

# Genetic Analysis of Calf Survival and Health in a Population of Dairy Calves in New York State

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## Introduction

Genetic selection for improved health and longevity is a major goal of dairy cattle breeders. However, little attention has been paid to the genetic components of calf and heifer survival. Death of youngstock represents an on-going concern among breeders of dairy cattle in Canada and the United States. However, the only genetic evaluations for calf mortality conducted in these countries are for the first 24 and 48 hours of life, respectively. This trait is also known as ‘stillbirth’. Calf and heifer losses in the United States were recently estimated as 9.6% mortality each year (NAHMS, 2007). Of these heifer losses, 7.8% occurred in preweaned heifers and 1.8% in heifers from weaning age to calving. The effects of calf and heifer mortality are widespread from an economic, genetic and animal welfare point of view. Costs include the loss in value of the calf, and the genetic loss, which is rather hard to quantify. To date, few genetic studies on calf mortality have been carried out, and for the most part these efforts have examined primarily preweaning mortality (Cundiff et al. (1986); Erf et al. (1990); Hansen et al. (2003)).

Previous research has shown that the most common causes of preweaning mortality are gastrointestinal diseases. The most common cause of post-weaning mortality is undifferentiated bovine respiratory disease (BRD). These problems are a very costly concern for dairy producers, as well as an important issue in terms of animal welfare. Furthermore, preweaning diseases have been associated with increased risk of morbidity later in the rearing period, and are likely to have impacts on the mature life of the animal, such as increased age at first calving and decreased lifetime profitability (Walter-Toews et al. (1986)). For instance, it has been shown that heifers treated for BRD within 90 days of birth were more likely to die after that time, as compared to untreated calves (Walter-Toews et al. (1986)). Also, calves contracting navel-joint illness in early calthood have exhibited significantly shorter herd longevity patterns, compared to calves receiving no treatment (Britney et al. (1984)). In addition, calthood diarrhea has been associated with lowered first lactation milk production (Svensson and Hultgren (2008)). The objective of this study was to estimate the genetic parameters of calf survival and health for a population of Holstein calves from New York (NY) State.

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## Material and methods

**Heifer rearing facility.** The commercial heifer raising facility that participated in this investigation is located in western New York. Annually, this farm raises approximately 3,000 heifers to varying target ages, based on the contractual arrangement between the facility and the farm of origin. Heifer calves typically arrive at the facility in the first 2-3 days of life. Upon arrival, calves are weighed, measured, and identified. Also, calves are sampled for serum total protein (TP) levels to provide a basis for calf survival contractual warranties. No guarantees on survival are made for the first 12 days of life, or if the heifer calf enters the facility with a TP score of  $\leq 53$ g/L. If heifers enter the facility with a TP score of 54 to 59 g/L, the heifer rearing farm shares any treatment or death losses with the herd of origin. Calves with a TP score of 60 g/L or higher, the facility refunds all fees and medication for any calf that dies. Calves were reared in individual pens in barns of 48 calves, and were weaned at approximately 7 weeks of age, during the study period.

**Data.** Data were recorded for 7,372 heifer calves at a commercial rearing facility in NY, from arrival at 1 to 7 days of age for the duration of stay at the facility. Performance and disease up to weaning, and mortality before and after weaning, were recorded. Analyzed data were limited to daughters of sires with at least 10 calves originating from farms which had sent at least 5 calves to be raised at the facility.

**Statistical analyses.** Calves from 264 sires and 36 herds were studied using survival analysis and two-trait sire model (survival from arrival to weaning and from weaning to exit) for calf survival and 3-trait sire model for calf health (preweaning undifferentiated respiratory disease (BRD), umbilical diseases (UMB), and bloat(BLT)). For survival analysis, the length of a calf's life was defined as time (in days) from arrival at the heifer raising farm until death; otherwise, the record was censored if the calf has left the farm to return to its source farm of origin. A lifetime record was considered completed (uncensored) if the calf received a termination code (i.e., death), indicating that the calf was either culled or died for any reason.

The general model (survival and linear models) included the fixed variables of arrival and weaning weight, total protein, season of birth, calving ease score. The random effect included the effect of herd-year class where herd was the source farm of origin. The Survival Kit software Version 5.1 (Ducrocq and Solkner (1998)) was used for the survival analysis, and DMU software package (Madsen and Jensen (2006)) was used for the multiple-trait linear models.

## Results and Discussion

**Survival Analysis.** Table 1 shows the relative mortality risks of the main effects included in the model. Results from the survival analysis showed an increased risk of mortality for calves with very light or heavy weight at arrival, low serum total protein, low weaning weight and for calves born in a difficult parturition. Weaning weight class had the greatest influence on mortality risk. The relative mortality risk for heifers who weighed between 75-111 lbs at weaning was 3.17 times greater than a heifer who weaned at an average weight of 131-150 lbs. Conversely, heifers who weaned in the heaviest weaning weight class (176-278 lbs) were approximately 40% more likely to survive than heifers who weaned in the average

weaning weight class. The heritability from the survival analysis was 0.063. This value comparable to lifetime survival heritability routinely used for genetic evaluations worldwide for the Holstein breed, ranging from 0.025 to 0.16 (Interbull (2010)).

