



Estimated genetic parameters for all genetically evaluated traits in Canadian Holsteins

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ABSTRACT

Genetic improvement is a crucial tool to deal with the increasing demand for high quality, sustainably produced dairy. Breeding programs are based on genetic parameters, such as heritability and genetic correlations, for economically important traits in a population. In this study, we estimated population genetic parameters and genetic trends for 67 traits evaluated on heifers and first-lactation Canadian Holstein cows. The data consisted of approximately 500,000 records with pedigree information collected from 1980 to 2019. Genetic parameters were estimated using bivariate linear animal models under a Bayesian approach. Analyses for the 67 traits resulted in 2,211 bivariate combinations, from which the estimated genetic parameters are reported here. The most highly heritable traits were fat percent (0.66) and protein percent (0.69), followed by stature (0.47). Lowest heritabilities (0.01) were observed for disease-related traits, such as lameness and toe ulcer, and calf survival. The genetic correlations between gestation length, calf size, and calving ease measured on both heifer and cows were close to unity. On the other hand, traits such as body condition score and pin width, cystic ovaries and sole ulcer, rear teat placement, and toe ulcer were genetically unrelated. This study reports genetic parameters that have not been previously published for Canadian Holstein cows, and provides updates of those previously estimated. These estimates are useful for building new indexes, updating existing selection indexes, and for predicting correlated responses due to inclusion of novel traits in the breeding programs.

Key words: heritability, genetic correlation, genetic trends

INTRODUCTION

The Canadian dairy industry has approximately 968,700 dairy cows on 10,371 farms. Among these animals, around 64.2% are enrolled in milk-recording programs, of which 39.8% are on supervised systems and 24.4% are on unsupervised systems. The Canadian dairy cattle population consists of 7 main dairy breeds, with 93% of cows registered as Holstein (Canadian Dairy Information Center, 2019). Demand for dairy products is likely to increase over the coming decades as global population and wealth increases. Although the genetic improvement of livestock has been very successful in increasing productivity, there is still pressure to improve the sustainability of the dairy industry and the traits contributing to it.

In Canada, genetic selection in Holstein cattle has been done through the Lifetime Performance Index, formerly known as Lifetime Profit Index (**LPI**), since it was introduced in 1991 and, more recently, through an alternative index called Pro\$. In the last 20 yr, 3 changes were made to LPI's main components; that is, production: durability: health and fertility, shifting their respective emphasis from 57:38:5 (2001) to 54:36:10 (2005), 51:34:15 (2008), and 40:40:20 (2016). The estimation of genetic parameters for economically important traits is a crucial component of animal breeding programs. Miglior et al. (2017) reviewed the development of phenotypes used in the Canadian dairy cattle selection program over time. Genetic parameters related to the Canadian Holstein population have been estimated for production (e.g., Miglior et al., 2007; Loker et al., 2012), conformation (e.g., Van Dorp et al., 2004), fertility (e.g., Jamrozik et al., 2005; Sewalem et al., 2010; Alves et al., 2020), and relatively more novel traits, such as metabolic diseases (e.g., Guarini et al., 2019), hoof health (e.g., Malchiodi et al., 2017) and milk properties (e.g., Nayeri et al., 2020). Martin et al. (2019) looked at the genetic correlation among a subset of 28 traits on Canadian Holstein cows from all trait groups, except hoof health. In addition to the importance of re-estimating these parameters using current data, a study involving all current routinely recorded

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traits in Canada has not yet been done. The knowledge of the (co)variance between conventional and relatively more novel traits is critical for updating selection indexes and predicting correlated responses when new traits are integrated in the breeding program. The objective of this study was therefore to estimate the genetic parameters for all 67 current routinely evaluated traits in primiparous Canadian Holstein cows.

MATERIALS AND METHODS

Data

Data for 67 traits measured on first-lactation cows and heifers were obtained from Lactanet (Guelph, ON, Canada) and were grouped into 5 categories: production (5), conformation (26), fertility (9), health (9), calving (8), workability (2), and hoof health (8). Trait names, abbreviations and definitions are presented in Table 1, whereas their respective descriptive statistics are presented in Supplemental Table S1 (<https://cgil.shinyapps.io/correlations/>).

