

Genetic selection for dairy calf disease resistance traits: opportunities and challenges

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Value in calf health

Reported incidence rates

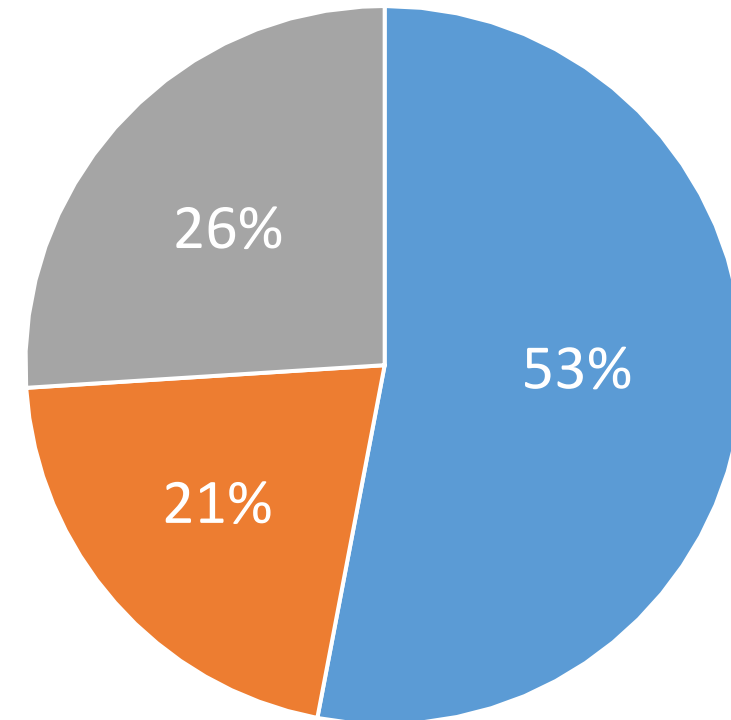
- Diarrhea: 23-44%
- Respiratory problems: 12-22%

(USDA 2010, 2018; Urie et al. 2018; Haagan et al. 2021)

