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Genomic evaluation of dairy heifer livability

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ABSTRACT

Differences in breeds and sire lines suggest the presence of a genetic component for heifer livability (HLIV). Genomic evaluation for this trait can increase profitability and improve animal health and welfare. Evaluations for HLIV were examined from 3,362,499 calf data records from heifers of all breeds born from 2009 to 2016. Data were obtained from the national cooperator database maintained by the Council on Dairy Cattle Breeding (https://www.uscdcb.com/). The total number of deaths reported was 134,753 (4.01%), which included herds with death loss between 1.5 and 25.5%. Age at death was evaluated and ranged from >2 d of age until the heifer left the herd, with a maximum of 18 mo of age. Records were not included until 3 yr after the birthdate so that live status of contemporaries could be confirmed by a calving date for those animals. Deaths observed until 2 d after birth were considered to be a stillbirth rather than a failure of HLIV. The scale used for analysis of HLIV was 0 (died) or 100 (live), and the heritability estimate was 0.7% based on sire model with restricted maximum likelihood estimation. Genomic predicted transmitting abilities for Holstein ranged from −1.6% to +1.6% with a standard deviation of 0.5%, and genomic predicted transmitting abilities for Jersey ranged from −0.5% to +0.5% with a standard deviation of 0.2%. The mean overall death loss was about 4%. Reliabilities of genomic predictions for young animals averaged 46% for Holsteins and 30% for Jerseys, and corresponding traditional parent average reliabilities averaged 16% and 12%, respectively. Correlations of HLIV were 0.44 with productive life, 0.18 to 0.22 with yield traits, and 0.29 with early first calving on proven Holstein bulls. The HLIV trait had a favorable genetic trend in recent years, likely because of the indirect selection associated with the correlated traits. The trait HLIV should receive 1% of emphasis on the Lifetime Net Merit index, resulting in economic progress worth $50,000/yr. By encouraging more comprehensive recording on calf mortality, the reliabilities of genetic predictions could increase significantly.
Key words: animal welfare, economics, genomic selection, heifer livability

INTRODUCTION

Heifer mortality is a major issue related to profitability and management in dairy farms. Raising replacement heifers ranks as the second largest cost on dairy farms after the feed and forage cost for cows (Chamberlain, 2012). Digestive and respiratory diseases comprise the majority of heifer deaths. Preweaning losses in dairy calves average 6.4%, with higher rates in small herds and lower rates in large herds. Postweaning losses, by comparison, average only 1.9% and are more similar across herd sizes. It has been estimated that 56% of all preweaned calf deaths were due to digestive problems, whereas 47% of postweaned calf deaths were associated with respiratory problems (NAHMS, 2014). Other studies also report that the major causes are gastrointestinal and respiratory diseases (Gonzalez-Peña et al., 2019, 2020).

Heifer mortality is associated with economic loss and is an important animal welfare issue (Gulliksen et al., 2009). These losses also limit selection opportunity, resulting in reduced genetic gain. Although US genetic evaluation in dairy cattle includes still birth (loss within 48 h of birth) and cow livability, little information is available on heifer livability (**HLIV**). There is currently a gap in knowledge of heifer survival from 48 h to start of productive life (Fuerst-Waltl and Sørensen, 2010).

Differences among breeds and sires suggest a genetic component of HLIV (Koch et al., 1994). Previous studies have identified low levels of heritability associated with calf mortality (or survival), ranging from 0.001 to 0.042 in Danish Holsteins (**HO**; Hansen et al., 2003; Fuerst-Waltl and Sørensen, 2010), 0.007 to 0.009 in Israeli HO (Weller et al., 2021), 0.001 to 0.063 in US HO (Henderson et al., 2011), 0.01 (SE = 0.0008) in UK HO (Pritchard et al., 2013), and 0.005 (SE = 0.0008) to 0.06 (SE = 0.003) in US dairy heifers (VanRaden

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et al., 2016; Vukasinovic et al., 2017). Together with good management practices, this low level of genetic component can be exploited in breeding programs to reduce heifer mortality. The objectives of this study were to develop a genomic evaluation system for HLIV and to estimate genetic correlations among this trait and traits already included in US dairy genetic evaluation system.

