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Short communication: A genetic study of mortality in Danish Jersey heifer calves

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ABSTRACT

The aim of this study was to estimate genetic parameters for mortality of Jersey heifer calves during the first 6 mo after birth, calculate the genetic trend of the trait, and estimate breeding values of widely used Jersey sires. More than 260,000 heifer calves were included in the study. The mortality traits included in the analysis were defined as mortality in 8 different periods from 24 h after birth to age 180 d (d 1–14, d 15–30, d 31–60, d 61–90, d 91–120, d 121–150, and d 151–180) and mortality over the entire period. A linear model was used for estimation of genetic parameters, breeding values of sires, and genetic trend. Fixed effects included in the model were herd-year class, month of birth, parity of mother, and whether the calf was sold to another farm in the first 6 mo. Both direct and maternal genetic effects were included in the model; however, the maternal genetic effect was very small and not significant. The mortality rate was highest in the first month after birth (7.8%). Total mortality in the first 180 d was 12.5%. Direct heritabilities of mortality were quite low, ranging from 0.002 to 0.03 on the observable scale and 0.025 to 0.076 on the underlying scale. Maternal heritabilities were even lower. The genetic correlation between mortality from d 1 to 14 and d 1 to 180 was estimated to be 0.88, although by definition, these 2 traits share the same observations for many records. No clear genetic trend existed over the last 20 yr; however, considerable genetic variation exists. The best and the worst sires differed by about 8% in their estimated breeding values of mortality in the first 180 d. Based on the results obtained in this study, genetic selection for reducing calf mortality should be possible.

Key words: mortality, Jersey calf, genetic parameter, breeding value

Short Communication

In recent years there has been increasing focus on the mortality of dairy cattle. In several breeds, mortality rates of cows have increased (McConnel et al., 2008), as well as stillbirth and prepubertal mortality of calves. This is not only a problem of economic importance, but also a major ethical issue. A few studies have investigated the genetic background of prepubertal mortality in dairy calves (Erf et al., 1990; Hansen et al., 2003; Fuerst-Waltl and Sørensen, 2010; Henderson et al., 2011; Van Pelt and De Jong, 2012). In Denmark, field records of mortality have been available for all Danish cattle over the last 20 yr. Newborn calves from the Jersey breed are known to have high mortality rates. The high frequency of mortality is partially explained by the common practice of euthanizing young male calves. However, mortality of Danish Jersey heifer calves has been reported to be around 12 to 13%. The comparable frequency of prepubertal mortality in the Danish Holstein and Danish Red breeds is 5 to 6% and 6 to 7%, respectively. Therefore, it appears that mortality is more of a problem in Jerseys than other dairy breeds. Hansen et al. (2003) found that heritabilities of prepubertal mortality in Danish Holstein were very low (<0.01). However, these estimates were affected by the relatively low frequency of mortality in their study (6.6%). No genetic parameters have been published on prepubertal mortality in Jerseys. The aim of this study was, therefore, to estimate genetic parameters for mortality from 24 h after birth to 180 d in Danish Jersey heifer calves. Previous studies have shown that the maternal genetic effects are considerable for stillbirth (Weller and Gianola, 1989; Steinbock et al., 2003; Hansen et al., 2004). Therefore, both direct and maternal additive genetic parameters for mortality were estimated in this study. Finally, breeding values of sires and genetic trends were calculated.

Records on all Danish Jersey heifer calves born from January 1998 to December 2006 that survived 24 h after birth were extracted from the Danish Cattle Database.

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Information on calving, transfers to other farms, death, and slaughter were available on all animals. Calves from herds with fewer than 100 records during the time period and records of twins and triplets were omitted from the study. The final data set consisted of 262,089 records. Pedigree was traced back as far as possible. Eight mortality traits were defined based on mortality in different periods: d 1 to 14, d 15 to 30, d 31 to 60, d 61 to 90, d 91 to 120, d 121 to 150, d 151 to 180, and d 1 to 180. Mortality in the defined periods included only mortality between the given days after birth, and not mortality until the given period. The model included a transfer code to account for a possible negative effect of moving calves between herds. Calves that were not transferred in the first 180 d were assigned to one group and calves that were transferred from d 14 to 30 were assigned to a second group (calves younger than 2 wk of age are not allowed to be transported in Denmark). Finally, calves transferred between d 31 and 180 were assigned to a third group. Transferring of calves in the first 180 d of life was rare, only 0.49% were moved between d 14 and 30, and 0.16% were moved between d 31 and 180. However, mortality rates were higher for transferred calves: 16.5 and 44.4% for calves transferred between d 14 and 30 and between d 31 and 180, respectively.