Value

- Economics
- Lifetime performance
- Societal opinions

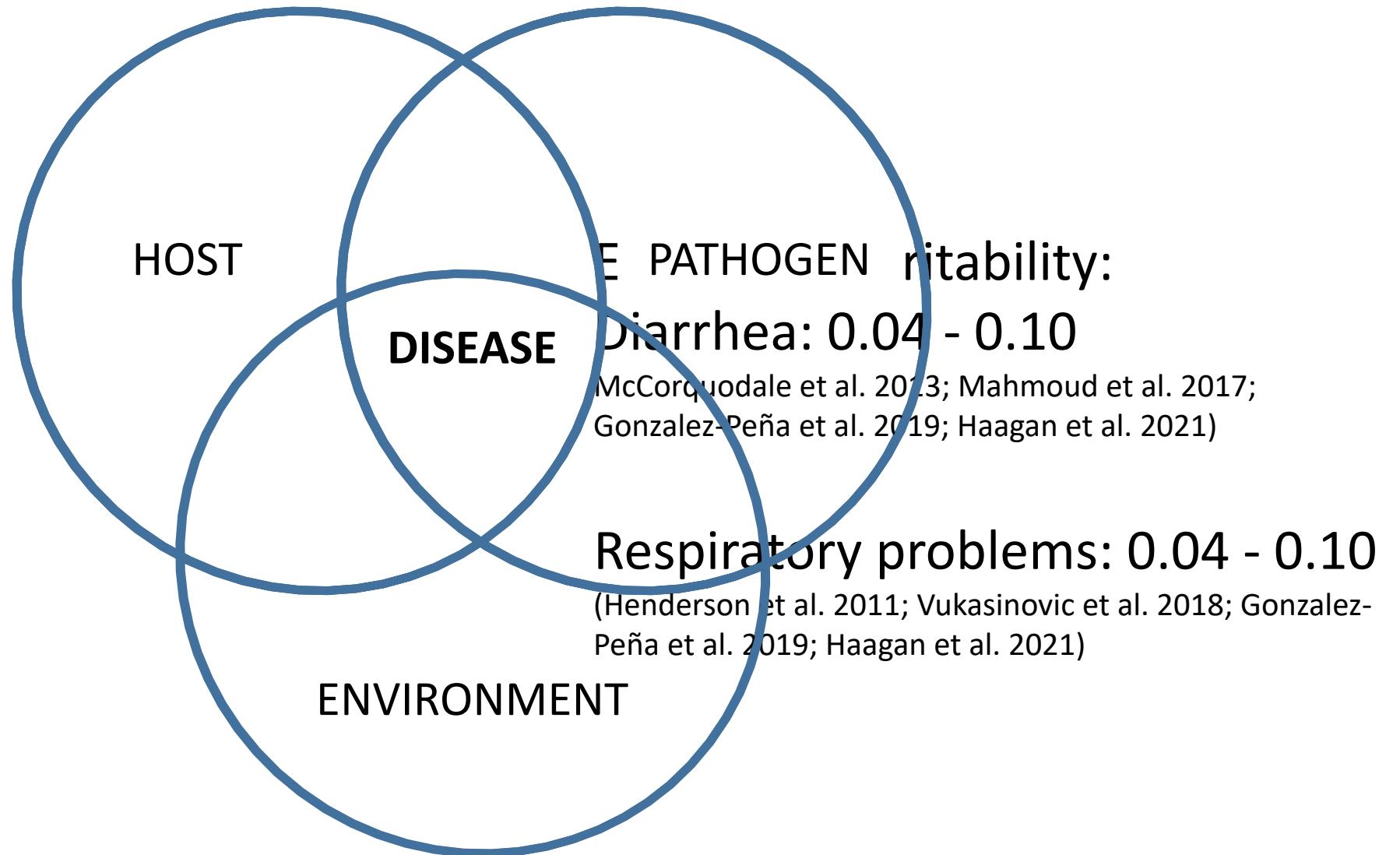
Causes of pre-weaning mortality



■ Diarrhea ■ Respiratory problems ■ Other

(Murray 2011)

