

## **A genetic evaluation for calf health: preliminary analysis**

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### **Abstract**

Growing consumer awareness means that the dairy industry needs to take proactive steps to improve animal health. Limited work has been conducted for improving Canadian calf health through genetics, and therefore, this study aimed to understand the current impact of calf health diseases on Canadian farms and to estimate genetic parameters for calf health traits. Calf health data comprised of 76,405 Canadian Holstein calf disease records for respiratory problems and diarrhea, collected on 1,890 Canadian dairy herds from 2009 to 2020. Incidence rates for respiratory problems were similar to values previously reported in literature, whereas diarrhea incidence rates were lower. Heritabilities of 0.01 and 0.04 were estimated for diarrhea and respiratory problems, respectively, which were lower than estimates reported in the literature. To maximise estimates stricter herd inclusion protocols, incorporating genomic information and splitting the traits by time of occurrence need to be investigated.

### **Introduction**

Emerging issues in dairy, related to animal welfare and social acceptability mean that the dairy industry must take proactive steps to improve animal health. Calf-hood diseases have a major impact on the economic viability of cattle operations, due to costs of treatment and long-term effects on performance (Svensson and Hultgren 2008; Mohd Nor et al. 2013). In the literature incidence rates for diarrhea range from 23% to 44%, while producers reported treating roughly 12% of pre-weaned calves for respiratory diseases (USDA 2010, 2018; Urie et al. 2018; Haagan et al. 2021). Though incidence reports are not available in Canada, diarrhea and respiratory diseases account for 53% and 21% of pre-weaned calf mortality in Canada, respectively (Murray 2011). Therefore, efforts to improve dairy calf health are vital.

From a genetic perspective, efforts aimed at breeding for increased disease resilience offer opportunities. Reported heritability estimates for respiratory disease and diarrhea range between 4% to 10% (Henderson et al. 2011; McCorquodale et al. 2013; Haagan et al. 2021), indicating the potential for genetic selection. In Canada, research has looked at improving overall cow health through initiatives such as Immunity+ provided by Semex, but this is proprietary, and no strategy for including calf health traits within national evaluations has been proposed. Therefore, the objective of this study was to understand the current impact of calf health diseases on Canadian farms and to estimate genetic parameters for calf health traits using existing data available. This work will provide the foundations for the inclusion of calf health traits within national Canadian genetic evaluations. Specifically, these results can be used to identify gaps in data collection methods which should be addressed in future developments for successful implementation of a national calf health selection strategy.

## Materials & Methods

**Data.** Calf health data recorded by dairy producers through management software was provided by Lactanet Canada (Guelph, Ontario). It comprised 76,405 Holstein calf disease records for respiratory problems and diarrhea, collected on 1,890 Canadian dairy herds from 2009 to 2020. All other calves present on the farm in a given year without a disease record were assumed to be healthy. To be considered in the analysis, records must have occurred within the first six months of the calf's life and each herd required a minimum annual disease incidence rate of at least 1%. This was calculated using the number of disease events in a herd per year over the total number of heifer calves raised on that farm in a given year. Additionally, herds had to have consecutive calf health records for years leading to and including 2020, or a minimum of three consecutive years of data available if there were no 2020 records. These metrics provided insight to which herds were consistently collecting calf disease information. A total of 62,168 records were used in the analysis after data validation and cleaning (Table 1).

**Table 1: Final datasets of calf health records.**

Trait	Diseased	Healthy	Total Records (Herds)
Diarrhea	18,887	101,857	120,744 (425)
Respiratory problems	43,281	212,502	255,783 (664)

**Models.** Univariate threshold animal models with a probit link function were used for both traits. A Bayesian approach based on the Gibbs sampling algorithm using the Markov chain Monte Carlo method with 1,000,000 iterations, 100,000 burn-in and 50 thinning interval was used for the analysis. Convergence of all chains was achieved, based on the Heidelberger and Welch, and Geweke convergence diagnostic tests. The general form of the model used was defined as:

$$l = Xb + Za + e \quad (1)$$

where  $l$  is a vector of underlying liabilities corresponding to the binary observation (0= healthy, 1= diseased),  $b$  is a vector of systematic fixed effects of year born-month born and herd,  $a$  is a vector of random additive genetic effects,  $e$  is a vector of random residuals and,  $X$  and  $Z$  are corresponding incidence matrices.

