US Genetic Evaluation for New Calf Health Traits: Diarrhea and Respiratory Illnesses

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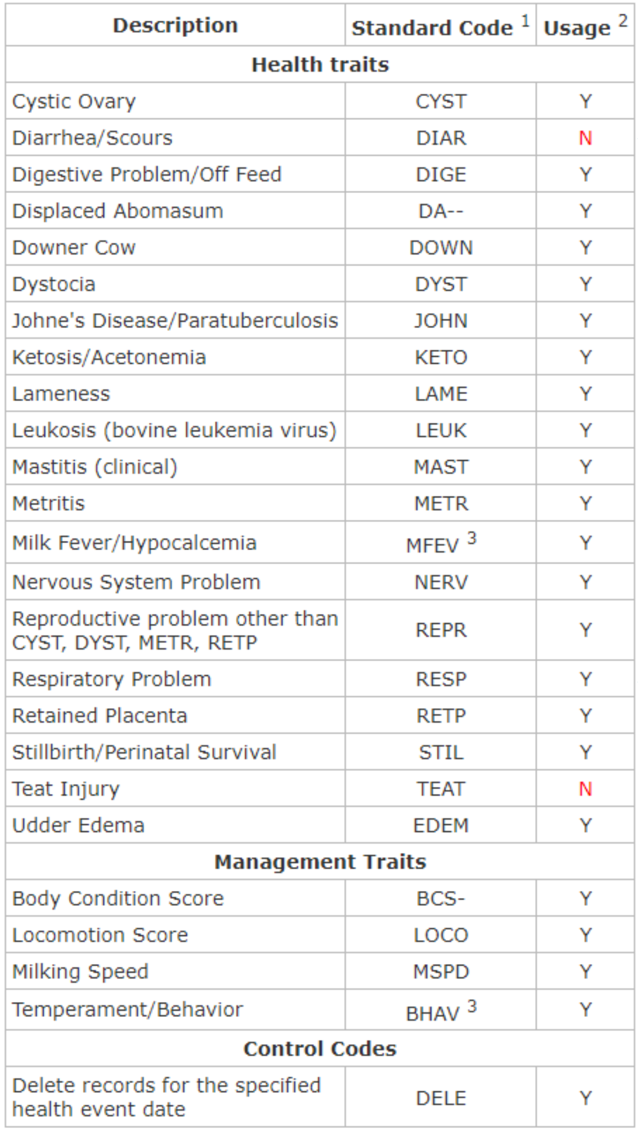
Background

- Calf health is a critical factor in the sustainability and profitability of dairy farming
- 75% of preweaned calf mortality is due to diarrhea (53-56%) and respiratory disease (21-23%)
- In postweaning mortality, respiratory disease accounts for 50% of cases
- Low heritability (0.02 – 0.21) and lack of centralized records/reporting
- No US national evaluation of calf health/disease traits, only heifer livability
- Is there enough good quality data leading to national evaluation?

Lynch et al., 2024; Gaddis et al., 2020; Cole et al., 2008

Format 6 (health data)

- Developed in 2008, latest revision in 2017
- Codes for 20 health traits and 4 management traits
- 6 cow health traits US national evaluation from 2018
  - DA, MFEV, KETO, MAST, METR, RETP



Description	Standard Code [1]	Usage [2]
Health traits		
Cystic Ovary	CYST	Y
Diarrhea/Scours	DIAR	N
Digestive Problem/Off Feed	DIGE	Y
Displaced Abomasum	DA--	Y
Downer Cow	DOWN	Y
Dystocia	DYST	Y
Johne's Disease/Paratuberculosis	JOHN	Y
Ketosis/Acetonemia	KETO	Y
Lameness	LAME	Y
Leukosis (bovine leukemia virus)	LEUK	Y
Mastitis (clinical)	MAST	Y
Metritis	METR	Y
Milk Fever/Hypocalcemia	MFEV [3]	Y
Nervous System Problem	NERV	Y
Reproductive problem other than CYST, DYST, METR, RETP	REPR	Y
Respiratory Problem	RESP	Y
Retained Placenta	RETP	Y
Stillbirth/Perinatal Survival	STIL	Y
Teat Injury	TEAT	N
Udder Edema	EDEM	Y
Management Traits		
Body Condition Score	BCS-	Y
Locomotion Score	LOCO	Y
Milking Speed	MSPD	Y
Temperament/Behavior	BHAV [3]	Y
Control Codes		
Delete records for the specified health event date	DELE	Y

