

Genetic Analysis of Calf and Heifer Losses in Danish Holstein

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Abstract

Especially in dairy breeds, mortality rates of cows but also stillbirth and postnatal mortality rates have increased during the last years. This is not only relevant with regard to economical losses but also to animal health and welfare. Thus, the aim of this investigation was to explore the genetic background of postnatal mortality in calves and replacement heifers in different age groups until first calving in Danish Holstein. The following periods were defined for analyses: P1 = 1-30d, P2 = 31-180d, P3 = 181-365d, P4 = 366d-age at first calving or a maximum age of 1200d if no calving was reported, P5 = 1d - age at first calving or a maximum age of 1200d if no calving was reported. Records of animals which were slaughtered or exported within a defined period were set to missing for this and consecutive periods while their records were kept for preceding periods. After further data restrictions records of more than 840 000 calves and heifers born in the years 1998 to 2007 were investigated. Mortality rates were 3.23, 2.66, 0.97, 1.92, and 9.36% for the defined periods P1-P5, respectively. For the estimation of genetic parameters a linear and a threshold sire model with the random effects herd*year*season and sire as well as the fixed effects year*month, number of dam's parity (parities >5 were set to 5), calf size and calving ease were applied. In total, the pedigree consisted of 4643 sires and 20 821 animals. Heritabilities for the linear model were low, ranging from 0.006 (P3) to 0.042 (P5). Heritabilities estimated by threshold models showed a wider range from <0.0001 (P2-P4) to 0.082 (P1). Total calf and heifer mortality is higher than stillbirth, thus, its economic impact on cattle breeding should not be neglected. A routine genetic analysis of juvenile mortality would therefore be valuable for monitoring cattle populations and for providing a basis for selection of fitter animals within dairy cattle breeding programs.

Keywords: Holstein, calves, heifers, genetic parameters, mortality

1. Introduction

Especially in dairy breeds, mortality rates of cows (e.g. McConnel *et al.*, 2008) but also stillbirth (Hansen *et al.*, 2004) and postnatal mortality rates (e.g. Norberg, 2008) have increased during the last years. This is not only relevant with regard to economical losses but also to animal health and welfare. Higher female calf or heifer mortality results in higher replacement and veterinarian costs but also in reduced possibility for selection and hence reduced genetic gain. Losses at higher ages up to first calving are even more economically important than early losses as replacement costs increase with higher ages. While genetic evaluations exist for stillbirth and longevity in cows in many countries worldwide

(www.interbull.org), to our knowledge no breeding values are available for losses of replacement animals. In the EU, information about survival is generally available due to the obligatory cattle registration (Regulation (EC) No. 1760/2000); still, there is nearly a complete lack of knowledge with respect to survival of young breeding stock between 24 or 48 hours and the start of productive life. Among the few existing studies in calf survival are works in Danish Holsteins (Hansen *et al.*, 2003) and Danish Jerseys (Norberg, 2008), reporting 6.6 and 12.5% of calves dying until an age of 180 days. For Norway, Gulliksen *et al.* (2009) reported a mortality rate of 3.7% in the first year of life in Norwegian dairy herds, while Svensson *et al.* (2006) observed 3.1% of calves dying up to an age of 90 days in south

western Swedish farms. However, in those studies only losses up to a maximum age of one year are covered. Heritability estimates for losses of replacement animals are also scarce. In the Danish studies by Hansen *et al.* (2003) and Norberg (2008) heritabilities were estimated and ranged from below 0.01 to 0.03. No estimates are however available for heifer losses or losses in the total replacement period.

In a review, Shook (1998) concluded that more genetic studies of calthood diseases and mortality were needed. Extensive knowledge and analysis of the genetics of juvenile survival are valuable for better understanding the biological background, monitoring cattle populations and possibly for providing a basis for selection. Thus, the aim of this investigation is to explore the genetic background of postnatal mortality in calves and replacement heifers in the Danish Holstein population in five periods using linear and threshold sire models. Furthermore, breeding values and genetic trends are estimated.

2. Materials and Methods

2.1. Animals

Records of all Danish Holstein heifer calves born in the years 1998 to 2007 that survived the first 24 hours after birth were extracted from the Danish Cattle Database (Danish Cattle, Skejby, Denmark). Data were restricted to herds with a minimum of 30 records and animals with complete life and calving history, single born calves and no transfer between herds. Heifers with an age at first calving lower than 550 or higher than 1200 days were discarded from analysis. Animals which were slaughtered or exported within a defined period and those being too young to theoretically reach the maximum age of the respective period were set to missing for this and consecutive periods while their records were kept for preceding periods. In total, records of 843 774 calves and heifers were investigated.