## Results

Incidence rates for each disease by year are presented in Table 2. The median incidence rate for each year was always lower than the mean for both traits. This was due to a number of herds with high incidence rates inflating the mean value. Given this, the median value should be seen as a better representation of the true average. For diarrhea, median incidence rate in herds ranged from 5% to 10% with the highest incidence rate seen in 2020. There was also a considerable increase in the number of herds collecting calf health data with this number rising from 54 herds in 2009 to 145 in 2020. For respiratory problems, median incidence rate in herds ranged from 8% to 12%, with the highest incidence rate seen in 2019. Again, there was a considerable increase in the number of herds collecting calf health data with this number rising from 133 herds in 2009 to 323 in 2020.

Variance components for each trait are presented in Table 3. Heritabilities were originally estimated on the liability scale and converted to the observed scale. Heritabilities of 0.01 and 0.04 were estimated for diarrhea and respiratory problems, respectively.

**Table 2: Descriptive statistics of diseases incidence rates in herds across years.**

Year	Diarrhea			Respiratory Problems		
	Mean %	Median %	Herds	Mean %	Median%	Herds
2009	10	5	54	16	8	133
2010	12	7	68	13	8	154
2011	12	8	86	15	10	187
2012	12	7	93	16	9	205
2013	11	7	98	16	10	230
2014	13	8	93	15	10	245
2015	13	8	107	16	10	253
2016	11	7	85	13	9	228
2017	11	6	98	14	10	260
2018	12	8	128	16	11	327
2019	13	8	166	17	12	355
2020	16	10	145	16	11	323

**Table 3: Variance components of disease traits in Canadian dairy calves.**

Parameters	Diarrhea	Respiratory Problems
Residual Variance	1.00	1.00
Genetic Variance (HPD)	0.02 (0.01 - 0.02)	0.05 (0.04 - 0.05)
Liability scale $h^2$ (HPD)	0.02 (0.01 - 0.02)	0.05 (0.04 - 0.05)
Observed scale $h^2$	0.01	0.04

HPD = Highest probability density

## Discussion

Reported incidence rates for respiratory problems were similar to the mean incidence rates previously reported in the literature, while for diarrhea values were lower (USDA 2010, 2018; Urie et al. 2018; Haagan et al. 2021). These differences may be due to several reasons, including quality of data collection and management practices. However, it is evident that consistent levels of calf disease were observed across years, indicating that there is an opportunity to reduce incidence rates and improve farm efficiency.

Heritabilities estimates for diarrhea and respiratory problems within this study were lower than estimates reported in the literature (Henderson et al. 2011; Mahmoud et al. 2017; Haagan et al. 2021). These differences could be attributed to several reasons including the lack of detailed information on individual calves, such as, birth weights and colostrum intake, which are directly related to the occurrence of respiratory problems and diarrhea (Henderson et al. 2011; Mahmoud et al. 2017). Another challenge is the uncertainty surrounding recording practices on farms. Farms without strict recording practices may have had sick animals that were assumed healthy in the current study, impacting model performance. Haagen et al. (2021) reported heritability estimates of 0.10 and 0.08 for respiratory problems and scours, respectively, with a similar lack of direct calf information as found in this study. The main difference was the use of genomic data for the estimation of genetic parameters. Furthermore, Vukasinovic et al. (2018) found higher estimates for respiratory problems by splitting the trait by age of occurrence, with heritabilities of 0.10 between 0 to 3d of age, 0.06 at 4 to 14d of age, and 0.05 at 15 to 50d of age, all above the estimate of 0.04 between day 0-365 of age. Given this, methods such as stricter herd inclusion protocols, incorporating genomic information, and looking at traits at specific times needs to be investigated with the current data to try to maximise model performance and improve parameter estimates.

## Conclusions

Growing consumer awareness means that the dairy industry needs to take proactive steps to improve animal health. In Canada, research has looked at improving overall cow health through initiatives such as Immunity+ provided by Semex, but no strategy for including calf health traits within national evaluations has been proposed. This study determined the current impact of calf health diseases on Canadian farms and provided initial estimates of genetic parameters for respiratory problems and diarrhea in Canadian dairy calves and, although the estimates were lower than those seen in other studies, they provide the foundations for future work. To improve estimates stricter herd inclusion protocols, incorporation of genomic information and splitting the traits by time of occurrence need to be investigated.

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