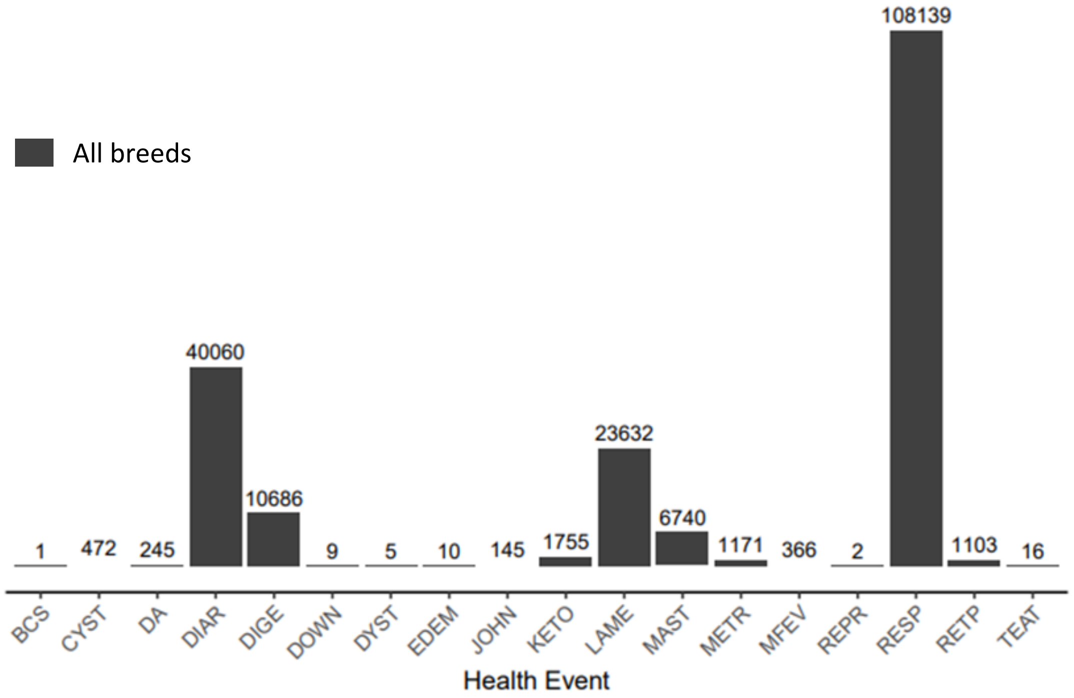
https://redmine.uscdcb.com/projects/cdcb-customer-service/wiki/Format_6#

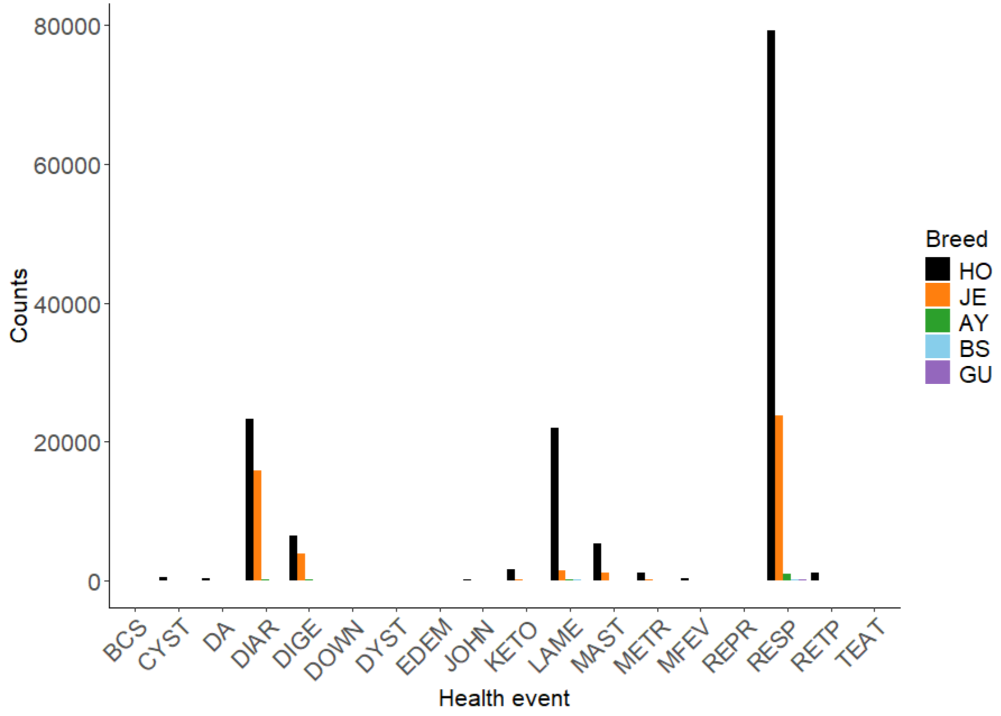
Objectives

Develop a comprehensive national genetic evaluation system for dairy calf health traits using producer-recorded health event data (Format 6)

