US genetic evaluation for new calf health traits: diarrhea and respiratory illnesses

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Abstract

Health records from US dairy herds are routinely collected through dairy records processing centers and stored in the national cooperator database using the health data format (Format 6). Currently, Format 6 includes 20 health event codes and 4 management codes. Since 2018, information from format 6 records have been utilized for routine genetic evaluations of six cow health traits. This study extends the use of Format 6 to calves, establishing a national genetic evaluation for calf diarrhea (DIAR) and respiratory illnesses (RESP). The analysis included 207,602 DIAR records (3–60 days of age) and 681,741 RESP records (3–365 days of age) from all breeds including 80.3% Holstein (HO) and 17.2% Jersey (JE) born between 2013 and 2024. Both traits were modeled as binary variables (0 = diseased, 100 = healthy), with overall incidence rates of 14.46% for DIAR and 16.05% for RESP. Heritability estimates from the all-breed model were 0.026 for DIAR and 0.022 for RESP. Predicted Transmitting Abilities (PTAs) were calculated using an animal model that accounted for fixed effects, including herd-year-season of birth and the parity group of the dam, along with random additive genetic effects. Genotyped animals with 69,200 imputed markers were used in calculation of genomic PTAs for HO and JE. Genome wide association analysis revealed two significant additive markers on chromosome 18 associated with DIAR in HO were within the CDH11 gene, known to have role in immunity, cell adhesion, and gut epithelium integrity. Additionally, two significant markers on chromosome 4 associated with RESP in HO fall within the DNAH11 gene, essential for motile cilia function in the respiratory tract, where mutations to this gene lead to chronic respiratory infections in humans. These findings suggest that routine genomic evaluations of these traits using producer-recorded health data would enhance calf health resulting in improved cow productivity.

Key words: Calf, health, data.

Introduction

To streamline the collection of health data, researchers from USDA along with industry partners and veterinary experts developed a standardized health record in 2008 (Format 6) (Cole *et al.,* 2008). This health data format, or Format 6, is also compatible with lactation yield records (Format 4) and reproductive records (Format 5). Currently, Format 6 includes 20 health event codes and 4 management codes. These event codes consist of up to four letters (e.g., DIAR for diarrhea or scours and RESP for respiratory problems) and have event detail sections for each health event. The structure of Format 6 is similar to other data formats, with the first 100 bytes of records including animal, sire, and dam identification, herd identification number, and calving date. Over time, Format 6 has undergone several revisions to meet the needs of dairy farmers and can easily accommodate additional traits in the future. The current version is available at https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Format_6 . Information from this health data format has been used in routine evaluation of six cow health traits (milk fever, displace abomasum, ketosis, mastitis, metritis, and retained placenta) since 2018 (Parker Gaddis *et al.,* 2014; 2020). With this precedent, a similar health evaluation system can be developed for calf heath traits, provided there are enough calf health records.

Dairy calf health is crucial for sustainable and profitable farming, with diseases like respiratory illnesses and diarrhea significantly impacting mortality and productivity (Gonzalez-Peña *et al.,* 2019; Lynch *et al.,* 2024a). Treatment costs average $25 per calf for diarrhea (Cangiano, 2023) and $40 for respiratory disease (Dubrovsky, 2020; Elmore *et al.,* 2023), with recurrent cases further increasing expenses. Research on bovine respiratory disease complex and diarrhea highlights the genetic factors influencing disease susceptibility. Heritability estimates for these conditions range from 0.02 to 0.24, varying based on disease prevalence, study design, statistical models, and data recording methods (Henderson *et al.,* 2011; McCorquodale *et al.,* 2013; Gonzalez-Peña *et al.,* 2019; Graham *et al.,* 2023; Lynch *et al.,* 2024a; Lynch *et al.,* 2024b). While heritability is low to moderate, genetic progress is achievable by improving prediction accuracy through large datasets and genomic selection (VanRaden *et al.,* 2009). Along with continued focus on improving environmental and nutritional conditions, genomics will offer new avenues for enhancing calf health.

Functional traits are characteristics of organisms that influence their performance, survival, growth, and reproduction. Effective recording and phenotyping strategies are essential for improving functional traits related to health and disease resistance in dairy calves. Systematic recording of health events, such as incidences of diseases, treatments administered, and recovery outcomes, provides valuable data for genetic evaluations (Egger-Danner *et al.,* 2014).

