Genomic predictions for dairy calf health traits

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Abstract

Healthy calves are important to the productivity and welfare of dairy herds. They are potential herd replacements as well as a source of livestock trading income. Further, healthy calves are important to the continuous improvement of animal welfare that is valued by farmers and consumers. In our dataset of ~20,000 calves with health records, the prevalence of stillbirth, preweaning mortality and scours was 4%, 2% and 6% respectively suggesting that there are opportunities to improve calf health. The aim of this study was to estimate variance components for novel calf traits and gather the perspectives of farmers about the relative importance of these traits. Univariate linear models that included a genomic relationship matrix were used to estimate variance components for stillbirth, preweaning mortality, scours, respiratory disease and calf vitality where heritability (h^2) estimates ranged from 1% to 11% depending on the trait. Calf vitality is a new, subjectively-scored trait where farmers describe calves on a scale from A (vigorous) to E (dead). The models included herd-year-season, sex, parity group and calving ease as fixed effects and these were found to be significant for most breed and trait combinations. Our survey found that calf traits were valued by farmers similarly to cow survival. They preferred new traits to be published separately, rather than in multi-trait indexes. As genetic variation in several calf health traits was measured and the value to farmers has been tested, we conclude that there is an opportunity to introduce new traits into routine evaluations that target genetic gain for calf health.

Key words: Calf health, stillbirth, vitality, breeding values

Introduction

Healthy calves are an important part of a dairy herd's natural cycle. Heifer calves become replacements that enable a herd to sustain or grow its size. Replacement heifers are costly to rear. In fact, Boulton et al. (2017) reported that it takes 1.5 lactations to repay the costs associated with the heifer rearing period. As morbidity increases, the costs associated with extra labour and treatments are expected to rise. As mortality rises, the total costs are spread over fewer surviving animals. There are economic, productivity and welfare benefits arising from healthier calves.

Compared to cow health traits, the genetic contribution to improved calf health and lower mortality is a relatively new area of research but it is a logical progression to the successful genetic improvement of traits like udder health (Abdelsayed et al., 2017) and fertility (Ooi et al., 2023) in cows and the number of stillborn calves (Cole et al., 2007).

This paper reports variance components for calf health traits and industry perspectives about trait expression and their relative importance for breeding purposes.

Materials and Methods

Health records for 19,824 calves were collected from ~50 Australian dairy herds as previously described by the authors (Axford et al., 2025a). Calf health events and deaths were coded as binary traits for analysis as 0 or 100 for each trait, where sick or dead was coded as 0 and healthy was 100. The traits were stillbirth (SB) (dead at birth or shortly thereafter), pre-weaning mortality (PWM) (born alive but died before weaning, estimated to be day 84), Health (presence of any health event), Scours (presence of any diarrhea event), Resp (presence of any respiratory disease). Vitality was a subjectively scored trait with 5 levels where A was a vigorous calf, B was a good calf, C was an average calf, D was a dull calf that lacked vigour and E was a dead calf.

Genetic parameters were estimated using univariate linear animal models that included a genomic relationship matrix (GRM) and fixed effects in ASReml 4.2 (Gilmour et al., 2022). The fixed effects were calving ease (CE) with 3 levels (no assistance, slight assistance and moderate/high assistance), dam parity at calving where parity was divided into 2 levels (parity 1 and parity 2+), sex of the calf and Herd Year Season (HYS) where season was divided into 2 levels (1 is January-June, and 2 is July-December). Calving ease was dropped in Jersey models because there were few cases of dystocia recorded in the dataset. Due to data limitations, direct-effect models were used. Mating data for dams and further detailed calf phenotypes were unavailable so gestation length, birth weight and colostrum were not included in the model. Animals were used in the EBV predictions if they were genotyped, sire by a recorded, AI sire and there was a minimum of 5 records in the HYS.

The general form of the model used to estimate variance components and genomic breeding values for each trait was as follows:

$$y = Xb + Zu + e$$

where **y** is the vector of the phenotypic records for each trait (SB, PWM, Health, Scours, Resp, Vitality); **b** is the vector of the fixed effects including HYS, parity group, CE for Holstein only, and sex; **u** is the vector of the random additive genetic effect and **e** is the vector of random residual effects; **X** and **Z** are design matrices that relate phenotypes to their corresponding fixed effects (**b**) and random additive genetic effects (**u**). It is assumed that

$$var(u) = GRM\sigma_u^2,\ var(e) = I\sigma_e^2$$

where σ_u^2 is the additive genetic variance, σ_e^2 is the residual variance, and **I** is an identity matrix.

This model was expanded to include two traits and was used to check the genetic correlation between calf traits of interest. Further, to test the relationship with cow traits, approximate genetic correlations were calculated using Peason correlations and then adjusted for reliabilities as we described earlier (Axford et al., 2025a).

The reliability of prediction for all traits was calculated using the standard errors of EBV, as follows:

$$reliability = 1 - \frac{PEV_i}{\sigma_u^2}$$

where, PEVi is the prediction error variance (squared error of the EBVi for animal i in the pedigree) and σ_u^2 is the estimated genetic variance in the prediction model.