Identify genetic markers associated with key health traits in dairy calves and their possible inclusion in genomic marker panel

Data extraction: calf health events distribution (2013-2024)





Data quality control (edits)

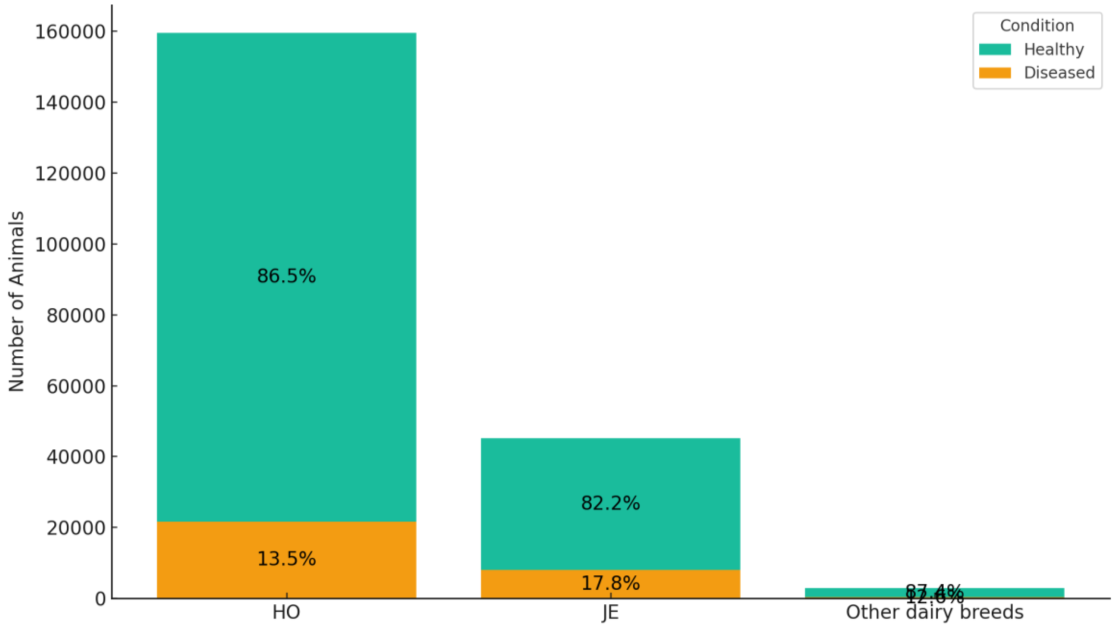
- Calves in the same herd-year (contemporaries) without the health event of interest were used as healthy animals
- For each event, first incidence reported is retained
- Herd-year incidence minimum 1% and maximum within 2 SD of mean
- Pedigree data: animals with missing sire keys were removed

Phenotypes and heritability estimates

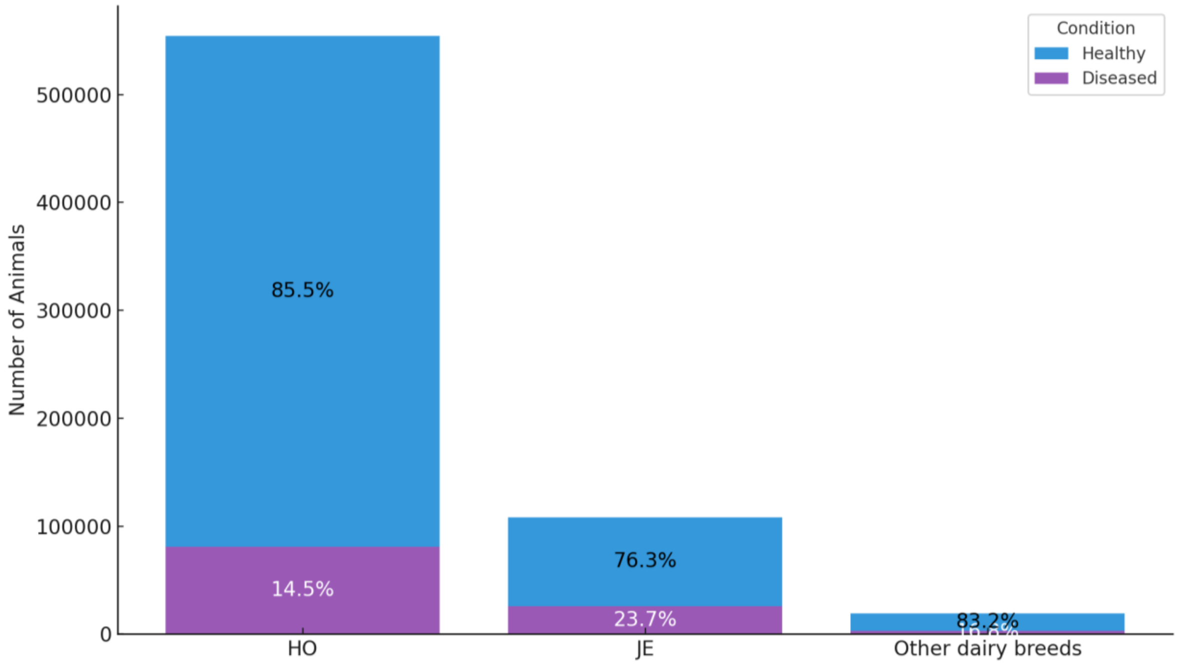
- Binary trait: **0** (diseased) and **100** (healthy)
  - DIAR: 207,602 total (14.46% diseased)
  - RESP: 681,741 total (16.05% diseased)
- Majority of data (>97%) from HO (80.3%) and JE (17.2%) breeds
- Higher incidence of both diarrhea and respiratory problems in JE as compared to HO
- Heritability estimates (blupf90): diar 0.026 and resp 0.022