Value in genetic selection



Data overview

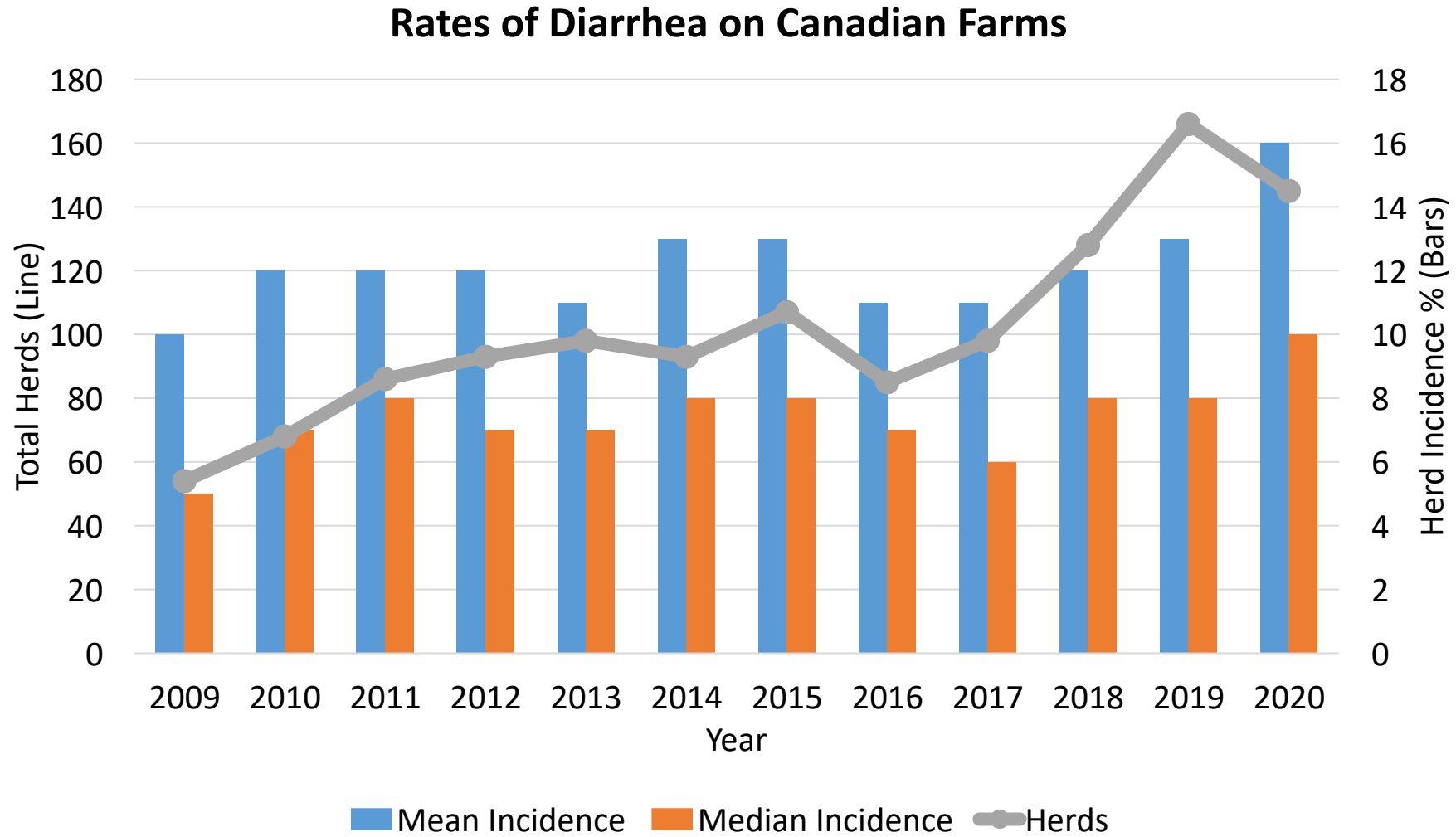
Calf disease data recorded by dairy producers with herd management software (DairyComp 305) were provided by Lactanet Canada