MATERIALS AND METHODS

Study Population and Phenotypes

Heifer livability was examined from the total of 3,362,499 calf data records for heifers of all breeds born from the years 2009 to 2016 from the national cooperator database maintained by the Council on Dairy Cattle Breeding (CDCB, https://www.uscdcb.com/). The main breeds included were 89.2% HO followed by 4.9% Jerseys (**JE**), 4.7% crossbreds, and 1.2% other breeds. Detailed breed information is presented in Table 1. More than 90% of usable records originated from Dairy Records Management Systems (https://www.drms.org/).

This study population included only herds with death loss between 1.5 and 25.5% to control the data quality. Owners can report one of several different codes such as "sold/transferred to another dairy alive" or "sold because of reproductive problems" or "sold for any other reason" when a calf leaves the herd or can report that the calf died or was killed on the dairy farm. The edited data included only records for heifer calves that remained on the dairy until first lactation or died or were killed by 18 mo of age. Records were not included until 3 yr after the birthdate so that live status of contemporaries could be confirmed by a calving date. Stillbirths, which included calves born dead or that died within 48 h of birth, were not included in this analysis because they were evaluated as a separate trait. The binary scale used for analysis in this study was 0 (died or killed) or 100 (live).

Table 1. Summary of different breeds used in heifer livability analysis

Breed	Number of calves	Percentage
Holstein	2,997,612	89.15
Jersey	165,651	4.93
Crossbred	159,592	4.75
Brown Swiss	19,605	0.58
Ayrshire	7,033	0.21
Guernsey	4,308	0.13
Milking Shorthorn	2,984	0.09
Red Holstein	2,631	0.08
All other breeds	3,083	0.09

As heifer mortality is affected by age at the first calving and parity of dam (Hansen et al., 2003), age of dam and parity of dam were included as fixed effects in this analysis. Embryo transfer heifers were recorded as a separate group as there was no information on the biological dams. Parity groups were separated from first to seventh parity dams, and more than seventh parity dams were grouped into a final class. First parity dams were further divided into 3 age groups (less than 22 mo, between 22 and 25 mo, and greater than 25 mo) because calves from dams with low calving age had significantly higher mortality (Hansen et al., 2003; Hutchison et al., 2017). Detailed information about parity groups of dams is given in Table 2.

Heritability Estimation

Heritability was estimated from a subset of 3,175,916 (94%) of the above phenotypes that were sired by the 9,961 HO bulls that had the most daughters observed. The use of a sire model allowed matrix inversion and standard error calculation in REML (VanRaden, 1986) with the following model:

$$\text{HLIV} = \text{HYS} + \text{group} + \text{sire} + e,$$

where HLIV is a binary trait scored 0 or 100, HYS is the fixed effect of herd-year-season of birth of the heifer, group is the fixed effect of sire's birth year group, sire is the random additive genetic effect of sire within group, and e is the residual error. The model included 7 sire birth year groups and a numerator relationship matrix among the sires. The sire component of variance $\left(\sigma_s^2\right)$ was multiplied by 4 and divided by the sum of the sire variance plus the error variance $\left(\sigma_e^2\right)$ to obtain the REML estimate of heritability, $\hat{h}^2 = \left(\frac{4 \times \hat{\sigma}_s^2}{\hat{\sigma}_s^2 + \hat{\sigma}_e^2}\right)$.

Table 2. Groups of calves based on number of parities and their fixed effects

Parity of dam (age of dam in months)	Number of calves (%)	Fixed effect
1 (<22)	222,734 (6.62)	−0.329
1 (22–25)	558,750 (16.62)	−0.048
1 (>25)	288,621 (8.58)	0.274
2	786,188 (23.38)	−0.353
3	517,755 (15.4)	−0.369
4	292,844 (8.71)	−0.272
5	141,460 (4.21)	−0.252
6	59,756 (1.78)	0.030
7	22,838 (0.68)	−0.075
8 (parity >7)	12,407 (0.37)	−0.019
9 (embryo transfer)	68,019 (2.02)	0.268
Missing information	391,127 (11.63)	1.391

