otimes \mathbf{I})$], with the residual covariance matrix $\mathbf{R}_0$). Models using trait definitions A

Table 1. Distribution of records by lactation

	Number of records	
Lactation	Parameter estimation	Breeding value estimation
1	1,495,441	7,684,455
2	1,137,682	5,370,587
3	790,602	3,499,842