The *primary objective* of this research was to develop a comprehensive US national genetic evaluation framework for dairy calf health traits. The *secondary objectives* were to identify genetic markers associated with key health traits in dairy calves and their possible inclusion in genomic marker panel, promote the adoption of genetic evaluation in breeding programs to improve calf health, and continuous improvement of genetic model and phenotypic data collection.

Materials and methods

Study population

Calf health records from dairy records processing centers were collected for calves born between 2013 and 2024. These records, maintained by producers and available in the national cooperator database (Format 6 - health data), provide comprehensive data on calf health events (Figure 1). The distribution of recorded health events in calves indicates that sufficient data are only available for diarrhea (DIAR) and respiratory illnesses (RESP), with most records representing Holstein (HO) and Jersey (JE) breeds. Both DIAR and RESP were treated as binary traits, where a score of 0

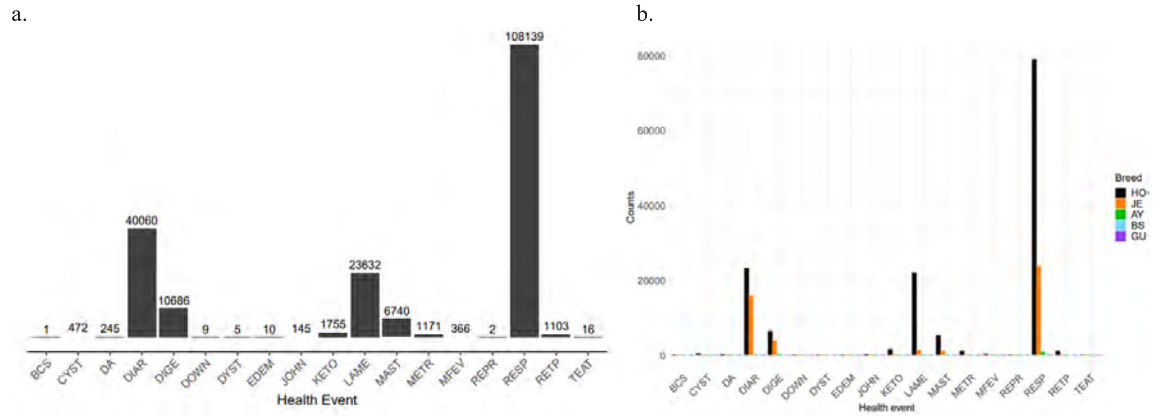


Figure 1. Distribution of calf health events recorded from year 2013-2024: (a) all breed health events (b) distribution of these health events across five major US dairy breeds.

indicated a disease event, and 100 represented a healthy animal. This scoring system allows breeding values to reflect disease resistance in percentage points. After quality control filtering, the final dataset included 207,602 animals for DIAR analysis and 681,741 animals for RESP analysis.

Heritability estimation

Variance components were estimated using the full dataset with BLUPF90 version 1.71 (Misztal *et al.,* 2018). The model accounted for fixed effects, including year-season, inbreeding, heterosis, and dam parity; while animal, herd-sire interaction, herd-year interaction, and residual effects were treated as random factors.

Traditional and genomic PTA

Predicted transmitting abilities (PTA) were estimated using the animal model: DIAR or RESP = HYS + PG + a + e, where DIAR or RESP is a binary trait (0 or 100), HYS is the fixed effect of herd-year-season of birth, PG is the fixed effect of parity group, a is the random additive genetic effect, and e is the residual error. Animal and residual error effects were distributed as N(0, $\mathbf{A}\sigma^2_a$) and N(0, $\mathbf{I}\sigma^2_e$), respectively where **A** is the numerator relationship matrix, **I** is an identity matrix, σ^2_a is the additive genetic variance, and σ^2_e is the residual variance. Traditional evaluations were conducted using a multibreed approach, while genomic evaluations followed a single-breed framework, consistent with the methodology used in the U.S. national genomic evaluation for other traits (VanRaden *et al.,* 2009; 2011).

Genomic PTA correlations with other traits

Relationships between genomic PTA for calf health traits (DIAR and RESP) and genomic PTA for 24 traits included in the Net Merit economic index (VanRaden *et al.,* 2025) were analyzed using Pearson correlation coefficients. This analysis included 4,292 proven Holstein bulls with reliabilities ≥ 85% and was performed using R version 4.4.1 (R Core Team, 2022).