Traditional PTA

Predicted transmitting abilities for HLIV were calculated using the following animal model:

$$\text{HLIV} = \text{HYS} + \text{PG} + a + e,$$

where PG is the fixed effect of the parity group of the dam and a is the random additive genetic effect of the animal. Animal and residual error effects were distributed as $N\left(0, \mathbf{A}\sigma_a^2\right)$ and $N\left(0, \mathbf{I}\sigma_e^2\right)$, respectively, where $\mathbf{A}$ is the numerator relationship matrix, $\mathbf{I}$ is an identity matrix, σ_a^2 is the additive genetic variance, and σ_e^2 is the residual variance. Traditional (pedigree-based) PTA were estimated using a model similar to those used for routine national genetic evaluations (VanRaden et al., 2014). Because the threshold model did not converge, analysis was done using linear model. All animals from the study population were used in traditional PTA estimation. Similar models for other traits analyzed included breed in the definition of unknown parent groups, but numbers of other breed phenotypes for HLIV were low and heritability was too small to justify estimating separate unknown parent groups. Those separate effects could be introduced in the future when the data includes more years and more records from other breeds.

Genomic PTA

Genomic evaluations were conducted using 79,294 SNPs used in routine US genomic evaluations. These SNPs were selected based on large effect high density and sequenced SNPs along with gene tests and causal alleles within lethal haplotypes (Wiggans et al., 2019). Animals were genotyped using 39 different arrays and were imputed to 79,294 markers with varying accuracy depending on array density and breed using Findhap version 3 (VanRaden et al., 2011). There were 2,922,969 genotyped HO and 371,275 genotyped JE used in this analysis and in the genomic predictions for all traits in the national evaluation. Only 8,494 HO and 1,272 JE animals contributed to the HLIV reference population, which requires traditional reliabilities to be 3 percentage points higher than parent average reliability. That population size compares to approximately 1 million HO used in the genomic reference for milk yield using the same reliability edit. Genomic PTA for HLIV were estimated only for HO and JE because too few reference animals had reliable phenotypic data to provide accurate genomic predictions in other breeds.

Allele substitution effects for the 79,294 SNPs used in the December 2019 US genetic evaluation were estimated from deregressed traditional PTA. An infinitesimal model with heavy-tailed priors was used, where smaller effects are regressed further toward 0 and markers with larger effects are regressed less to account for a nonnormal distribution of marker effects (VanRaden, 2008). Genomic PTA were calculated by combining 3 terms in an index: (1) direct genomic prediction, (2) parent average computed from the subset of genotyped ancestors using traditional relationships, and (3) published parent average (VanRaden et al., 2009; de Oliveira et al., 2018).

Genetic correlations were approximated as the product-moment correlations among genomic PTA for traits using the CORR procedure in SAS version 9.4 (SAS Institute Inc.). The correlations were calculated from 237 HO and 195 JE bulls born from 2010 to 2014 with ≥70% and ≥50% reliability, respectively, for HLIV. Average reliabilities for HLIV were 75% for HO and 56% for JE bulls, whereas average reliabilities for most other traits were near 99%. Correlations were classified high (>0.6), moderate (0.2–0.6), and low (<0.2).

Economics

Relative value for HLIV was computed as standard deviation (**SD**) of transmitting ability times economic value. The average cost of heifer loss was estimated to be $500. The absolute economic values times SD for all other traits in net merit sum to $377 (VanRaden et al., 2018). The emphasis of HLIV on Lifetime Net Merit index (**NM$**) is calculated from its value times its SD divided by the sum across all traits of their values times SD.

RESULTS AND DISCUSSION

Heifer Mortality

The total number of deaths reported during first 18 mo of life for heifers was 134,753 (4.01%) for all breeds. The losses were higher in JE (5.06%) than HO (3.92%). Figure 1 shows monthly loss of calves in the first 18 mo, and differences between JE and HO in those months were shown in Supplemental Figure S1 (https://doi.org/10.6084/m9.figshare.14538579.v1, Neupane, 2021). The average age of heifer death was 144 d, and the first 2 mo had higher proportions of heifer deaths as compared with other months.