69,695 Holstein records for respiratory problems and diarrhea

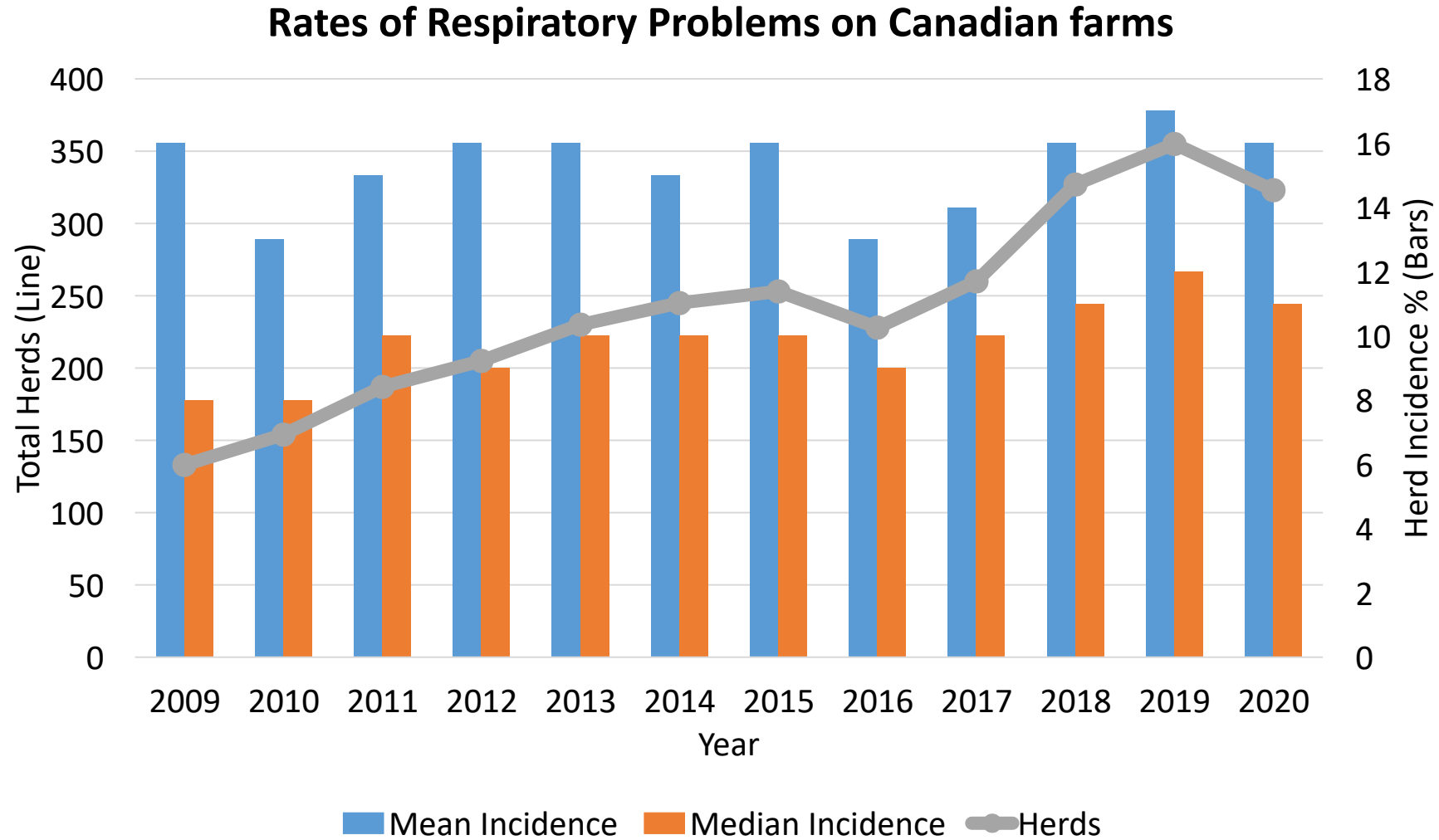
- 62,361 calves
- 1,617 Canadian dairy herds
- Collected between 2006 and 2021