Allele effects

Additive allele effects for all the 69,200 markers were calculated using the densemap.f90 program. Genes within significant markers were identified using the *Bos taurus* ARS-UCD 2.0 assembly (https://www.ncbi.nlm.nih.gov/datasets/genome/GCF_002263795.3/).

Results and discussion

Incidence of diarrhea and respiratory illnesses

Based on the distribution of incidence data and findings from the literature, diarrhea events were defined as occurring between days 3 and 60, while respiratory events were defined as occurring between days 3 and 365 (Figure 2). Notably, the distribution of RESP was bimodal with a second spike in respiratory cases around day 100, coinciding with the weaning and relocation period, which can be stressful for calves. These distributions of disease occurrence were consistent with previous studies (Gonzalez-Peña *et al.,* 2019; Zhang *et al.,* 2022; Lynch *et al.,* 2024b). Most of the data (> 97%) were from HO (80.3%) and JE (17.2%). The mean and median ages of RESP were 98.1 d and 94 d in JE, compared to 75.3 d and 57 d in HO. Similarly, the mean and median ages of DIAR were 10.3 d and 9 d in JE, and 11.8 d and 10 d in HO. The incidence of both DIAR and RESP was higher in JE compared to HO. The detailed distribution of the incidence of diarrhea and respiratory events in HO, JE and other breeds is presented in Table 1.

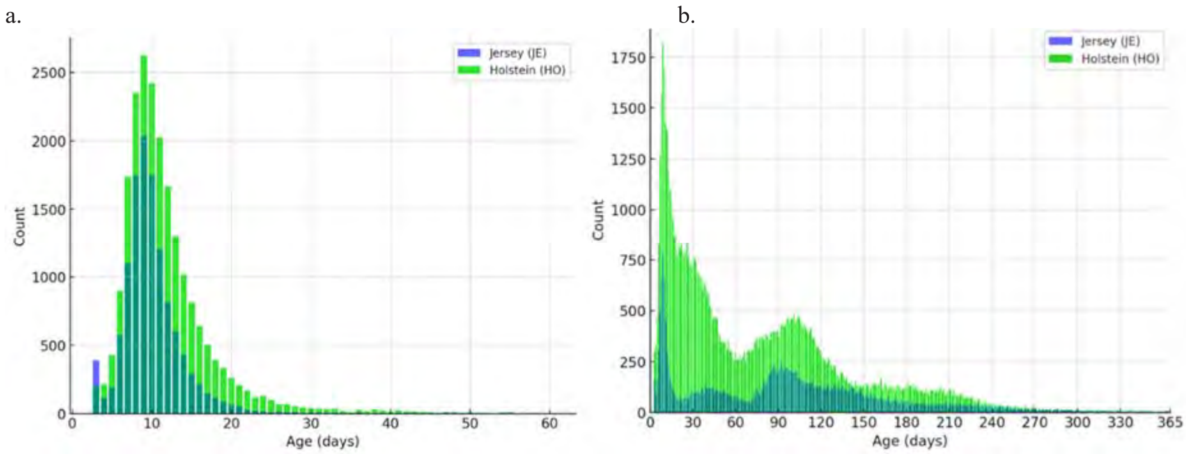


Figure 2. Distribution of calf health diseases in Holstein and Jersey calves born between years 2013 to 2024: (a) diarrhea within 3 to 60 days and (b) respiratory illness within 3 to 365 days.

Table 1. Summary of study population, breeds and disease incidence for diarrhea (DIAR) and respiratory illnesses (RESP) traits.

Traits (Breeds)	Diseased (%)	Healthy (%)	Total (%)
DIAR (HO)	21,605 (13.5)	137,994 (86.5)	159,599 (76.9)
DIAR (JE)	8,042 (17.8)	37,088 (82.2)	45,130 (21.7)
DIAR (other dairy breeds)	363 (12.6)	2,510 (87.4)	2,873 (1.4)
Total DIAR	30,010 (14.5)	177,592 (85.5)	207,602 (100)
RESP (HO)	80,608 (14.5)	474,026 (85.5)	554,634 (81.4)
RESP (JE)	25,629 (23.7)	82,604 (76.3)	10,8233 (15.9)
DIAR (other dairy breeds)	3,175 (20.2)	15,699 (79.8)	18,874 (2.7)
Total RESP	109,412 (16.1%)	572,329 (83.9)	681,741 (100)

Heritability

A strong herd-year and moderate herd-sire effect were observed in all models. The heritability estimates for DIAR using the all-breed model ranged from 0.022 to 0.026, while estimates for RESP ranged from 0.018 to 0.022, with or without the inclusion of herd-sire and herd-year variance components. These estimates were within the lower end of previously reported heritability estimates for calf health, which range from 0.02 to 0.24 (Henderson *et al.,* 2011; McCorquodale *et al.,* 2013; Gonzalez-Peña *et al.,* 2019; Graham *et al.,* 2023; Lynch *et al.,* 2024a). These variations may be attributed to differences in disease incidence, statistical modeling approaches, data recording methods, and data editing practices. Producer-recorded data is often incomplete and noisy, with missing records, inconsistent case reporting, and varying disease definitions across farms.