2.2. Definition of periods

Evidence from an earlier study (Hansen *et al.*, 2003) suggests that survival of calves and

heifers is different at different stages of their life and may therefore be controlled by different genes. For analysing survival data of juvenile cattle, the following periods were defined: 1-30 days (P1), 31-180 days (P2), 181-365 days (P3), 366 days-first calving (a maximum of 1200 days, P4). Additionally, the full period between 1 day after birth and first calving was defined as P5. The calves and heifers were scored as 1 if they died within the respective period and 0 otherwise, resulting in a binary data structure.

2.3. Method and Models

In previous studies on calf mortality within the first 180 days of life, those binary traits were analysed with linear rather than threshold models (Hansen *et al.*, 2003; Norberg, 2008) although the latter could result in more accurate estimates of variance components (Gianola and Foulley, 1983). The main reasons for using linear instead of threshold models are that these are generally less computationally demanding. Predicted breeding values were shown to be highly correlated in previous studies (e.g. Carlén *et al.*, 2006). Besides, genetic correlations are reported to be correct for binary traits using linear models (Heringstad *et al.*, 2005; Negussie *et al.*, 2008). For this analysis, both methodologies – a linear sire and a threshold sire model - were applied. The pedigree of the 4643 sires was traced back as far as possible, finally consisting of 20 821 animals.

Linear Sire Model: Variance components were estimated in univariate and bivariate linear sire models using the average information (AI) REML procedure (Jensen *et al.*, 1997) as implemented in the DMU software (Madsen and Jensen, 2006). Effects included in the models were as follows:

$$Y_{ijklmno} = hys_i + YM_j + Parity_k + Ease_l + Size_m + sire_n + \varepsilon_{ijklmno}$$

where $Y_{ijklmno}$ = individual observation of mortality in periods 1-5, hys_i = the random effect of herd*year*season i (herd = 1,...,3099; year = 1998,...,2007; season = 1,...,4), YM_j = the fixed effect of year*month j , $Parity_k$ = the fixed effect of the dam's parity k ($k = 1, \dots, 5$)

with parities >5 set to 5), $Ease_l$ = the fixed effect of calving ease l ($l = 1, \dots, 4$), $Size_m$ = the fixed effect of calf size m ($m = 1, \dots, 4$), $sire_n$ = the random genetic effect of sire n ($n = 1, \dots, 4643$) and $\varepsilon_{ijklmno}$ = the random residual.

Threshold sire model: Variance components were estimated by univariate threshold sire models based on the generalized linear mixed model theory and applying a binomial distribution with a logit link function using the same software as for linear models. The same effects as for the linear sire analysis were accounted for. Heritabilities were calculated using the variance of the logit link function, which implies a correction of the residual variance by the factor $\pi^2/3$ (Southey *et al.*, 2003). For further comparison of the estimated heritabilities, the formula of Dempster and Lerner (1950) was used to transform heritabilities from the observable to the underlying scale.

3. Results and Discussion

3.1. Frequencies

Of 513 868 heifers which were not exported or slaughtered or too young for being considered in the analysis, 9.36% died until first calving. The mean age at dying was 189.9 ± 263.6 days. The 10% and 25% quantiles were 8 and 13 days, respectively, the median 65 days. Mean frequencies of mortality in all periods are shown in Figure 1. Even if the percentages may not just be added up due to different data size of single periods, the mortality until 180 days seems to be slightly lower than the one reported by Hansen *et al.* (2003) in the same population. One reason therefore may be that in the previous study both sexes were considered with male calves showing a higher mortality of 7.78% until 180 days while only 5.60% of females died in the same period. Generally it should be taken into account that mortality is certainly underestimated as additionally e.g. twins and multiples or animals with incomplete information were excluded from analyses. In Austrian Fleckvieh heifers

(dual purpose Simmental), the mortality rates were distinctly lower for the period born alive to first calving (6.11%, Fuerst-Waltl and Fuerst, 2009), while in Danish Jersey heifers (Norberg, 2008) the mortality was already 12.5% up to an age of 180 days. For comparison, the average stillbirth rate (born dead or died within 24 hours, both sexes) in Danish Holsteins in the year 2008 was 9.5% for first and 5.4% for second and higher calvings, respectively (Team Avlsværddivurdering Dansk Kvæg, 2009). Thus, the more costly mortality of replacement stock is on average higher than stillbirth.