The total heifer loss was less than the reported average loss of 8.3% (NAHMS, 2014) because of potential underreporting of losses in DHI data, better management in DHI herds, or recent improvements in calf management and calving ease. The stillbirths, which account for 5.6% of calf loss in dairy calves, were excluded from

calf losses in the current study and by NAHMS (2014). Heifer mortality has been reported to be highest in first month of life (Pritchard et al., 2013). Because many death losses and their causes are unknown, death loss categorization scheme will be highly helpful to resolve these issues (Lombard et al., 2019).

Heritability

Variance components (REML estimates ± SD) were 0.54 ± 0.05 for sire variance and 304.42 ± 0.33 for error variance, resulting in an estimated heritability of 0.0072 ± 0.0007. This estimate is higher than the 0.005 heritability reported by VanRaden et al. (2016) that also used sire model REML. The heritability estimate likely increased because new edits excluded data with incomplete reporting from earlier years and because many new records were added in recent years. The genetic and genomic evaluations used the previous lower estimate rather than the new higher estimate of heritability.

The low heritability estimate of HLIV was similar to those found in studies from different countries (Hansen et al., 2003; Fuerst-Waltl and Sørensen, 2010; Henderson et al., 2011; Pritchard et al., 2013; Vukasinovic et al., 2017). A recent study from Weller et al. (2021) observed similar heritability of 0.007 for calf survival from birth to 305 d and 0.009 for survival to first calving. Hansen et al. (2003) also found similar and even lower heritability estimates ranging from 0.0001 to 0.008 in Danish HO calves during first 6 mo of age also using a linear sire model. Similarly, Fuerst-Waltl and Sørensen (2010) also found the heritability estimates of 0.006 to 0.042 in Danish HO using a linear and threshold sire model. Pritchard et al. (2013) estimated heifer survival heritability as 0.01 for survival up to 750 d in UK HO. Henderson et al. (2011) found heritability estimate was lower (0.001) for survival up to weaning but higher (0.036) from weaning to 1 mo before calving. However, Vukasinovic et al. (2017) found much higher heritability estimates of 0.06 for calf livability , which measured livability for 2 to 365 d in US HO calves. The main reason for differences in heritability across studies is a lack of uniformity in trait definitions for HLIV along with geographical differences, data set sizes, and model used in analysis. Most of the heritability estimates in other studies only evaluated HLIV through first few months of life.

As HLIV is affected by various environmental factors, heritability estimates were low. These estimates can be increased with standardizing environment conditions and increasing accuracy of recording. The use of calf birth certificate and death categorization can help in increasing these estimates (Lombard et al., 2019). Although heifer losses can be improved quickly through better management, genetic selection will have a permanent effect with small gains accumulating over generations. Similar improvement has been made in other reproductive and disease traits with low heritability in cattle.

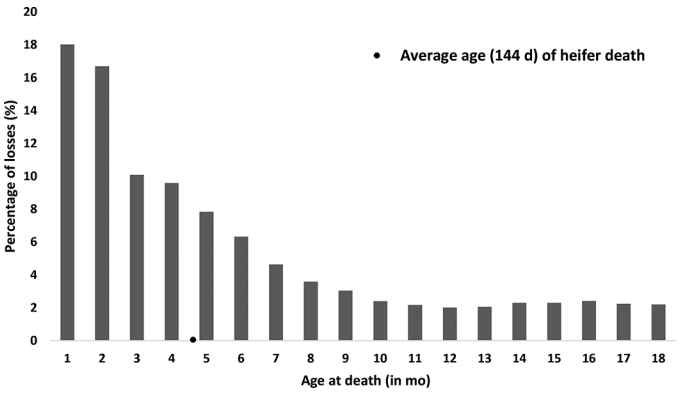

Figure 1. Heifer losses in first 18 mo for animals born between 2009 and 2016.