A herd inventory file for all calves reared in each herd was used to identify healthy calves within herd

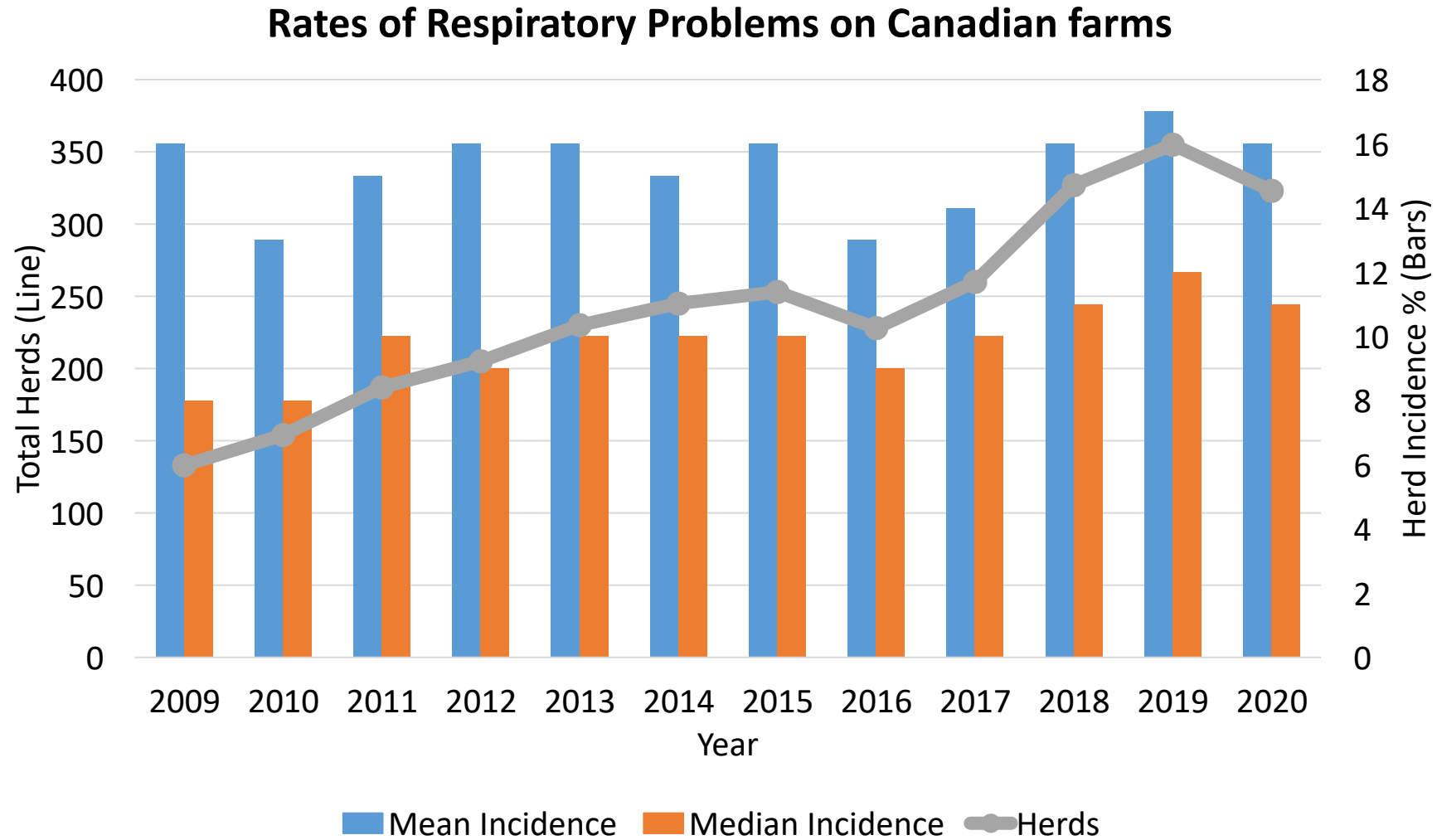
Incidence rates



Incidence rates



Incidence rates



Analysis edits

Edits:

Age of occurrence:

- <60 days for Diarrhea
- <180 days for Respiratory Problems

Herds required three consecutive years of records

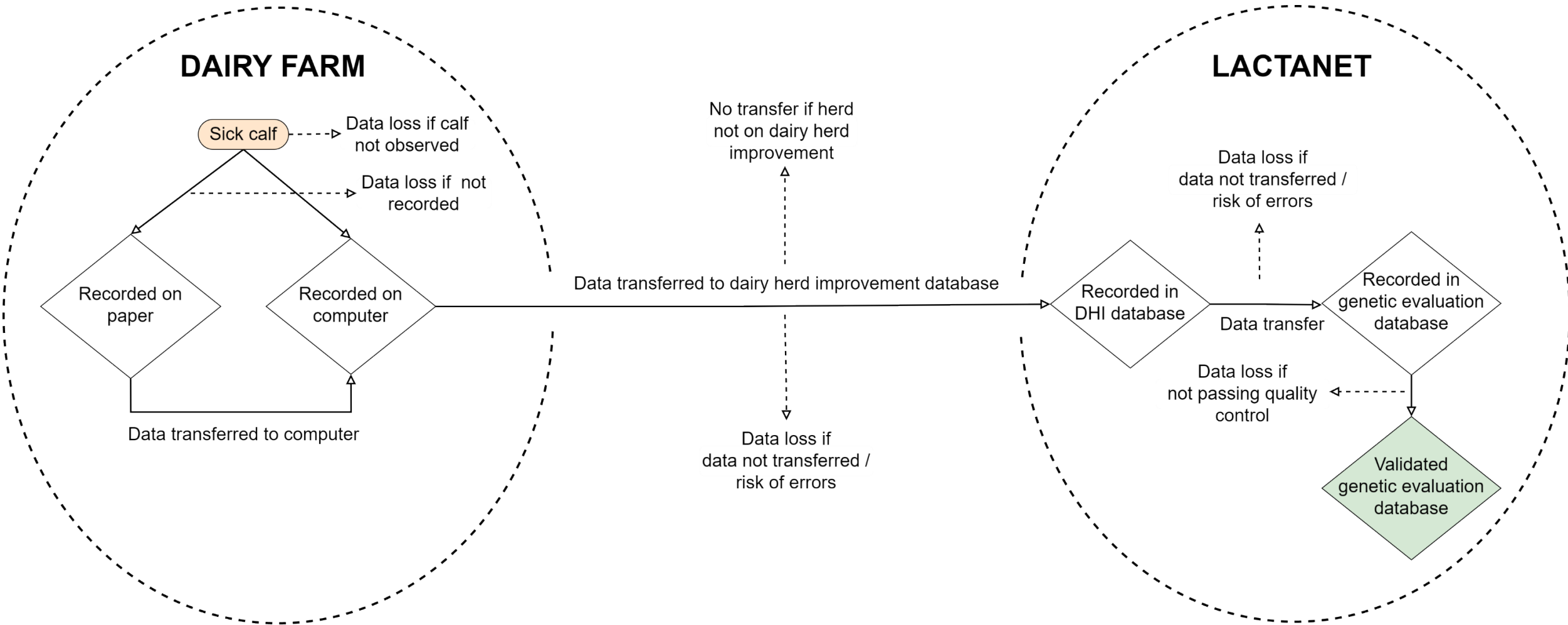
Two datasets created with herd-years requiring a minimum of 1% / 5% incidence