Edits were applied to remove contemporary groups (herds) with fewer than 5 animals, and animal records exceeding 3.5 standard deviations above or below the overall trait mean. Within the health file, additional editing steps were applied separately for each disease according to literature (Koeck et al., 2012b; Jamrozik et al., 2016; Guarini et al., 2019). Milk fever was not included in this study, given its low occurrence in first-lactation cows (<1%). The fertility traits included in the analysis were edited as in Jamrozik et al. (2005), and hoof lesions were edited following Malchiodi et al. (2017).

A subset of the data was generated by randomly sampling (sample_n function in R) herds for estimation of (co)variance components and genetic parameter. This resulted in files with about 500,000 animals with records over the past generations on at least 1 trait within each trait category. The birth year of animals with recorded phenotypes ranged from 1980 up to 2018. The final pedigree file comprised more than 14 million animals. Four seasons of calving were defined as January to March, April to June, July to September, and October to December. Age at calving classes included 8 levels (17–24, 25, 26, 27, 28, 29, 30–31, >31 mo).

Statistical Models

Bivariate linear animal models were used to estimate (co)variance components using Bayesian methods via Gibbs sampling in the GIBBS1F90 software (<http://nce.ads.uga.edu/html/projects/programs/Linux/32bit/gibbs1f90>; Misztal et al., 2002). The software

uses noninformative inverse Wishart distribution as a priori distributions for (co)variance components for all dispersion parameters. A single chain with a minimum length of 505,000 was generated, in which the first 5,000 iterations were discarded as burn-in. An initial thinning interval of 10 cycles was used, which was increased when needed to overcome autocorrelation between sampled values. Convergence was monitored by visual inspection of trace plots of variance components. Longer chains were generated when convergence criteria were not achieved.

The linear animal models used are presented in Table 2. In general, the models can be described as follows:

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}\mathbf{a} + \mathbf{W}\mathbf{h} + \mathbf{e},$$

where \mathbf{y} is the vector of observations; \mathbf{b} is the vector of fixed effects; \mathbf{a} is the vector of random additive genetic effects; \mathbf{h} is the vector of random herd-year effects; \mathbf{e} is the vector of random residual effects; \mathbf{X} , \mathbf{Z} , and \mathbf{W} are design matrices relating observations in \mathbf{y} to factors in the model. The covariance matrix was defined as

$$\begin{bmatrix} \mathbf{a} \\ \mathbf{h} \\ \mathbf{e} \end{bmatrix} \sim MVN \left(\begin{bmatrix} \mathbf{0} \\ \mathbf{0} \\ \mathbf{0} \end{bmatrix}, \begin{bmatrix} \mathbf{G} \otimes \mathbf{A} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{I} \otimes \mathbf{H} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{I} \otimes \mathbf{R} \end{bmatrix} \right),$$

where \mathbf{G} is the covariance matrix of random additive genetic effects between traits, \mathbf{H} is the covariance matrix of random herd-year effects between traits, and \mathbf{R} is residual covariance matrix between traits. The \mathbf{A} matrix is the additive genetic relationship matrix; and \mathbf{I} is an identity matrix. The nonlinear (score) traits, were analyzed using a linear model, as literature indicates that analyzing these traits with a linear model does not affect model fit and has little effect on the ranking of animals (Negussie et al., 2008; Neuenschwander et al., 2012). Phenotypic correlations (r_p) were estimated as

$$r_p = r_g \sqrt{h_1^2 h_2^2} + r_{hy} \sqrt{hy_1^2 hy_2^2} + r_e \sqrt{e_1^2 e_2^2},$$

where, for trait i , $h_i^2 = \sigma_{ai}^2 / \sigma_{pi}^2$, $hy_i^2 = \sigma_{hyi}^2 / \sigma_{pi}^2$, $e_i^2 = \sigma_{ei}^2 / \sigma_{pi}^2$, $\sigma_{ai}^2 =$ additive genetic variance, $\sigma_{hyi}^2 =$ herd-year variance, $\sigma_{ei}^2 =$ residual error variance, $r_g =$ additive genetic correlation, $r_e =$ residual error correlation, $r_{hy} =$ herd-year correlation. The phenotypic variance (σ_{pi}^2) was estimated as $\sigma_{ai}^2 + \sigma_{hyi}^2 + \sigma_{ei}^2$. Both σ_{hyi}^2 and r_{hy} were zero for traits that did not have herd-year effect in their models. For all parameters, posterior