Traditional and Genomic PTA

Summary statistics of sire evaluations for HO and JE are reported in Table 3. Genomic PTA for HO ranged from −1.6% to +1.6% with a SD of 0.5%, and genomic PTA for JE ranged from −0.5% to +0.5% with SD of 0.2% with mean death losses of about 4%. Reliabilities of genomic predictions for young animals averaged 46 ± 4% for 2,402,141 for HO and 30% ± 4% for 371,275 for JE. The SD of traditional PTA and the reliabilities were lower in both HO and JE. The SD of true transmitting ability in HO was estimated to be 0.7%.

Gonzalez-Peña et al. (2019) found a similar mean reliability of 47.3% in US HO cattle for the calf livability trait recorded between 2 and 365 d age, which included 1,926,261 phenotypes and 325,025 genotypes. The inclusion of genomic data substantially improves reliabilities for health traits in dairy cattle (Parker Gaddis et al., 2014; Vukasinovic et al., 2017). The lower reliability of JE and other breeds was the result of far fewer phenotypic and genotypic records in other breeds as compared with HO. Another factor affecting reliabilities was the low number of genotyped sires in the reference population used for estimation in breeds such as Ayrshire, Guernsey, and Brown Swiss (data not shown). The low observed heritability (0.007) of HLIV can be explained by large environmental and error variance for binary traits with low incidence. In this study, calves from older than 2-yr-old dams performed better than the youngest dams; however, age-parity dif-

Table 3. Summary statistics of bull evaluations for heifer livability, including genomic and pedigree-based PTA

		Genomic PTA		Pedigree-based PTA	
Breed	Bull status[1]	Mean ± SD	REL[2]	Mean ± SD	REL[3]
Holstein	Old	1.5 ± 0.5	51	1.2 ± 0.6	23
	Young	1.6 ± 0.5	46	1.2 ± 0.8	16
Jersey	Old	0.4 ± 0.2	33	0.3 ± 0.4	17
	Young	0.5 ± 0.2	30	0.3 ± 0.4	12

[1]Old = bulls that have daughter records; young = bulls without daughter records.
[2]REL = average reliability of bull's genomic PTA.
[3]REL = average reliability of bull's parent average or PTA.

ferences were not large (Table 2). Hansen et al. (2003) also reported that calves from dams with a low calving age (23 mo) had significantly higher mortality than for a calving age at 28 mo.

Genetic Evaluations and Correlations With Other Traits

Approximate genetic correlations between PTA of HLIV and PTA of other traits included in NM$ are presented in Table 4. Moderate correlations for HLIV in HO included 0.44 with productive life, 0.18 to 0.22 with yield traits, and 0.29 with early first calving on proven bulls. Fertility traits (daughter pregnancy rate, heifer conception rate, and cow conception rate) had low positive correlations with HLIV. The JE bulls had a similar correlation pattern but with lower magnitude than HO, as shown in Table 4. The lower correlations in JE as compared with HO may be the result of breed differences or lower average reliability due to fewer phenotypes and genotypes. The reported correlations with absolute values >0.10 in HO or >0.15 in JE were statistically significant ($P < 0.05$).

Interestingly, the correlation between HO HLIV and cow livability was only moderate (0.31). Weller et al. (2021) and Pritchard et al. (2013) found a similar moderate correlation of 0.30 and 0.31 respectively, whereas Henderson et al. (2011) found correlation of 0.13. This low to moderate correlation suggests that survival in the milking herd and survival in the rearing period are 2 different traits (Pritchard et al., 2013). The survival of cows is also affected by other events that occur later in life such as physiological stress due to greater milk production, udder and teat disorders, and metabolic disorders (Miller et al., 2008). However, the genetic correlation between survival of heifer calf and milking cow indicates common disease resistance factor comprising genetic component (Heringstad et al., 2005).