Calf disease data overview

Analyses		Trait	Diseased	Healthy	Records (Herds)
Single trait	1%	DIAR	12,662	52,980	65,642 (122)
		RESP	29,388	128,885	158,273 (288)
	5%	DIAR	11,058	28,907	39,965 (61)
		RESP	26,307	76,131	102,438 (180)
Multiple trait	1%	DIAR only	6,161		
		RESP only	8,868	33,756	53,683 (96)
		Both diseases	4,898		
	5%	DIAR only	4,797		
		RESP only	5,659	16,164	31,103 (45)
		Both diseases	4,483		

DIAR= Diarrhea; RESP= Respiratory problems

Data infrastructure



Model

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_{hys}\mathbf{hys} + \mathbf{Z}_a\mathbf{a} + \mathbf{e}$$

where

- \mathbf{y} is a vector of the observed binary phenotype (0= healthy, 1= diseased)
- \mathbf{b} is a vector of systematic fixed effects of year born-season
- \mathbf{hys} is a vector of random effects of herd-year-season at birth
- \mathbf{a} is a vector of random additive genetic effects
- \mathbf{e} is a vector of random residuals
- \mathbf{X} , \mathbf{Z}_{hys} and \mathbf{Z}_a are corresponding incidence matrices

Genetic parameter estimation

Dataset	Calf Traits	Single trait h^2	Multiple trait h^2	Genetic correlation
1% Data	Diarrhea	0.043	0.044	0.53 (0.07)
	Respiratory problems	0.027	0.043	
5% Data	Diarrhea	0.060	0.066	0.62 (0.07)
	Respiratory problems	0.037	0.071	