As estimating both direct and maternal genetic effects with a threshold model was not possible with the software used in this study, a linear animal model was used for estimation of all (co)variance components. Effects included in the model were as follows:

$$\mathrm{M}_{\mathrm{ijklmn}} = \mathrm{HY}_{\mathrm{i}} + \mathrm{BM}_{\mathrm{j}} + \mathrm{PM}_{\mathrm{k}} + \mathrm{TG}_{\mathrm{l}} + \mathrm{a}dir_{\mathrm{m}} + \mathrm{a}mat_{\mathrm{n}} + \mathrm{e}_{\mathrm{ijklmn}},$$

where $\mathrm{M}_{\mathrm{ijklmn}}$ = prepubertal mortality, HY_{i} = fixed effect of herd-year class, BM_{j} = fixed effect of month of birth (1, 2, 3, . . . , 12), PM_{k} = fixed effect of parity of the mother (1, 2, . . . , 5), TG_{l} = fixed effect of transfer group (1, 2, or 3), $\mathrm{a}dir_{\mathrm{m}}$ = random direct additive genetic effect of animal o, $\mathrm{a}mat_{\mathrm{n}}$ = random maternal additive genetic effect of animal p, and $\mathrm{e}_{\mathrm{ijklmn}}$ = random residual.

In addition, the direct genetic correlation between mortality from d 1 to 14 and d 1 to 180 was estimated using a bivariate analysis; however, the maternal genetic effect was excluded due to computational limitations. For estimation of the genetic trend and breeding values of sires, a sire model was used. The same data set was analyzed and the same fixed effects were included in this model. All analyses in this study were carried out with the AI-REML algorithm using the DMU package (Madsen and Jensen, 2010). The convergence criterion used was a change in the norm of the update vector less than 10^{-5}. Heritabilities were transformed to the underlying scale by the approximate formula proposed by Dempster and Lerner (1950).

In Figure 1, the mean mortality for each of the 8 defined periods is presented. Mortality over the entire period (i.e., from d 1 to 180) was 12.5%. Mortality was highest in the first month after birth (7.8%). All fixed effects had a significant effect on mortality in all time periods. The risk of mortality increased with increasing parity of mother, which is in contradiction to what was found in Norwegian Red cattle (Gulliksen et al. 2009). Calves born in the winter period had a higher risk of dying than calves born in the spring and summer, and this result agrees well with the results reported by Gulliksen et al. (2009).

Phenotypic standard deviations, direct and maternal additive genetic variances, and direct and maternal heritabilities of mortality in the different periods after birth are presented in Table 1. The direct heritability was largest, both on the observed scale (0.029) and the underlying scale (0.076), when estimated on data from the entire period (i.e., from d 1 to 180). All direct heritabilities of the mortality traits analyzed were significant. Hansen et al. (2003) estimated direct heritabilities for prepubertal mortality in Danish Holstein heifers and they found direct heritabilities of mortality from d 1 to 14 and from d 1 to 180 on the observable scale to be 0.0033 and 0.0061, respectively, and on the underlying scale to be 0.024 and 0.025. The results reported here and by Hansen et al. (2003) correspond well with what presented for Brown Swiss by Erf et al. (1990), who found a direct heritability of 0.008 on the observable scale for early mortality (d 1 to 7). In the study on heifer loss in the total replacement period for Danish Holstein by Fuerst-Waltl and Sørensen (2010), heritabilities in early life (1–30 d after birth and 30–180 d after birth) were estimated to be 0.017 and 0.022, respectively, with a linear model and 0.082 and 0.001 with a threshold model. Henderson et al. (2011) found a very small heritability (0.0006) for mortality from d 1 to weaning when applying a linear model. Another recent study on Holstein calves by Van Pelt and De Jong (2012) reported heritabilities for mortality from d 3 to 365 to be 0.011 on the observable scale and 0.040 on the underlying scale, whereas the heritability from d 15 to 30 was 0.001 on the observable scale. Based on those studies, heritabilities of prepubertal mortality seem to be higher in Jersey than in the other dairy breeds, at least when presented on the observable scale. Some of the difference may be explained by the higher frequency of prepubertal mortality in Jerseys, as heritabilities of binary traits depend on the frequency.