Mistal et al., 2002

Incidence by breed

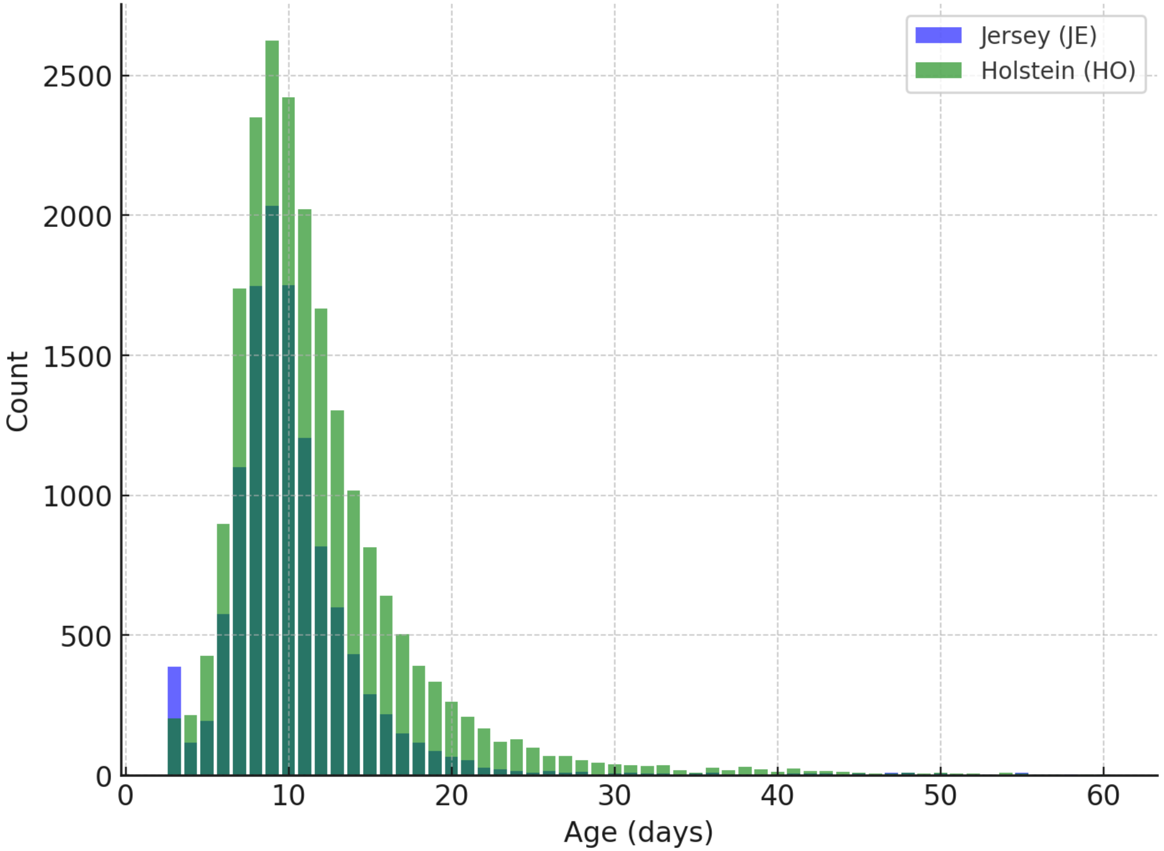


DIAR

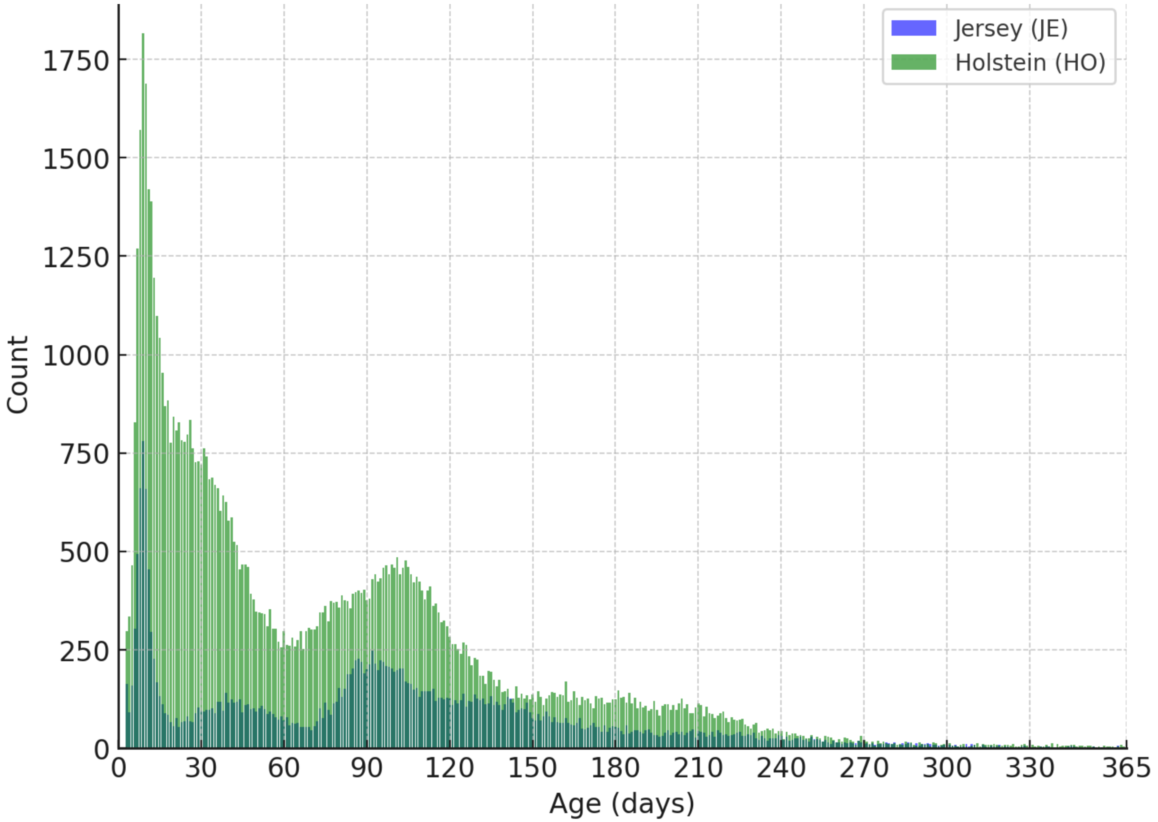


RESP

Age distribution of diarrhea and respiratory events in HO and JE calves



Diarrhea



Respiratory problems

Predicted transmitting abilities (PTAs)

- Predicted Transmitting Abilities (PTAs) were calculated using the animal model: DIAR/RESP = HYS + PG + a + e