All heritability standard errors < 0.01

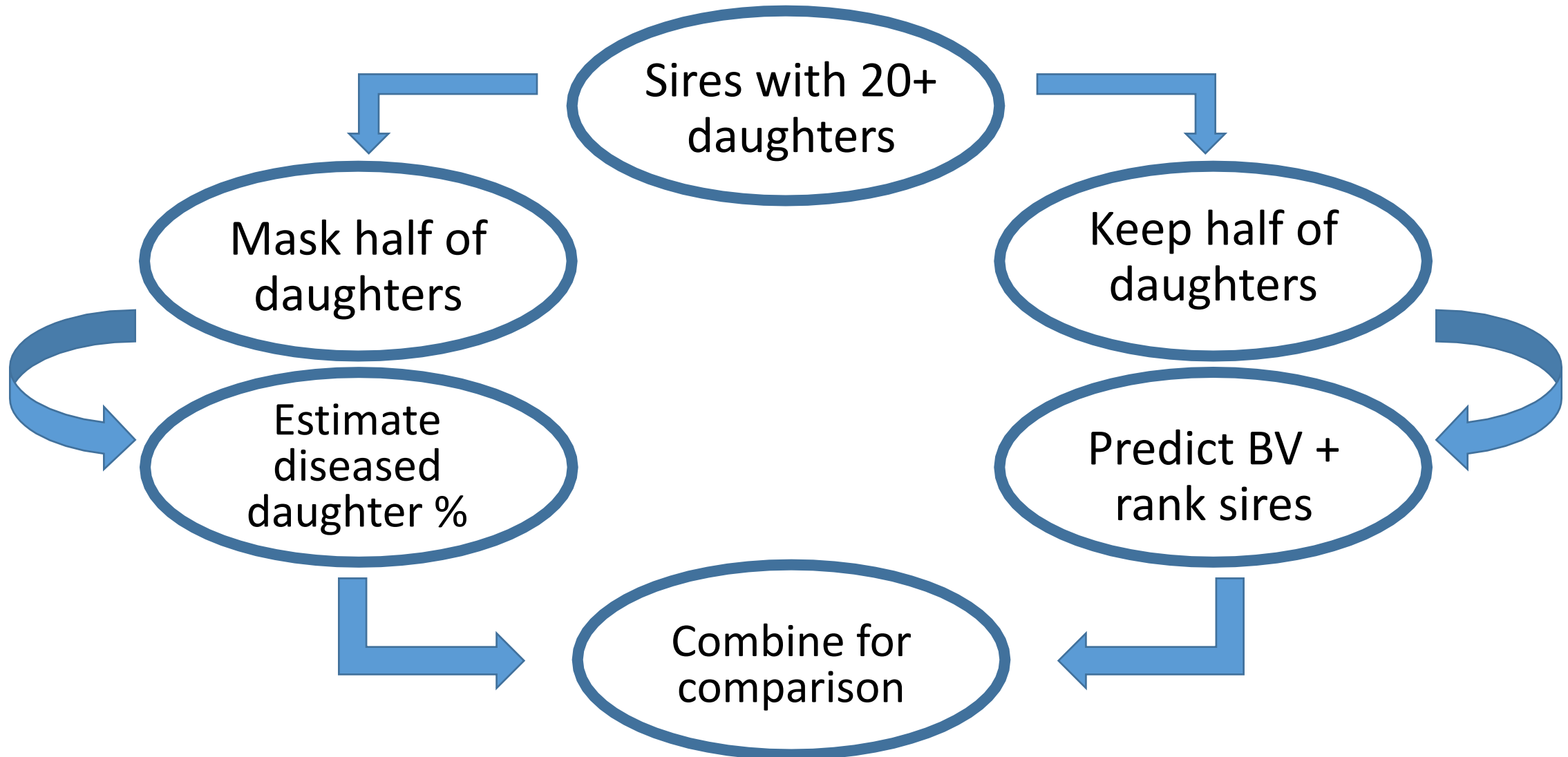
Genetic correlation with production (1st lactation)

Dataset	Calf Traits	Milk Yield	Fat Yield	Protein Yield
1% Data	Diarrhea	0.06 (0.05)	0.05 (0.05)	0.07 (0.05)
	Respiratory problems	0.02 (0.04)	0.07 (0.04)	0.05 (0.04)
5% Data	Diarrhea	0.09 (0.05)	0.05 (0.05)	0.09 (0.05)
	Respiratory problems	0.02 (0.04)	0.10 (0.04)	0.05 (0.04)

Genetic correlation with mastitis (1st lactation)

Dataset	Calf Traits	Clinical Mastitis	SCS150
1% Data	Diarrhea	0.37 (0.29)	-0.07 (0.12)
	Respiratory problems	0.11 (0.14)	-0.06 (0.08)
5% Data	Diarrhea	0.18 (0.36)	-0.14 (0.13)
	Respiratory problems	0.08 (0.19)	-0.09 (0.09)

Sire comparison



Diarrhea

Analysis	Data	Sires	Percentage of diseased daughters		
			Top 10%	Bottom 10%	Difference
Single trait	1%	737	14%	20%	1.4x
	5%	466	20%	30%	1.5x
Multiple trait	1%	629	15%	21%	1.4x
	5%	363	24%	36%	1.5x

Respiratory problems

Analysis	Data	Sires	Percentage of diseased daughters		
			Top 10%	Bottom 10%	Difference
Single trait	1%	1,607	14%	19%	1.4x
	5%	1,083	21%	27%	1.3x
Multiple trait	1%	629	19%	29%	1.5x
	5%	363	24%	36%	1.5x

Opportunities and challenges

Use of a multiple trait model for analyzing traits

Data collection practices need to be improved

- collaborative effort between producers, industry, academia and veterinarians

Differences in sire performance can be identified

Other avenues to explore:

- Epidemiological model approach
- Colostrum

Acknowledgements



IOWA STATE UNIVERSITY

