Genomic Evaluation for Calf Health in Canada

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Abstract

A genomic evaluation for calf health traits was developed for the Holstein breed in Canada effective August 2025. The new Calf Health index aims to increase resistance to the two most prevalent calf diseases on Canadian farms, respiratory problems (RESP) and diarrhea (DIAR). Producer-recorded respiratory problems and diarrhea health events recorded in the first 180d and 60d, respectively, of a heifer calf's life, are used in the genetic evaluation. RESP and DIAR, coded as binary traits, are used in a two-trait linear animal model considering a fixed year-season effect and random herd-year-season, animal, and residual effects for both traits. Genetic parameters were estimated by the MC EM REML method using 310 662 calf records from 1 179 herds. Heritability estimates were 0.05 for RESP and 0.04 for DIAR, with a genetic correlation of 0.53 between the traits. A Single-step genomic evaluation was implemented using the MiX99 software. A June 2025 evaluation test run had 355 355 records for RESP and 144 495 for DIAR, collected from 1 442 Canadian herds from 2007 to 2025. There were 74 013 calves with health records that were genotyped and a total of 119 715 genotyped animals in the reference population. The overall prevalence for RESP and DIAR was 19.5% and 21.1%, respectively. The Calf Health index combines genomic estimated breeding values for RESP and DIAR at equal weightings. Calf Health evaluations are published as a relative breeding value, with a mean of 100 and standard deviation of 5 for base bulls, where higher values represent greater resistance to calf health diseases. No genetic trend was observed and only weak relationships with other routinely evaluated traits were present. From a sire comparison analysis, clear differences were found when comparing high and low RBV sires in terms of daughter disease rates, highlighting the potential of the evaluation. Genetic selection for improved calf health is a valuable tool for animal welfare, lifetime animal production, and overall herd profitability.

Key words: Calf health, diarrhea, respiratory problems, single-step, genomic evaluation

Introduction

In recent years, genetic and genomic evaluations of dairy cattle have begun to prioritize animal health. In Canada, national genomic evaluations for dairy cattle now contain various health-related traits, including mastitis resistance, metabolic diseases, hoof lesions, and fertility disorders (Jamrozik et al., 2013, Jamrozik et al., 2016, Malchiodi et al., 2020, Jamrozik et al., 2021). To date, only traits related to the mature cow have been included. However, recent studies have shown the potential for improving calf health through genetic selection, with heritabilities ranging between 0.02 to 0.24 (Gonzalez-Peña et al., 2019; Lynch et al., 2024a). The two major calf disease classes are respiratory problems (RESP) and diarrhea (DIAR). Both diseases can be caused by several pathogens which makes control of the diseases difficult on farms. Prevalence rates of RESP are typically reported between 12 and 22%, while DIAR ranged from 23 to 44% (Windeyer et al., 2014, Urie et al., 2018, USDA, 2018; Gonzalez-Peña et al., 2019). Furthermore, RESP and DIAR account for roughly 75% of preweaning mortality, highlighting the impact of calf disease on dairy farms (NAHMS, 2007, Murray, 2011).

To address this, Lactanet Canada (Guelph, ON) has developed a new genomic evaluation for both RESP and DIAR, as part of a new calf health index, officially released in August 2025 for the Holstein breed. The objectives of this study were to describe the current impact of calf diseases on Canadian farms, the methodology of the genomic evaluation, and highlight the differences in sire performance.

Materials and Methods

Data and Trait Definitions

A detailed examination of the calf health (CH) recording and traits in Canadian Holsteins can be found in Lynch et al. (2024b). Calf disease data are recorded by Canadian dairy producers on a voluntary basis since 2007. The 'healthy' herd mates were determined using herd inventory data. The two calf disease traits with sufficient records were RESP and DIAR. Only Holstein records for female calves were considered for genetic evaluations. RESP and DIAR are expressed as binary traits where 0 represents no case and 1 represents at least one disease case occurring within the defined timeframe. For RESP the first 180d of life is considered while birth to 60d is used for DIAR. To ensure accurate and continuous data recording within individual herds, at least 2 recorded cases for a given disease were required within the dataset, with a minimum of 4 months between the 1st and the last record for a trait. Also, a minimum disease frequency of 1% within a herd-birth year was required.

Using the above criteria, data used in the June 2025 evaluation included 378 587 total records, with 355 355 and 144 495 for RESP and DIAR, respectively. A total of 121 263 records had values for both traits.