  covariates: parity of dam and herd-year-season of birth(hys)

- All breed model for traditional pedigree-based evaluation and breed specific (JE and HO) for genomic evaluation
- All animals genotyped on various platforms were imputed to 69,200 markers using Findhap version 3

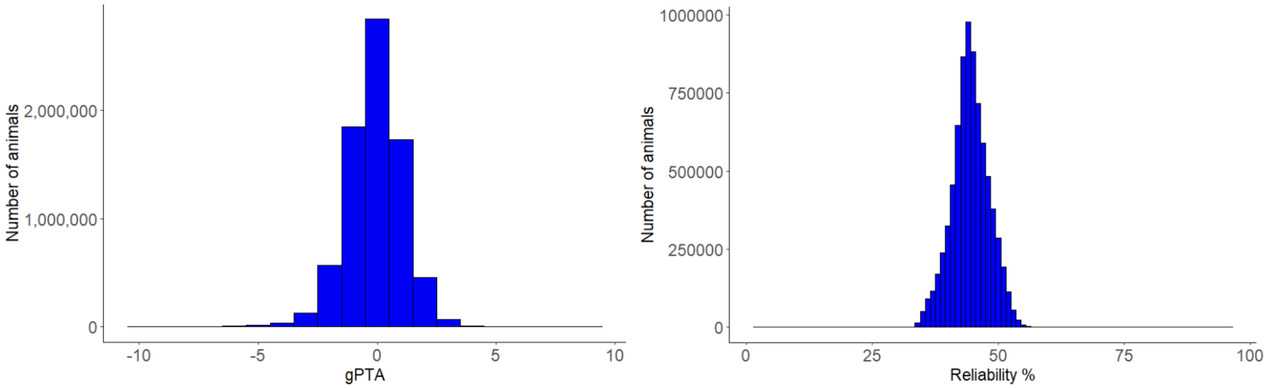
Wiggans et al., 2019; VanRaden et al., 2011