To gather the perspectives of farmers and service providers about the importance of calf traits in breeding programs, an online survey was conducted between October 2023 and June 2024 using SurveyMonkey (https://uk.surveymonkey.com/). Respondents were asked about their business and herd demographics, calf record keeping, trait preferences and opinions about the expression of genetic traits. A total of 109 responses were received, of which 66% were farmers with further demographic details available in Axford et al. (2025b).

Results & Discussion

Disease prevalence

Table 1 reports the prevalence of morbidity and mortality for Holstein and Jersey calves. The prevalence of SB was lower (4% compared to almost 7%) to our earlier Australian study of a larger national dataset (Axford et al., 2024) and the prevalence of PWM was similar (~2%). This dataset was more recent (calves born 2020-2023) and involved farmers that agreed to participate in this calf research who may prioritise calf health and recording which could explain the lower mortality rate. As expected, scours was the most commonly recorded disease, followed by respiratory disease. Few cases of other health events were recorded, for example miscellaneous (96 cases), deformities (26 cases), and pink eye (20 cases). Stillbirth explained five times more deaths than scours and respiratory disease combined, suggesting that this was a major calf welfare issue on participating dairy farms.

The novel trait of calf vitality had fewer records (n=3,651) as roughly half of the herds routinely recorded this trait. Twenty-one percent of recorded calves were scored as A - “vigorous”, 28% B - “good”, 26% C – “average”, 6% D – “dull”, and 19% E – “dead”. Many herds (40%) only recorded vitality scores for dead calves which explains the high percentage of “E” scores in the dataset.

Table 1: Across herd prevalence of morbidity and mortality in Holstein and Jersey calves, expressed as a percent.

	Holstein (n=11,182) Overall mean % (SE)	Jersey (n=949) Overall mean % (SE)
Pre-Weaning Mortality	2.0 (0.1)	2.7 (0.5)
Respiratory disease (lived and died)	0.4 (0.1)	0.1 (0.1)
Respiratory disease (died)	0.1 (0.0)	0.0 (0.0)
Scours (lived and died)	5.9 (0.2)	4.8 (0.7)
Scours (died)	1.0 (0.1)	1.5 (0.4)
Stillbirth	4.1 (0.2)	4.8 (0.7)

Genetic parameters

After editing to include animals with a genotype, recorded AI sire and at least 5 records per HYS, there were 7,504-10,513 records for Scours, SB and PWM. HYS were removed if the Vitality records included only calves scored as E – “dead” leaving 1,693 Vitality records remaining. The heritability ranged between 1-11% depending on the trait. Either low disease prevalence, smaller sample size or a combination of the two meant that variance components for Jersey cattle could not be estimated.

Table 2: Genetic variance (VarG), phenotypic variance (VarP), and heritability (h^2) estimates for calf health traits in Holstein cattle from univariate linear models.

Trait	VarG (SE)	VarP (SE)	h^2 (SE)
Holstein			
PWM	0.43 (0.38)	76.91 (1.07)	0.01 (0.01)
Scours	17.48 (4.05)	390.25 (6.44)	0.04 (0.01)
Stillbirth	5.68 (2.07)	230.86 (3.59)	0.03 (0.01)
Vitality	44.66 (15.16)	392.69 (13.82)	0.11 (0.04)

Stillbirth, as the major cause of early life mortality, had a heritability estimate of 4% (for the direct effect). At least in Holstein cattle, selecting for calving ease contributes to lower stillbirth rates as the genetic correlation is favourable (0.7 between stillbirth direct and calving ease, Axford et al., 2024). However, other significant effects, such as parity, are uncontrollable as there will always be heifer calvings. Therefore, adding stillbirth into sire selection protocols is an important step in improving calf welfare.

Calf scours was the most prevalent disease reported in this study and others (Neupane et al., 2021, Urie et al., 2018). As is common for health traits, including mastitis (Abdelsayed et al., 2017), the proportion of variance explained by genetics is low. In our case, the heritability of scours was 4% and this was similar to a recent Canadian study (4-6%, Lynch et al., 2024). The mean sire EBV for scours was 0.05

(±1.86 SD) as shown in Figure 1 and mean reliability was 0.27 (±0.11 SD).