Table 1. Abbreviations, trait names and their short definitions

Abbreviation	Trait name	Short definition
FY	305-d fat yield	Total fat yield in the lactation standardized to 305 d
Fat%	305-d fat (%)	Fat percentage based on a 305-d lactation records
MY	305-d milk yield	Total milk yield in the lactation standardized to 305 d
PY	305-d protein yield	Total protein yield in the lactation standardized to 305 d
Protein%	305-d protein (%)	Protein percentage based on 305-d lactation records
CO	Cystic ovaries	Presence of follicles greater than 25 mm in diameter in the ovaries
DA	Displaced abomasum	When the abomasum becomes filled with gas and rises to the top of the abdomen
CK	Clinical ketosis	Decreased appetite with evidence of elevated milk, urine or breath ketones
LAM	Lameness	Change in an animal's walking pattern resulting in dysfunction of the locomotion system
MAST	Clinical mastitis	Inflammation of the udder resulting in abnormal milk from ≥ 1 quarters
METR	Metritis	Presence of an abnormally enlarged uterus containing fetid watery red brown fluid
RP	Retained placenta	Failure to eliminate afterbirth within 24 h of calving
SCS	SCS	Based on the SCC of the milk—used as an indicator of mastitis
BHB	Beta-hydroxybutyric	Amount of BHB in milk; used as an indicator of ketosis
AFS	Age at first service	Age in days when a heifer is first inseminated
FSTC	First service to conception ¹	Number of days between the first and last insemination that resulted in a calf
CTFS	Calving to first service	Number of days between calving and first insemination after calving
DO	Days open	Total number of days open from first insemination after calving to conception date
NRR	Nonreturn rate ¹	Measure if an animal is confirmed pregnant 56 d after insemination
NSC	Number of services per conception ¹	Number of times an animal was inseminated before becoming pregnant
CE	Calving ease ¹	Measure from 1 (unobserved/unassisted) to 3 (c-section)
CS	Stillbirth ¹	Calf survival after 24 h postbirth (0 = survived, 1 = stillbirth)
GL	Gestation length ¹	Number of days pregnant
CZ	Calf size ¹	Size of calf scored by producers from 0 (small) to 3 (large)
BCS	BCS	Amount of fat deposition in the tailhead, loin and pelvic region
BD	Body depth	Depth of the body at the rear rib from 1 (shallow) to 9 (deep)
BQ	Bone quality	Flatness of bone from 1 (coarse) to 9 (flat)
CW	Chest width	Width at the chest floor from 1 (narrow) to 9 (wide)
FAN	Foot angle	Angle of hairline at the hoof from 1 (low) to 9 (steep)
FA	Fore attachment	Attachment to the abdominal wall from 1 (weak) to 9 (strong)
FTP	Front teat placement	Teat placement from the center of the quarter from 1 (wide) to 9 (close)
HD	Heel depth	Depth of the heel on the outside claw from 1 (shallow) to 9 (deep)
HFE	Height at front end	Difference in height at the withers compared with the back of the animal from 1 (low) to 9 (high)
LS	Loin strength	Strength of vertebrae between back and rump from 1 (weak) to 9 (strong)
MSL	Median suspensory	Depth of the cleft (fore/rear) from 1 (weak) to 9 (strong)
PS	Pin setting	Height of pin bones relative to height of hook bones from 1 (high) to 9 (low)
PW	Pin width	Distance between point of pins from 1 (narrow) to 9 (wide)
RAH	Rear attachment height	Distance from the top of the udder at the back of the cow to the base of the vulva from 1 (low) to 9 (high)
RAW	Rear attachment width	Width of the milk secreting tissue at the top of the udder at the back of the cow from 1 (narrow) to 9 (wide)
RTP	Rear teat placement	Teat placement from the center of the quarter from 1 (wide) to 9 (close)
RLRV	Rear legs rear view	Turn of the hock when viewed from rear from 1 (hocked-in) to 9 (straight)
RLSV	Rear legs side view	Degree of curvature of rear leg at the hock from 1 (straight) to 9 (curved)
RA	Rump angle	Height of pin bones relative to height of hip bones from 1 (high) to 9 (low)
SRL	Set of rear legs	Degree of curvature (side view) from 1 (straight) to 9 (curved)
ST	Stature	Height at rump from 1 (short) to 9 (tall)
TL	Teat length	Average length of the rear teats from 1 (short) to 9 (long)
THP	Thurl placement	Horizontal position of thurl between the hook and pin bones from 1 (back) to 9 (ahead)
UD	Udder depth	Distance from hock to floor of udder from 1 (deep) to 9 (shallow)
UT	Udder texture	Softness and expandability from 1 (fleshy) to 9 (soft)
DC	Dairy capacity	Angle, openness and spring of ribs from 1 (nonangular) to 9 (angular)
DD	Digital dermatitis	1 = nonaffected or 2 = affected
HHE	Heel horn erosion	1 = nonaffected or 2 = affected
ID	Interdigital dermatitis	1 = nonaffected or 2 = affected
IH	Interdigital hyperplasia	1 = nonaffected or 2 = affected
SH	Sole hemorrhage	1 = nonaffected or 2 = affected
SU	Sole ulcer	1 = nonaffected or 2 = affected
TU	Toe ulcer	1 = nonaffected or 2 = affected
WL	White line disease	1 = nonaffected or 2 = affected
MSP	Milking speed	Speed of milking from 1 (very slow) to 5 (very fast)
MT	Milking temperament	Temperament during milking from 1 (very nervous) to 5 (very calm)