Predicted Transmitting Ability (PTA): genomic and pedigree

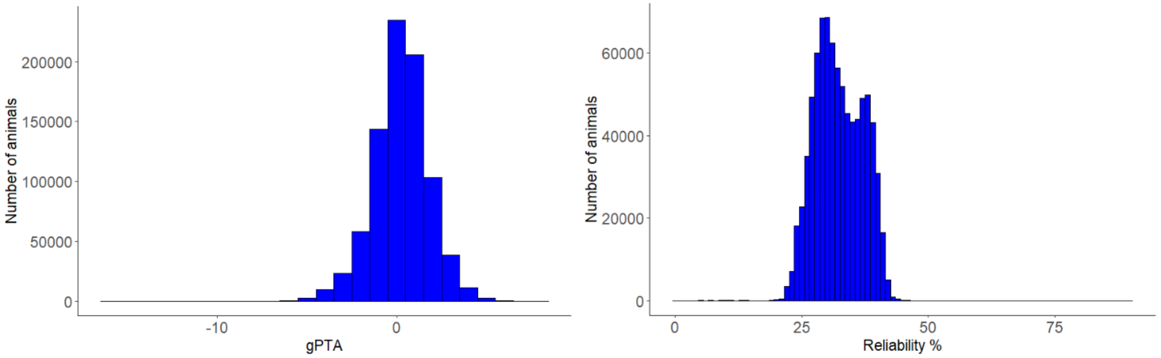
Trait	Genomic PTA mean ± SD (reliability)		Traditional PTA mean ± SD (reliability)	
	Old	Young	Old	Young
DIAR-JE	0.07 ± 0.36 (34)	0.08 ± 0.47 (33)	-0.01 ± 0.36 (15)	0.06 ± 0.52 (15)
RESP-JE	0.04 ± 0.41 (42)	-0.01 ± 0.48 (39)	0.03 ± 0.42 (21)	-0.04 ± 0.51 (18)
DIAR-HO	-0.01 ± 0.25 (47)	-0.03 ± 0.34 (45)	-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)