Traditional and genomic PTA

The traditional and genomic PTA for DIAR and RESP in young and old animals are presented in Table 2. Holsteins exhibited higher genomic reliabilities for both diarrhea and respiratory traits compared to JE, possibly due to the greater number of genotyped and phenotyped animals included in the study. As expected, reliabilities of genomic PTA were higher than traditional ones. Toghiani *et al* (2024) also reported that the predictive ability of genomic PTA surpassed the parent average in predicting cow performance deviation for yield, productive life, somatic cell score, fertility, and health traits in US HO and JE heifer calves.

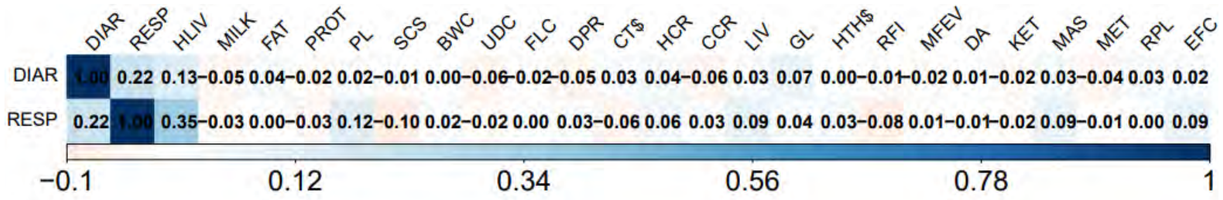
Genomic PTA correlations with other traits

Genomic PTA correlations between calf health traits and other traits in daughter-proven Holstein bulls are shown in Figure 3. Correlation between DIAR and RESP was 0.22, while correlations of heifer livability with DIAR and RESP were 0.13 and 0.35, respectively. Respiratory illnesses and diarrhea, being major causes of pre- and post-weaning deaths in dairy calves, are expected to correlate with heifer livability, which considers heifer deaths from >2 days to 18 months (Neupane *et al.,* 2021). Correlations of these two health traits with other traits were low. Other studies also have showed that calf health traits such as bovine respiratory disease complex and diarrhea have limited genetic overlap with economically important traits such as milk yield, growth, and fertility (Heringstad *et al.,* 2007; Fuerst-Waltl *et al.,* 2012).

Table 2. Summary statistics of bull evaluations for calf health traits (DIAR- diarrhea, RESP-respiratory illnesses), including genomic and pedigree-based Predicted Transmitting Ability (PTA).

	Genomic PTA mean ± SD (reliability)		**Traditional PTA mean ± SD (reliability)**	
Trait	**Old**	**Young**	**Old**	**Young**
DIAR-JE	0.07 ± 0.36 (34)	0.08 ± 0.47 (33)	-0.01 ± 0.36 (15)	0.06 ± 0.52 (15)
RESP-JE	0.04 ± 0.41 (42)	-0.01 ± 0.48 (39)	0.03 ± 0.42 (21)	-0.04 ± 0.51 (18)
DIAR-HO	-0.01 ± 0.25 (47)	-0.03 ± 0.34 (45)	-0.00 ± 0.25 (19)	-0.04 ± 0.26 (12)
RESP-HO	-0.04 ± 0.36 (60)	-0.11 ± 0.51 (59)	-0.02 ± 0.35 (26)	-0.08 ± 0.36 (17)

Young animals were born on or after 2020, old animals were born before 2020.