Model

The model is a two-trait linear animal model for RESP and DIAR. The same model is used for both traits, considering the fixed effect of year-season and random effects of herd-year-season (**HYS**), animal additive genetic, and residual. In matrix notation, the model can be written as:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Z_1h} + \mathbf{Z_2a} + \mathbf{e},$$

where y is a vector of observations (binary RESP and DIAR traits), **b** is a vector of the fixed effect, **h** is a vector of HYS effects, **a** is a vector of animal additive genetic effects, **e** is a vector of residuals, and $\mathbf{X}$, $\mathbf{Z_1}$, and $\mathbf{Z_2}$, are the respective incidence matrices. Random effects were assumed to be normally distributed, with means equal to zero.

Model assumptions are that: $v(\mathbf{h}) = \mathbf{I} \otimes \mathbf{HYS}$, $\mathbf{I}$ is an identity matrix and **HYS** is the covariance (2x2) matrix for HYS effects, $v(\mathbf{a}) = \mathbf{H} \otimes \mathbf{G}$, $\mathbf{H}$ is a combined pedigree-genotype relationship matrix, $\mathbf{G}$ is the additive genetic covariance, $v(\mathbf{e}) = \mathbf{R}$, $\mathbf{R}$ is a diagonal matrix of residual effects.

Genetic Parameters

Co-variance components and genetic parameters were estimated by MC-EM-REML as implemented in MiX99 (MiX99 Development Team, 2017) using a 2024 data extract including 310 662 records from 1 179 herds. The edits described above were also applied to the genetic parameter estimation dataset. The same model as described for genetic evaluation purposes above was used, but the combined pedigree-genomic relationship matrix **H** was replaced by an additive relationship matrix **A**.

Genomic Evaluation

A two-trait component-wise Single-Step GTABLUP method (Mantysaari et al., 2017) was implemented at Lactanet Canada using MiX99 and related software (MiX99 Development Team, 2017), with the assumption that 80% of the total genetic variance was explained by SNP effects. The June 2025 data included 119 715 genotyped animals, of which 74 013 were genotyped females with phenotypes and 8 570 were genotyped sires with phenotyped daughters. Animals are genotyped either with 50K SNP panel or a low-density panel and imputed to 50K using F-Impute (Sargolzaei al., 2014). Groups for unknown parents are not included in the model. The SNP effects, to be used for calculating Genomic Estimated Breeding Values (**GEBV**) for genotyped animals not included in the single-step core analysis, are estimated from the GEBV of reference animals (as in Lourenco et al., 2015).

Reliability of GEBV is approximated by a weighted (80:20) average of Direct Genomic Value (**DGV**) and animal model reliabilities (Sullivan et al., 2005). The DGV reliabilities are calculated using SNP prediction error co-variances with the SNP-BLUP-REL software (Luke, Finland). Animal model reliabilities are calculated with the EDC and reliability software of Sullivan (2023).

Relative Breeding Values

The CH index combines the two individual RESP and DIAR traits at equal weighting. The index and the individual traits are published. The evaluations are expressed as Relative Breeding Values (**RBV**) with a mean of 100 and SD of 5 for base bulls that for April 2025 are those born 2010-2019 and with an 'official' status. A higher RBV value means a greater resistance to calf health diseases. Sire evaluations are defined as 'official' for RESP and DIAR when they have at least 20 phenotyped daughters from 5 herds for the respective trait and a minimum reliability of 70%. Sires are official for CH when they are official for both contributing traits.

Sire Comparison Validation

To investigate the difference in performance of top and bottom performing sires, a random cross-validation study was conducted. For each trait, official sires with at least 30 phenotyped daughters were included in the analysis. Randomly half of each sire's phenotyped daughters had their phenotype changed to missing, while the remaining half were used to predict sires' RBV. Sires were then ranked according to their RBV. The daughters with their phenotype set to missing for the evaluation were used to determine the sires' daughter disease rate for both the calf diseases, therefore acting as an independent sample. Sires with an RBV greater than 110 and lower than 90 were then compared based on their percentage of disease daughters for each calf disease. This process was repeated five times and averaged across iterations to get an accurate representation of sire performance across different sample groups.

Results and Discussion

Incidence Rates

Incidence rates across years for RESP and DIAR are shown in Figure 1. On average, the incidence rates for RESP and DIAR were 19.5% and 21.1%, respectively, which were similar to values reported in the literature (Lynch et al. 2024a). Greater fluctuation has been seen in DIAR incidence rates, whereas RESP has remained relatively stable. This fluctuation may be due to several factors, including changes in herds reporting information and quality of reporting over time.