¹Measured in heifers and cows.

mean, posterior standard deviation (PSD), and 95% highest posterior density were calculated. Genetic trends for bulls, cows, and overall (bulls + cows) were calculated by taking the mean EBV for animals born in a specific year. Only the overall trends will be used when discussing the results.

RESULTS AND DISCUSSION

Analysis of the 67 traits resulted in 2,211 bivariate combinations. The descriptive statistics, as well as the posterior variance components and genetic trends, are available online: <https://cgil.shinyapps.io/correlations/>. Supplemental Tables S1 to S7 show the descriptive statistics, posterior mean, PSD, and the 95% highest posterior density of the estimated parameters. As previously mentioned, knowledge of genetic parameters is crucial for animal breeding programs, not only for best linear unbiased prediction, but also to predict genetic gain, indirect selection response, and to build and update selection indexes. Given the plethora of results produced by this project, the authors chose only to discuss genetic parameters. All correlations reported herein therefore refer to genetic correlations, unless otherwise stated. The reported heritability values are the mean of all estimated heritabilities for a given trait. Trait initials are defined again in the text to facilitate the reader's understanding.

Heritability, as well as genetic correlations, are based on similarity among relatives, quantified by pedigree information (Falconer, 1981). Heritability measures the expected proportion of the differences in performance due to additive genetic effects (narrow-sense heritability). Higher values indicate a higher relationship between the performance of parents and offspring for a given trait. On the other hand, low heritable traits mean that an animal's performance is less useful in identifying the individual's breeding value for the trait. Pedigree errors and data noise can bias heritability estimations downwards, whereas the reduction of environmental and residual components increases the accuracy of heritability estimates. A precise definition and improved consistency in measurements is a way to reduce data noise. It is worth emphasizing that low heritability does not necessarily imply a lack of genetic variability (Berry et al., 2019). In addition, even though some traits present low heritabilities (<0.05), they might have sufficient genetic variance and high economic value, justifying selection for these traits.