	DIAR	RESP	HLIV	MILK	FAT	PROT	PL	SCS	BWC	UDC	FLC	DPR	CT$	HCR	CCR	LIV	GL	HTH$	RFI	MFEV	DA	KET	MAS	MET	RPL	EFC
DIAR	1.00	0.22	0.13	−0.05	0.04	−0.02	0.02	−0.01	0.00	−0.06	−0.02	−0.05	0.03	0.04	−0.06	0.03	0.07	0.00	−0.01	−0.02	0.01	−0.02	0.03	−0.04	0.03	0.02
RESP	0.22	1.00	0.35	−0.03	0.00	−0.03	0.12	−0.10	0.02	−0.02	0.00	0.03	−0.06	0.06	0.03	0.09	0.04	0.03	−0.08	0.01	−0.01	−0.02	0.09	−0.01	0.00	0.09

Figure 3. Genomic predicted transmitting ability correlations between calf health traits, diarrhea (DIAR) and respiratory illnesses (RESP), and 24 Net Merit traits in proven Holstein bulls (reliability >= 85%, n = 4,292).

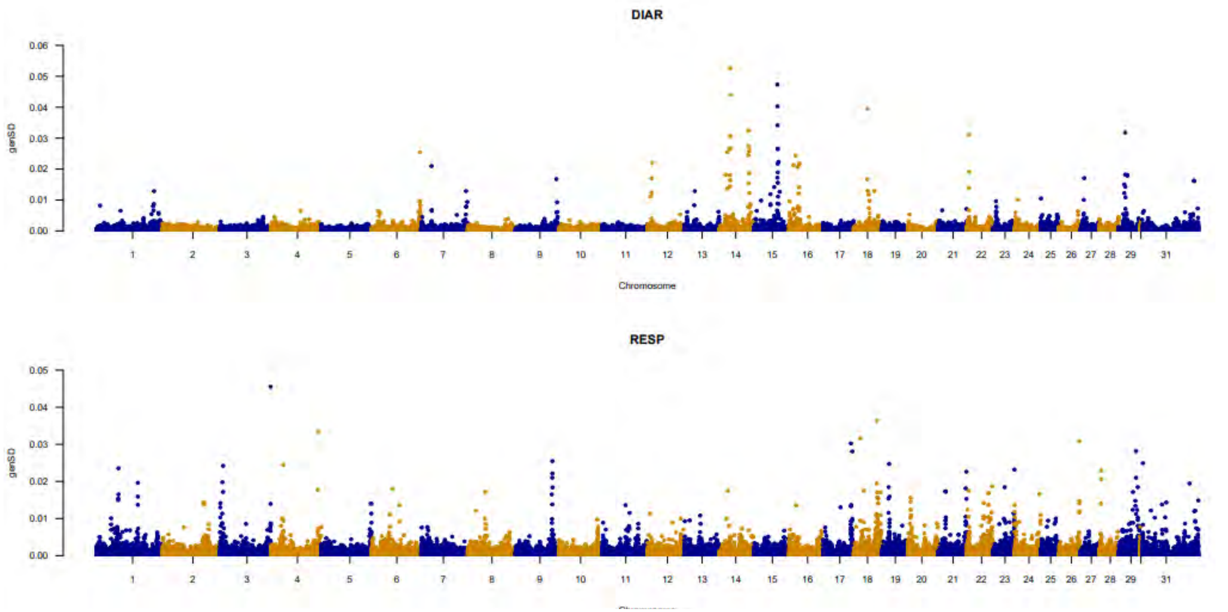


Figure 4. Marker effects (additive genetic SD) for diarrhea (DIAR) and respiratory illnesses (RESP) traits in Holsteins

Allele effects

The additive allele effects for DIAR and RESP in Holsteins (HO) are shown in Figure 4, with distinct peaks across multiple chromosomes. Notably, two significant additive markers on chromosome 18 associated with DIAR in HO were within the cadherin 11 (CDH11) gene, known to have role in immunity, cell adhesion, and gut epithelium integrity. CDH11 expression is upregulated in the intestines of patient with inflammatory bowel disease (Franzè *et al.,* 2020). Additionally, two significant markers on chromosome 4 associated with RESP in HO fall within the dynein axonemal heavy chain 11 (DNAH11) gene. DNAH11 is essential for motile cilia function in the respiratory tract, where mutations to this gene lead to chronic respiratory infections in humans (Bartoloni *et al.,* 2002).

Conclusions

This genetic evaluation system enhances dairy farmers' ability to improve calf health through selective breeding. By integrating new calf health traits diarrhea and respiratory illnesses into the US national genetic evaluation system, breeders can select for genetically resilient calves. This approach will contribute to improved herd health and increased profitability in dairy production. These findings support the feasibility of incorporating DIAR and RESP into national genetic evaluations in the near future.

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