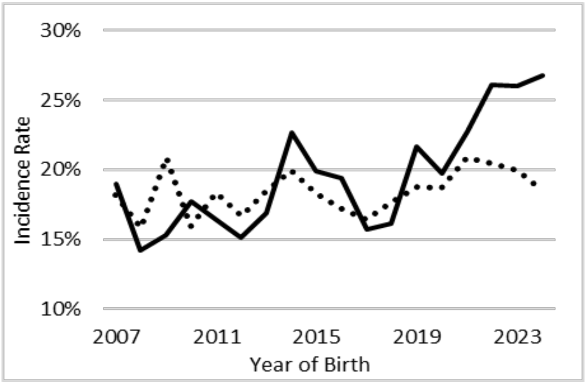

Figure 1: Incidence rates across years for Respiratory Problems (dotted line) and Diarrhea (solid line).

Genetic Parameters

Heritability and genetic and phenotypic correlation estimates for RESP and DIAR are shown in Table 1. The heritabilities for RESP and DIAR were 0.054 and 0.044, respectively. Estimates were similar to those reported in the literature for calf disease traits and other health related traits in the Canadian Holstein population (Lynch et al. 2024a, Jamrozik et al., 2013, Jamrozik et al., 2016, Malchiodi et al., 2017, Jamrozik et al., 2021).

Table 1: Heritabilities with standard error in parentheses, genetic correlations (above diagonal), and phenotypic correlations (below) diagonal for Respiratory Problems (RESP) and Diarrhea (DIAR).

	RESP	DIAR
RESP	0.054 (0.010)	0.53
DIAR	0.13	0.044 (0.013)

Genomic Evaluations

In the June 2025 preliminary evaluation run there were 1 393 Holstein sires with an official CH evaluation. The RBV for CH evaluation ranged from 78 to 114 for this group and averaged 100. The average reliability was 87% and ranged from 72 to 99% for official sires. The average reliability of genotyped, young Holstein bulls without daughter records that were identified as being controlled by an AI organization (N=3 744) was 70%.

Proof correlations were estimated between CH index, RESP and DIAR and other routinely evaluated traits in Canada using 937 Holstein sires born since 2010 with an official LPI and CH index. The proof correlation between RESP and DIAR was 0.39, which is similar but slightly lower than the genetic correlation estimate. This highlights some difference in the two traits and that the CH index is useful to make effective progress in both traits, since the proof correlation for RESP and DIAR with CH is 0.83 and 0.84, respectively. For other routinely evaluated traits, little to no correlations were found. No proof correlations above |0.20| were found between CH and RESP for any other trait currently being evaluated. For DIAR, the only proof correlations stronger than 0.20 were for Calving Ability (-0.20) and Calving Ease of daughters at first and later calvings (-0.21 and -0.20, respectively). Direct selection on the CH index is therefore important to make progress in the calf health traits analyzed.

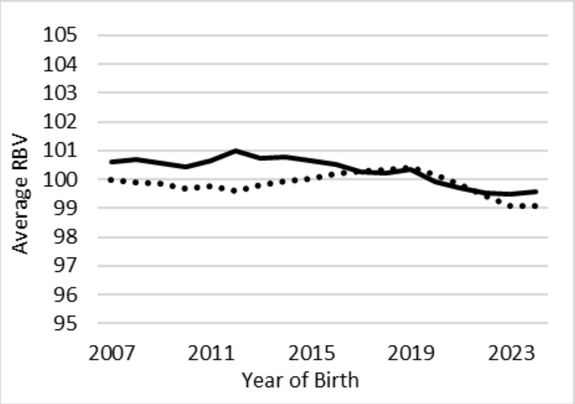

Figure 2: Genetic trend for Holstein females with records for Respiratory Problems (dotted line) Diarrhea (solid line).

The genetic trend for CH in females with records in the evaluation is shown in Figure 2. The genetic trend has been relatively flat since the onset of trait recording. Since there is little to no relationship with other traits under selection in the Canadian Holstein population, this is expected.

Sire Comparison

On average, daughters born to sires with an RBV less than 90 were 1.8 times more likely to exhibit DIAR compared to daughters born to sires with an RBV greater than 110, while for RESP they were 1.3 times more likely. These differences help highlight the difference in sire performance and show the potential of the evaluation to help improve the health of young dairy calves. These results are in line with a similar approach conducted by Lynch et al. (2024b).

Conclusions

Genetic improvement of Calf Health is highly valuable as it impacts replacement loss, lifetime performance, animal welfare, and overall profitability. The first genomic evaluations for the Calf Health index and the contributing traits, DIAR and RESP, were published in August 2025 by Lactanet for the Canadian Holstein breed. The introduction of the CH index in the Canadian national selection index LPI within its Health and Welfare subindex is scheduled for April 2026.

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