When selecting for new traits, it is essential to remember that even though it is possible to intensely select for a single trait, consideration must be given to the genetic correlations that exist with other economi-

cally important traits. The genetic correlation expresses the magnitude and direction in which a pair of traits are linearly genetically associated and can be caused either by linkage disequilibrium of genes affecting the 2 traits independently or by the pleiotropic effects of single genes. Traits could be phenotypically correlated but not share any genetic background, meaning that the phenotypic correlation is determined solely by the environmental correlation. In this case, selection on one trait has no effect on the response of the other (Walsh and Lynch, 2018). On the other hand, for highly heritability traits, the genetic correlation has the largest contribution to the observed (phenotypic) correlation. The dual nature of phenotypic correlation often makes it a poor approximation of genetic correlations, as even the sign of these correlations may differ (Falconer, 1981). However, differences between phenotypic and genetic correlations may also be a consequence of imprecise estimates of genetic correlations (Cheverud, 1988; Koots and Gibson, 1996). It is important to highlight that traits with an antagonistic relationship (e.g., production and fertility) can still be improved simultaneously through selection. The inclusion of antagonistic traits in a selection index may reduce the rate of genetic gain in either trait due to a reduction in selection intensity; however, genetic gain is still possible in both traits (Berry, 2013).

Genetic selection aims to change the population mean genotypic value and, consequently, the observed phenotypes. This shift of the mean is caused by very small changes in allele frequency over the genome under a polygenic model. This change in allele frequency is cumulative and permanent (Walsh and Lynch, 2018). Changes in allele frequency are also expected to affect genetic correlation (Bohren et al., 1966). Given that selection can cause changes in correlation values over time, there is a need to frequently re-estimate these parameters.

Divergence in genetic parameters among studies are likely related to the differences in data structure, statistical models, and the population sampled. Koots and Gibson (1996) stated that variation in estimated genetic parameters for different populations can be also related to poor estimation of residual variances. Although genomic information was not included in this study, Forni et al. (2011) and Veerkamp et al. (2011) found that estimates by REML and single-step genomic REML (ssGBLUP) were similar, with ssGBLUP resulting in smaller standard errors due to the inclusion of genomic information. Cesarani et al. (2019), working with simulated data, also reported similar results between REML and ssGBLUP, depending on the genotyping strategy applied.

Table 3. The posterior mean¹ of the genetic correlation (above diagonal), heritability (diagonal), and phenotypic correlation (below diagonal) for production traits²

Item	Fat%	FY	MY	Protein%	PY
Fat%	0.66	0.49	-0.52	0.66	-0.22
FY	0.36	0.31	0.48	0.09	0.64
MY	-0.29	0.46	0.33	-0.57	0.86
Protein%	0.50	0.07	-0.32	0.68	-0.08
PY	-0.14	0.81	0.59	0.08	0.24

¹Posterior standard deviations (PSD) for heritability estimates varied from 0.0013 to 0.0014, whereas for genetic and phenotypic correlations, they varied from 0.0009 to 0.0030 and 0.0002 to 0.0008, respectively. Individual PSD are given in Supplemental Table S2 (<https://cgil.shinyapps.io/correlations/>).

²Fat% = fat percentage, FY = fat yield, MY = milk yield, protein% = protein percentage, PY = protein yield.

Heritability

Production. Heritability estimates of production traits varied from 0.24 protein yield (**PY**) to 0.68 (protein %; Table 3). Similar results were reported by Jamrozik and Schaeffer (1997), with heritabilities of 0.32, 0.28, and 0.28 for milk yield (**MY**), fat yield (**FY**), and PY, respectively. Likewise, Kadarmideen et al., (2003) reported heritabilities of 0.28, 0.21 and 0.19 for MY, FY, and PY, respectively. Cassell (2009), working with US Holstein cattle, estimated heritability of 0.30 for yield traits (milk, fat, protein) and 0.58 and 0.43 for fat percentage and protein percentage, respectively. Although yield trait heritabilities were similar to the ones estimated in our study, higher estimated values were found for fat percentage and protein percentage. As already discussed, these divergences are expected, given the different statistical models and populations used in each study.