Favorable genetic correlations with milk (0.22), fat (0.14), and protein (0.18) indicate that selection to increase production is already improving calf health. Similarly, moderate correlation with productive life helps to decrease replacement heifer cost resulting from correlated response in HLIV and also assists in genetic improvement programs through added selection intensity resulting from beneficial genetic correlations. The HLIV has low favorable correlations with SCS (−0.08), gestation length (−0.21), and cow conception rate (0.15) that all aid in selection of healthy animals. Favorable genetic correlation for size (0.1), feet and legs composite (0.06), and udder composite (0.08) indicate heifers that were more likely to survive to maturity and produce more as a cow (Henderson et al., 2011). However, negative correlation with BW composite (−0.21) might suggest unfavorable association with dystocia (Pritchard et al., 2013). Low to moderate positive correlation with fertility results in a healthy calf with better conception rates. Gonzalez-Peña et al. (2019) reported similar favorable genetic correlations of those traits with calf diarrhea but smaller correlations with calf mortality and respiratory disease. Other correlated factors that could be targeted for direct selection include heifer diseases such as bovine respiratory disease

Table 4. Approximate genetic correlations (Pearson product-moment) from genomic evaluations for heifer livability and other traits of 237 Holstein and 195 Jersey bulls with ≥70% and ≥50% reliability for heifer livability, respectively

Trait	Holstein	Jersey
Milk	0.22**	0.09
Fat	0.14*	−0.02
Protein	0.18*	0.07
Productive life	0.44***	0.23*
Cow livability	0.31***	0.12
Daughter pregnancy rate	0.04	0.22*
Heifer conception rate	0.09	0.17*
Cow conception rate	0.15*	0.07
Early first calving	0.29***	0.12
Body size	0.10	−0.21**
Udder composite	0.08	0.08
Feet and legs composite	0.08	−0.02
Gestation length	−0.21**	−0.13
SCS	−0.08	−0.21*

*$P < 0.05$, **$P < 0.01$, and ***$P < 0.001$.

complex and scours, as these conditions are favorably correlated with HLIV (Neibergs et al., 2014; Gonzalez-Peña et al., 2019). Our data suggested that inclusion of HLIV in NM$ will also result in higher yield, longevity, increased fertility, and decreased disease incidence.

Economic Impact

As rearing of replacement heifers accounts for a major cost in most farms, heifer survival has large economic benefits on a phenotypic basis. Heifer losses affect selection intensity within herds for other traits that will ultimately result in reduced genetic gain. The direct genetic contribution of HLIV to profit is much less than its phenotypic contribution due to the low heritability. The correlation before and after including HLIV in NM$ was 0.9999 for HO. There was strong genetic correlation (0.55) between genomic HLIV PTA with NM$. This situation resulted from favorable correlations with most other traits already included in NM$.

Current assumptions assess a $200 value to newborn heifers and $1,400 to freshening heifers (VanRaden et al., 2018). Most deaths occur early in life, but rearing expenses also may be higher in those early months. Average cost of heifer loss is estimated to be around $500. However, there is higher loss of cost if the heifer dies in later months, if correlated health costs are added, or if bull calf losses are added. These costs were not included in this study.

Relative value for HLIV was computed from its SD of transmitting ability (0.007) times economic value ($500), which equals $3.50, and from the sum of the SD times absolute economic values for all other traits in NM$, which equals $377 (VanRaden et al., 2018). Thus, HLIV would receive $3.50/($377 + $3.50) = 0.9% of total emphasis in NM$. With about 1% of emphasis in the NM$, the extra economic progress from including HLIV is expected to be about $50,000 per year.

CONCLUSIONS

Genetic evaluation of HLIV is important from economic, genetic, and animal welfare perspectives. This study showed that HLIV is positively correlated with yield traits, NM$, productive life, and fertility traits, signifying that indirect selection for this trait is already occurring and that direct selection will help to improve herd performance over time. Our data suggest that HLIV genomic PTA can be predicted with reliabilities averaging 46% for young and 51% for well-proven HO sires along with moderate success in JE sires (reliabilities of 30–33%). Selection of HLIV in dairy calves resulted in decreased cost of replacement heifers along with more productive and healthier cows. By encouraging more precise and detailed recordings on calf mortality, the reliabilities of evaluations can increase substantially. Implementation of dairy calf birth certificates and death loss categorization will help in the goal of reducing calf morbidity and mortality. Hence, routine genetic evaluation of HLIV is valuable to select cattle with increased profitability and improved animal health and welfare.

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