**Table 1. Risk ratio of mortality<sup>s</sup> for calving ease (CE), total protein (TP), season (SEA), no. of disease treatments (DIS), arrival (AW) and weaning weight (WW).**

Class <sup>y</sup>	CE	TP	SEA	DIS	AW	WW
1	1	1.17	1	1	1.15	3.17
2	1.14	1.11	0.8	0.92	1.12	1.70
3	1.6	1	1.04	1.12	1	1
4	1.57	0.92	0.98	1.55	1.16	0.77
5					1.49	0.61

<sup>s</sup>Values greater or lower than 1 (reference class) indicate greater or lower mortality risk, respectively, associated with that factor.

<sup>y</sup>CE: 1 = unobserved/unassisted, 2 = easy pull, 3 = hard pull and 4 = excessive force or surgery needed

TP: 1 = 30-49 g/L; 2 = 50-59 g/L; 3 = 60-69 g/L; 4 = 70-80 g/L

SEA: 1 = January to March, 2 = April to June, 3 = July to September, 4 = October to December

DIS: 1 = no disease experienced, 2 = 1 disease occurrence, 3 = 2 disease occurrences, 4 = 3 or greater diseases

AW: 1 = 49-74 lbs; 2 = 75-83 lbs; 3 = 84-92 lbs; 4 = 93-101 lbs; 5 = 102 lbs and above

WW: 1 = 75-110 lbs; 2 = 111-130 lbs; 3 = 131-150 lbs; 4 = 151-175 lbs; 5 = 176-278 lbs

**Linear model for survival traits.** The first survival trait (survival from arrival to weaning) had genetic and herd-year variance close to zero, resulting in a very low heritability (0.001). However, the second survival trait, survival from weaning to exit from the rearing facility, had higher genetic variance and heritability (0.036). Additionally, the two survival traits were favorably genetically correlated at 0.58. The low heritability for the first survival trait is likely due to the lower than average mortality in the preweaning period at this facility (2.7% vs. an average mortality of 7.8% as cited above). The low rate of mortality in the preweaning period is most likely due to the incentives in saving costs when TP was over a given threshold. Hansen et al. (2003) estimated genetic parameters of postnatal mortality in Danish Holstein. One of the binary traits considered by these authors was D1-180, with this interval indicating the period of risk of mortality in days after birth (Hansen et al. (2003)). The heritability for this trait was much lower (0.0072) than the findings of the current study. A more recent study also estimated genetic parameters of mortality in a population of Danish Holstein calves (Fuerst-Waltl and Sørensen (2009)). Similar to the current study, heritabilities for survival were lower (< 0.025) in early life and increased (0.042) as a mature heifer (Fuerst-Waltl and Sørensen (2009))

**Linear model for health traits.** During the preweaning period, 38.4%, 6.2% and 4.4% of calves experienced BRD, UMB and BLT, respectively. Table 2 includes genetic parameters and residual correlations for the three health traits. The heritability estimate for BRD was higher than the previously estimated heritability (0.05) for this disease in Norwegian Red Holstein calves (Heringstad et al. (2008)). To the knowledge of the authors, heritabilities for umbilical disease and bloat in dairy calves have not been previously reported in the literature. Correlations between UMB and BRD, as well as between UMB and BLT were both estimated to be close to zero. However, the genetic correlation between BRD and BLT was positive and moderately strong (0.62). This positive correlation between the two traits could

be due to the adverse impact BRD may have on the vagus nerve. Calves that have suffered BRD intermittently develop BLT from damage to the thoracic portion of the vagus nerve or enlarged thoracic lymph nodes that cause failure of eructation, problems swallowing and compromised forestomach motility (Divers and Peek (2008)).

**Table 2. Estimates of genetic parameters<sup>&</sup> for preweaning undifferentiated respiratory disease (BRD), umbilical diseases (UMB), and bloat(BLT).**

Trait	BRD	BLT	UMB
BRD	0.09	0.62	-0.03
BLT	0.01	0.04	-0.07
UMB	-0.11	-0.01	0.14

<sup>&</sup>Heritabilities on diagonal, genetic correlations above diagonal and residual below diagonal

## Conclusion

Results suggest that there was significant genetic variance among Holstein sires for calf survival from weaning to the growing period, and for calf health during the preweaning period. Heritabilities of the calf survival and health traits were low. However, the heritability for BRD was higher in the current study than has previously been reported in dairy calves. The genetic correlation between BRD and BLT was moderately high, likely due to the negative effect BRD may have on the vagus nerve, consequently influencing the occurrence of BLT. Although the heritabilities for survival reported in the present study are low, genetic variability is sufficient for selection to be implemented, if recording of survival prior to 1st lactation was available on a large number of animals.

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