3.2. Genetic parameters

Heritabilities for mortality in the different observed periods between born alive and first calving ranged from 0.006 (P4) to 0.042 (P5) for the linear sire model (Table 1). Heritabilities estimated by bivariate analyses were similar to those estimated by univariate analyses (data not shown). Heritabilities for calf and heifer mortality in Danish Holstein were in accordance to those reported in Austrian Fleckvieh (Fuerst-Waltl and Fuerst, 2009), where the values for P1 and P2 were approximately 0.01 while heritabilities in P3 and P4 did not significantly differ from zero. They are also in the range of previous studies in Danish Holstein (Hansen *et al.*, 2003) and Jersey calves (Norberg, 2008) up to an age of 180 days. Heritabilities estimated by threshold models were distinctly higher for P1 and P5, being 0.082 and 0.076, respectively, while the values for P2-P4 were lower than 0.001. The latter finding might have been caused by the lower frequencies in these periods. The heritabilities on the underlying continuous scale calculated by the formula of Dempster and Lerner (1950) using the values on the observable scale were generally higher than the ones estimated by the threshold models. Partly they seem to be unrealistically high, presumably because of the very low incidences. Furthermore, it should be taken into account that the variances are very small for P2-P4.

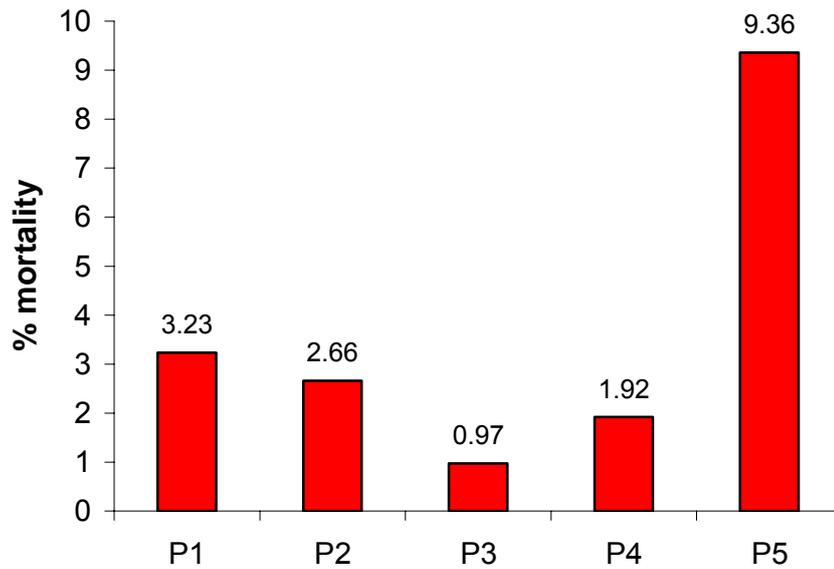


Figure 1. Mortality in % in different periods (P1 = 1-30 days; P2 = 31-180 days, P3 = 181-365 days, P4 = 366 days - first calving, and P5 = 1 day - first calving).

The genetic correlations between the different periods and P5 ranged from 0.756 (P1-P5) to 1.000 (P4-P5). As the frequencies and heritabilities for later postnatal mortality are rather low, and the genetic correlations between periods are reasonably high (data not shown), either two periods (P1 and P2+P3+P4) or the full period (P5) could be taken into account for future developments aiming at routine evaluations. The advantage of two periods is that a relatively small number of records are lost during the first 30 days due to export or slaughtering and that information on bulls is sooner available.

3.3. Breeding values and genetic trend

No clear genetic trend could be observed for P5 and the 336 bulls with birth years 1990-

2002 (Fig. 2). The relative average breeding values (positive values are favourable; mean = 100, $s = 10$ for 86 base animals = 5-7 year old bulls) varied around 100 units and were nearly identical for both estimation methods. The Spearman rank correlation for breeding values of the bulls with a minimum of 100 records ($N = 336$) estimated by linear and threshold models was 0,991. Thus, only little changes in ranking of bulls occurred depending on evaluation method. The best bull based on the linear analysis had 249 offspring and a relative breeding value of 125 and ranked forth in the threshold analysis with a relative breeding value of 129 and an average mortality rate of 3.6%. The worst bull was the same for both methods; having relative breeding values of 42 and 51 (linear and threshold, respectively) with a mortality rate of 30.7% of his 117 female offspring.

Table 1. Variance components (hys = herd*year*season, res=residual), heritabilities (h^2_{lin} estimated by linear sire models, h^2_{DL} calculated by the formula of Dempster and Lerner, 1950, h^2_{th} estimated by threshold sire models), and their standard errors (as subscripts) estimated for calf and heifer mortality in different periods (P1 = 1-30 days; P2 = 31-180 days, P3 = 181-365 days, P4 = 366 days - first calving, and P5 = 1 day - first calving).

