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Phenotypic and genetic relationships between age at first calving, its component traits, and survival of heifers up to second calving

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ABSTRACT

The aim of this study was to answer the question whether models for genetic evaluations of longevity should include a correction for age at first calving (AFC). For this purpose, phenotypic and genetic relationships between AFC, its component traits age at first insemination (AFI) and interval from first to last insemination (FLI), and survival of different periods of the first lactation (S1: 0 to 49 d, S2: 50 to 249 d, S3: 250 d to second calving) were investigated. Data of 721,919 German Holstein heifers, being inseminated for the first time during the years from 2003 to 2012, were used for the analyses. Phenotypic correlations of AFI, FLI, and AFC to S1 to S3 were negative. Mean estimated heritabilities were 0.239 (AFI), 0.007 (FLI), and 0.103 (AFC) and 0.023 (S1), 0.016 (S2), and 0.028 (S3) on the observed scale. The genetic correlation between AFI and FLI was close to zero. Genetic correlations between AFI and the survival traits were -0.08 (S1), -0.02 (S2), and -0.10 (S3); those between FLI and the survival traits were -0.14 (S1), -0.20 (S2), and -0.44 (S3); and those between AFC and the survival traits were -0.09 (S1), -0.06 (S2), and -0.20 (S3). Some of these genetic correlations were different from zero, which suggests that correcting for AFC in genetic evaluations for longevity in dairy cows might remove functional genetic variance and should be reconsidered.

Key words: age at first calving, survival, longevity, age at first insemination

INTRODUCTION

Longevity is an economically important (Allaire and Gibson, 1992) and publicly discussed trait in dairy cows. Routine genetic evaluations for this trait are conducted in all major dairy breeding countries (Miglior

et al., 2005; Interbull, 2016). After years of routine genetic evaluations for longevity, some recent studies have reviewed this trait complex (Sasaki et al., 2015; van Pelt et al., 2015; Heise et al., 2016). In research studies (Ducrocq, 2005; Sewalem et al., 2007; Sasaki et al., 2015; van Pelt et al., 2015) as well as routine genetic evaluations in many countries (Interbull, 2016), longevity is corrected for age at first calving (AFC), either in the form of a covariate (Sewalem et al., 2007) or as a fixed class effect (Ducrocq, 2005). In the following countries, which participate in Interbull genetic evaluations, longevity is corrected for AFC in either form: Canada, Czech Republic, Denmark-Finland-Sweden, France, Germany, Great Britain, Hungary, Ireland, Israel, Italy, Netherlands, Poland, Republic of South Africa, Slovenia, Spain, and Switzerland. In Australia, Belgium, New Zealand, and the United States, longevity is not corrected for AFC (Interbull, 2016). In genetic evaluations, this is only justifiable if AFC predominantly reflects environmental factors with no genetic correlation to longevity. There are reasons to reconsider this hypothesis: AFC can be dissected into age at first insemination (AFI), time from first to last (or successful) insemination (FLI), and gestation length. All these traits are functional traits and were shown to be heritable in previous studies (AFI: Mäntysaari et al., 2002; Jamrozik et al., 2005; FLI: Berry et al., 2003; Liu et al., 2008; gestation length: Jamrozik et al., 2005; Norman et al., 2009). Especially, FLI is a widely used reproduction trait and part of the total merit index in various countries, including Germany (Interbull, 2016). Phenotypically, impaired reproductive performance increases the risk of culling (Rajala-Schultz and Gröhn, 1999), and positive genetic correlations between more favorable expressions of reproduction traits and survival were also reported (Campos et al., 1994; Haile-Mariam et al., 2003). Despite the mentioned results, literature on genetic relationships between AFC or AFI and survival is scarce. Furthermore, most previous studies on genetic relationships between survival and other traits considered survival of relatively long periods; for example, survival of the complete first

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lactation (Visscher and Goddard, 1995; Dematawewa and Berger, 1998; Haile-Mariam et al., 2003). Recent studies (Sasaki et al., 2015; van Pelt et al., 2015; Heise et al., 2016) suggest that the genetic background for survival of different periods within the same lactation is not the same. The aim of this study was to investigate the genetic relationships between AFC, its underlying traits, and survival of different periods of the first lactation. Knowledge about these relationships is crucial for appropriate modeling of longevity in routine genetic evaluations.

MATERIALS AND METHODS

Data

The data used in this study originate from national routine genetic evaluations for Holstein cattle in Germany (VIT, 2016) and were selected by applying the selection steps described in Table 1. The traits AFI and FLI were restricted to plausible ranges: 330 to 800 d for AFI and 0 to 210 d for FLI. Additionally, the interval from last insemination to first calving was required to be within the range from 265 to 295 d. The last step included sampling of herds within 5 federal states in Germany such that at least 100,000 records were in each data set. This procedure resulted in 5 sample data sets consisting of in total 721,919 cows (111,388 to 174,102 each) from 10,643 sires.

Trait Definitions

The individual records for AFI, FLI, and AFC were derived from the available data of the sampled animals. Following Heise et al. (2016), 3 survival traits within the first lactation were defined as follows: the first par-

ity was divided in the periods 0 to 49 d (**S1**), 50 to 249 d (**S2**), and 250 d from calving until the second calving (**S3**). If a cow survived until the end of a period, given that she had survived all previous periods, her observation for survival was coded “1”; if she was culled in the period of consideration, her observation for survival was coded “0”; and if the cow was sold or culled in one of the previous periods, her observation record of survival for the regarded period was considered missing.

Phenotypic Analyses

Survival rates and risk of culling for S1 to S3 were estimated following Kaplan and Meier (1958) with the `survfit()` function from the survival package (Therneau, 2016) in R (R Core Team, 2016).

To evaluate phenotypic relationships between AFI, FLI, and AFC and the survival traits S1 to S3, the traits AFI, FLI, and AFC were coded as discrete variables (monthly steps for AFI and AFC, ranging from 12 to 21 mo and from 21 to 32 mo, respectively; 21-d steps for FLI, ranging from 0 to 147 d). Univariate logit threshold models were fitted as

$$\mathbf{y}^* = \mathbf{X}\mathbf{b},$$

where \mathbf{y}^* is a latent variable that is linked to \mathbf{y} via a logit-function; \mathbf{y} is a vector comprising survival observations (1/0) for S1, S2, or S3; \mathbf{X} is an incidence matrix linking observations to classes of fixed effects; and \mathbf{b} is a vector of fixed effects (AFI, FLI, or AFC). This resulted in 9 models with survival traits as dependent variables and AFI, FLI, and AFC as independent variables. The analysis was conducted using the function `glm()` from the R package `stats` (R Core Team, 2016).

Table 1. Data selection steps and criteria

Step: Selection of	Criterion
(1) Insemination bulls	(a) Holsteins only (b) Semen used in at least 10 herds
(2) Insemination records	(a) Bulls from step 1 (b) Conventional (non-sexed) frozen semen only
(3) Cows	(a) Holsteins only (b) Both parents known (c) Stayed in the same herd until first calving (d) All inseminations on the cow passed step 2 (e) Known record of first calving (f) Record of first insemination within the years 2003 to 2012
(4) Herds	(a) At least 20 first inseminations (from step 3) on heifers per year from 2003 to 2015 (b) Sampling of herds within 5 of the German federal states
(5) Sires	(a) Per sample: more than 5 daughters per sire

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