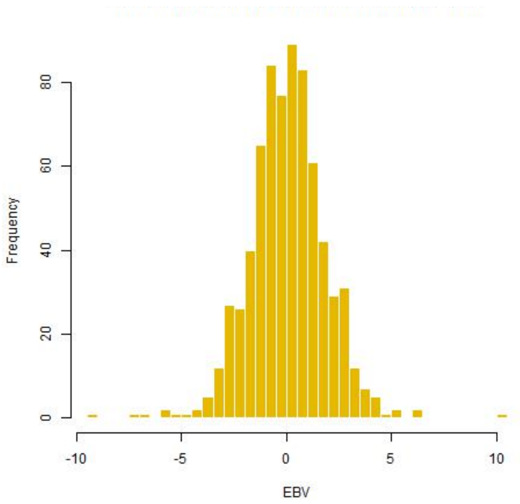

Figure 1. Distribution of EBV for scours in Holstein sires

Scours is a major contributor to PWM. About half of the calves that were born alive but died before weaning were recorded as having died from scours in this study. Interestingly, the genetic correlation between the two was only 0.18. PWM had a very low heritability estimate of only 1% in this study, which is lower than the 9% reported by Zhang et al. (2022) with a similar model. Despite significant efforts to obtain a dataset of sufficient size, traits with low prevalence are especially challenging in genetic analysis and emphasise the need for more systematic approaches to data recording, at scale, such as automatic milk feeders and calf health sensors.

Vitality was an experimental trait that is thought to reflect both health and behavioural characteristics and the interaction between the two. For example, a calf that is highly motivated to drink more milk may achieve higher intakes that promote good health. Despite having the least records, the heritability estimate for vitality was highest (11%). It is likely that the multiple levels partially explain the higher heritability compared to the remaining calf traits. There was a moderate relationship between vitality and scours (genetic correlation 0.46) suggesting that the trait of vitality is capturing different information compared to scours alone. There were no significant genetic correlations between vitality and traits of the cow, such as Cow Survival, Likeability (another subjectively scored trait) and the Balanced Performance Index (BPI, national breeding index).

Survey

From this research, it is clear that genetic variation from calf health traits can be measured and EBVs could be incorporated into routine genetic evaluation. However, the availability of EBVs is not enough to instigate practice-change on-farm. As genetic selection decisions are the domain of farmers, their opinions are important. On a preference scale of 1-5 where 5 was most important, the mean score ranged between 3.5 (±1.1) for heifer survival from weaning to first calving and 3.8 (±1.1) for calf health, as shown in Figure 2. These scores were lower than production traits but higher than scores for new traits such as feed saved and heat tolerance. Calf trait scores were similar to traits that are included in BPI, such as cow survival, mastitis and type traits.

With regard to the expression of calf traits, respondents preferred that calf traits were presented so that higher ABVs reflect healthier calves (88%) and preferred traits to be presented separately rather than in a multi-trait index. We suggest that the preference for single trait presentation is related to the desire for transparency when new traits are first released.

Conclusions

The genetic selection for calf traits is a natural extension to the highly successful genetic improvement of traits affecting the productive life of cows. Like many other health traits, the calf traits we studied are characterised by low heritability yet are highly valued by farmers. There are opportunities to improve the welfare of calves and lower the costs associated with rearing replacements by adding calf health traits to routine genetic evaluations.

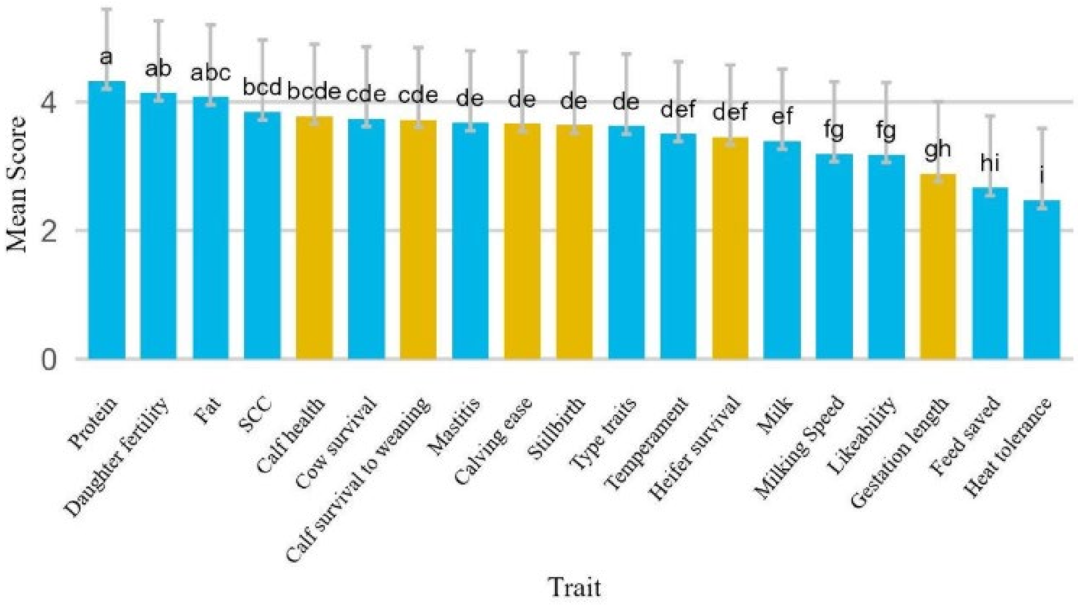

Figure 2. Weighted mean scores (bars) and standard error (whiskers) for calf (yellow) and cow (blue) trait preferences where 5 is most important and 1 is least important. Bars with no common letters identify scores that are significantly different (p<0.05).

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