	Linear Model			Threshold model ¹		Heritabilities		
	σ^2_{hys}	σ^2_{sire}	σ^2_{res}	σ^2_{hys}	σ^2_{sire}	h^2_{lin}	h^2_{DL}	h^2_{th}
P1	.0010 _{<.0001}	.0001 _{<.0001}	.0300 _{<.0001}	.6159 _{.0140}	.0815 _{.0096}	0.017	0.102	0.082
P2	.0009 _{<.0001}	.0001 _{<.0001}	.0249 _{<.0001}	<.0001 _{.0060}	<.0001 _{.0001}	0.022	0.151	<0.001
P3	.0002 _{.0005}	<.0001 _{<.0001}	.0094 _{<.0001}	<.0001 _{.0141}	<.0001 _{.0002}	0.009	0.127	<0.001
P4	.0005 _{<.0001}	<.0001 _{<.0001}	.0183 _{<.0001}	<.0001 _{.0128}	<.0001 _{.0003}	0.006	0.052	<0.001
P5	.0051 _{<.0001}	.0009 _{<.0001}	.0789 _{.0002}	.4968 _{.0099}	.0731 _{.0074}	0.042	0.128	0.076

¹ Residual variance = 1, for calculation of heritabilities correction of the residual variance by the factor $\pi^2/3$

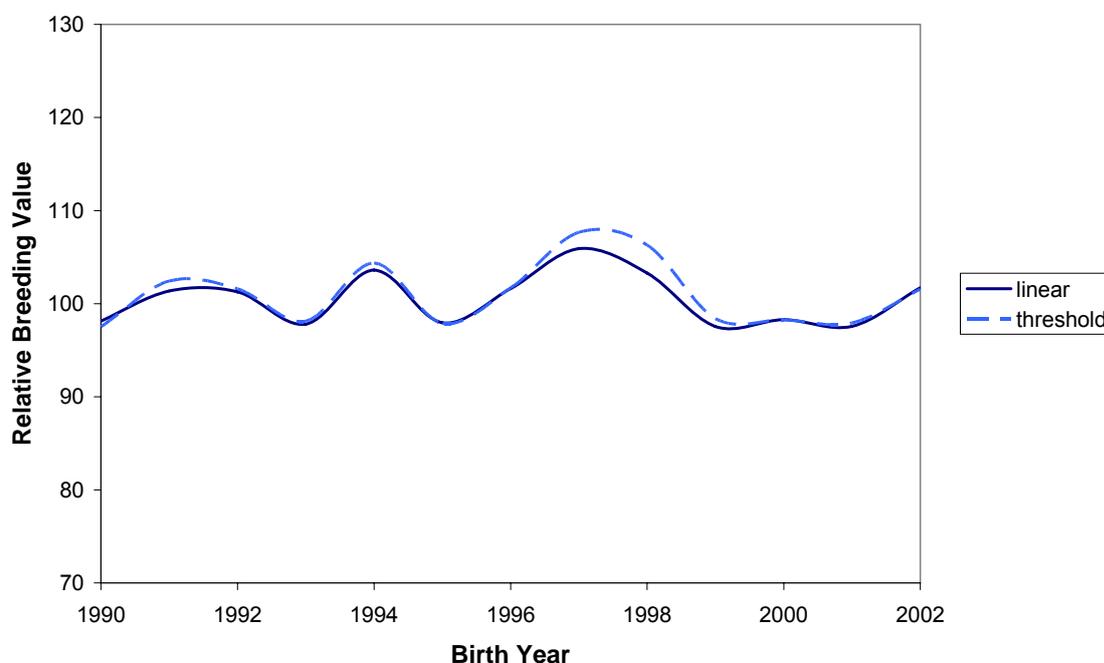


Figure 2. Genetic trend in breeding values for Danish Holstein bulls with a minimum of 100 records (N=336, mean=100, s=10 points; positive values are favourable) for losses between 1 day after birth and first calving (P5) and the linear and threshold sire model.

4. Conclusions

Calf and heifer mortality may have seemed to be too low for being considered in breeding programs so far. However, with a mortality of 9.36% of single born females until first calving or a maximum age of 1200 days in Danish Holstein, the percentage of mortality is higher than the stillbirth rate. The economic impact on cattle breeding and ethical issues should not be

neglected with regard to this trait. Genetically improving this trait is practicable as long as genetic and phenotypic variation is reasonably high. Based on the results obtained in this study selection against higher postnatal mortality should be possible. A routine genetic evaluation would be valuable for monitoring cattle populations and for providing a basis for selection of fitter animals in the Danish Holstein cattle breeding program.

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