Estimated genomic PTAs and reliabilities

DIAR

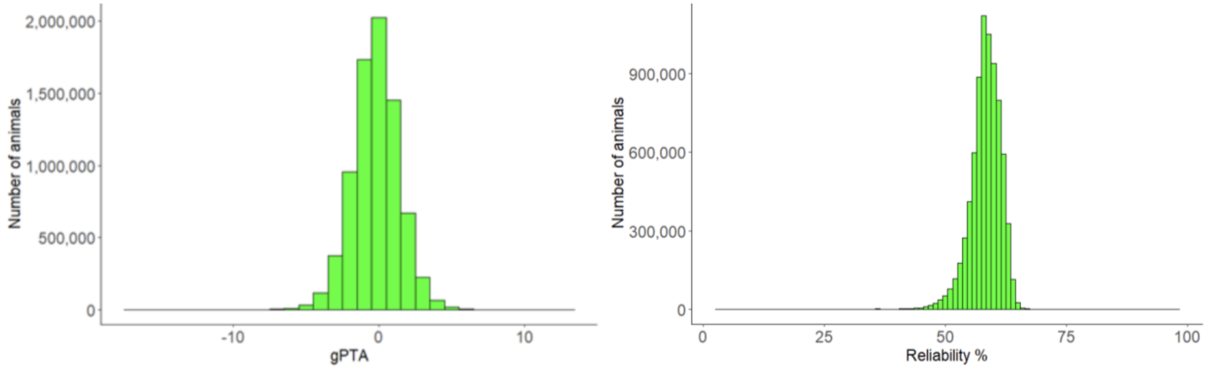


HO

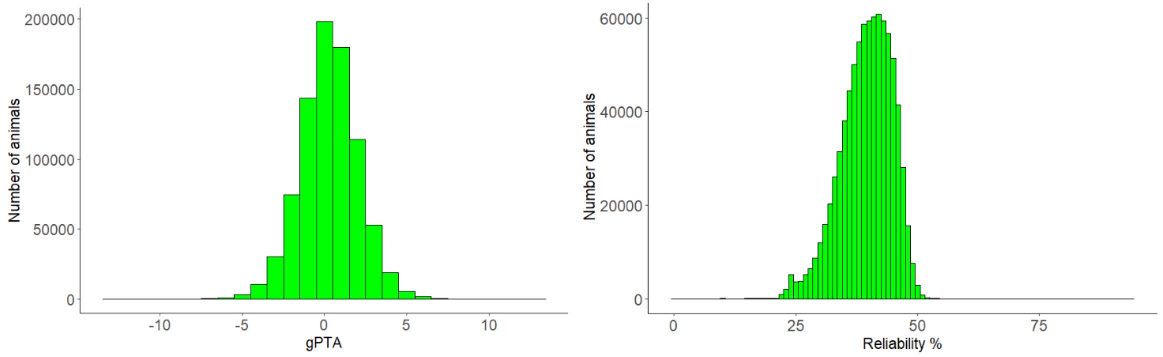


JE

RESP

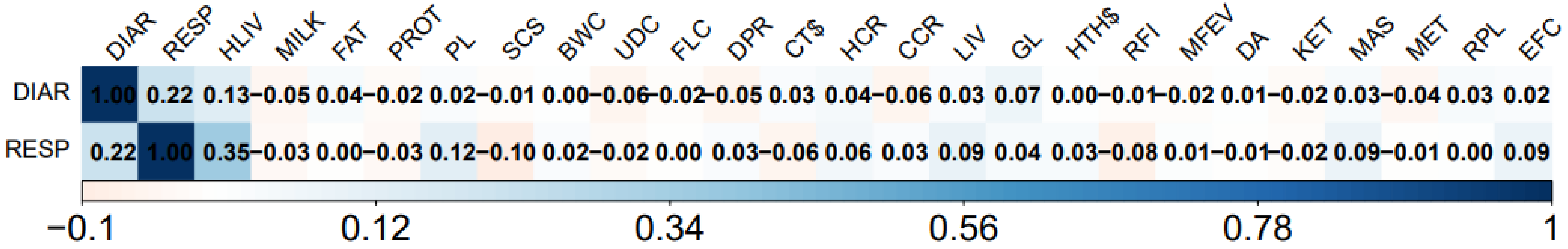


HO

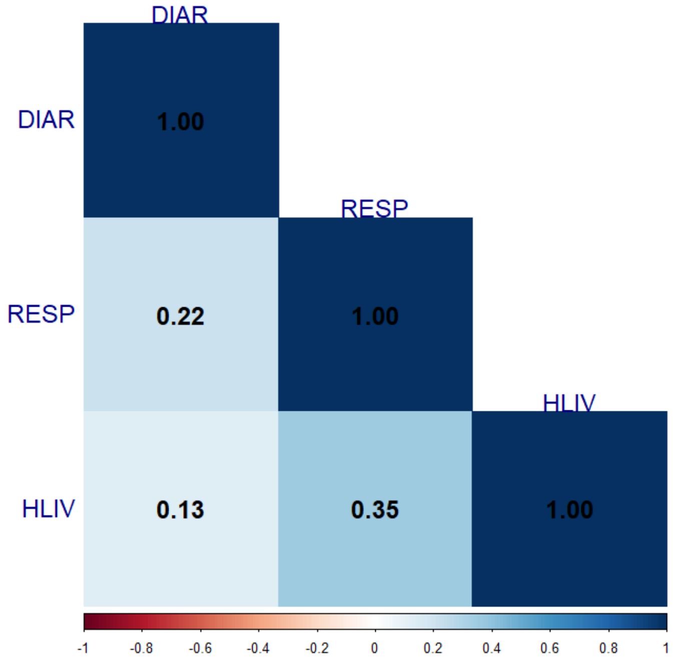


JE

gPTA correlations with net merit traits

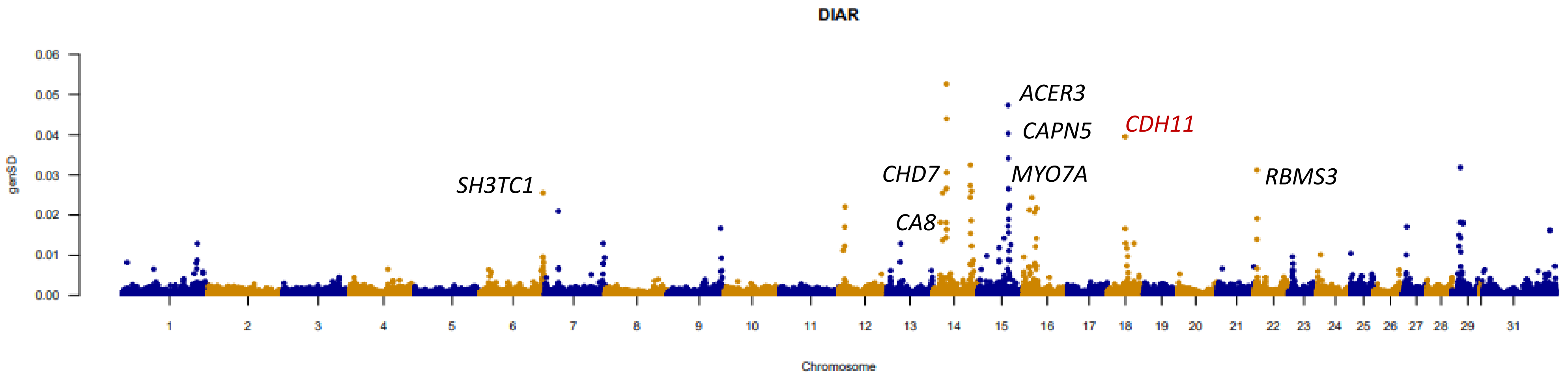


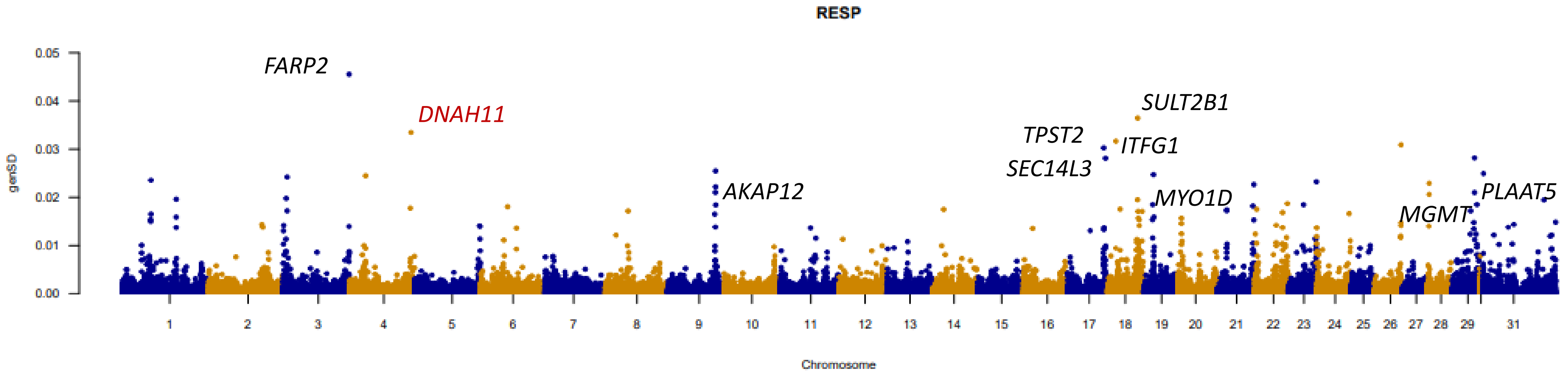
	DIAR	RESP	HLIV	MILK	FAT	PROT	PL	SCS	BWC	UDC	FLC	DPR	CT$	HCR	CCR	LIV	GL	HTH$	RFI	MFEV	DA	KET	MAS	MET	RPL	EFC
DIAR	1.00	0.22	0.13	−0.05	0.04	−0.02	0.02	−0.01	0.00	−0.06	−0.02	−0.05	0.03	0.04	−0.06	0.03	0.07	0.00	−0.01	−0.02	0.01	−0.02	0.03	−0.04	0.03	0.02
RESP	0.22	1.00	0.35	−0.03	0.00	−0.03	0.12	−0.10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



	DIAR	RESP	HLIV
DIAR	1.00		
RESP	0.22	1.00	
HLIV	0.13	0.35	1.00

Additive marker effects (HO): within genes





Future work

- Genome wide association study and pathway analysis with different models for calf health traits (calf livability, diarrhea, and respiratory illnesses)
- Collection and continuous data flow
- Additional/new traits for calf health
- Accurate recordings of phenotypes and improved models

Conclusions

- National genetic evaluation system will provide dairy farmers with powerful tools to enhance calf health through selective breeding
- More precise and detailed recordings on calf health data will result in increased reliabilities
- Continuous flow of data is necessary
- Selection of healthy calf will result in profitability and sustainability of herds

Acknowledgments & disclaimers

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