Conformation. Conformation trait results were divided into 4 groups based on the scorecard sections established by Holstein Canada (www.holstein.ca), and included mammary system, feet and legs, dairy strength, and rump. There are currently 26 confor-

mation traits being genetically evaluated in Canada, which are recorded by Holstein classifiers with a 1 to 9 linear score, except for pin width (**PW**), rear attachment height, rear attachment width, stature (**ST**), teat length, udder depth, which are measured in centimeters. Body condition score and rump angle are also recorded differently, with a 1 to 5 score and in angles, respectively. Although these 8 traits are transformed into a 1 to 9 linear score for the national genetic evaluations, we considered them on their observed measure or score.

Heritability for conformation traits ranged from 0.04 set of rear legs to 0.47 (**ST**). Within scorecards, udder depth (0.41; mammary system), bone quality (0.27; feet and legs), **ST** (0.47; dairy strength), and rump angle (0.36; rump) were the most heritable traits (Tables 4, 5, 6, and 7).

Fertility. Heritabilities of all fertility traits are given in Table 8. They ranged from 0.01 (first service to conception measured on heifers, nonreturn rate (**NRR**), **NRR** measured on heifers, number of services measured on heifers) to 0.06 [calving to first service (**CTFS**), days open (**DO**)] and are in line with the literature (Berry et al., 2016; Fleming et al., 2019). Fleming et

Table 4. The posterior mean¹ of the genetic correlation (above diagonal), heritability (diagonal), and phenotypic correlation (below diagonal) for mammary system traits²

Item	FA	FTP	MSL	RAH	RAW	RTP	TL	UD	UT
FA	0.26	0.28	0.04	-0.48	0.23	-0.01	-0.10	0.70	0.38
FTP	0.12	0.29	0.32	-0.06	0.18	0.63	-0.27	0.14	0.32
MSL	0.17	0.19	0.16	-0.25	0.41	0.55	-0.02	0.02	0.73
RAH	-0.57	-0.05	-0.40	0.23	-0.40	-0.06	0.07	-0.41	-0.41
RAW	0.44	0.13	0.48	-0.24	0.18	0.19	0.00	-0.10	0.23
RTP	0.00	0.22	0.28	-0.02	0.08	0.30	-0.17	-0.05	0.31
TL	-0.02	-0.10	0.01	0.00	0.03	-0.07	0.29	-0.13	-0.05
UD	0.82	0.14	0.03	-0.34	-0.10	-0.01	-0.06	0.41	0.40
UT	0.37	0.16	0.39	-0.47	0.32	0.14	-0.01	0.14	0.13

¹Posterior standard deviations (PSD) for heritability estimates varied from 0.0016 to 0.0021, whereas for genetic and phenotypic correlations, they varied from 0.0040 to 0.0110 and 0.0008 to 0.0030, respectively. Individual PSD are given in the supplemental Table S2 (<https://cgil.shinyapps.io/correlations/>).

²FA = fore attachment, FTP = front teat placement, MSL = median suspensory ligament, RAH = rear attachment height, RAW = rear attachment width, RTP = rear teat placement, TL = teat length, UD = udder depth, UT = udder texture.

Table 5. The posterior mean¹ of the genetic correlation (above diagonal), heritability (diagonal), and phenotypic correlation (below diagonal) for feet and legs traits²

Item	BQ	FAN	HD	RLRV	RLSV	SRL
BQ	0.27	-0.06	0.02	0.23	0.20	0.38
FAN	0.01	0.08	0.83	0.24	-0.35	0.36
HD	0.04	0.36	0.08	0.17	-0.34	0.37
RLRV	0.28	0.08	0.09	0.11	-0.24	0.47
RLSV	0.13	-0.07	-0.07	-0.16	0.21	-0.33
SRL	0.17	0.08	0.10	0.23	-0.07	0.04

¹Posterior standard deviations (PSD) for heritability estimates varied from 0.0013 to 0.0020, whereas for genetic and phenotypic correlations, they varied from 0.0059 to 0.0140 and 0.0008 to 0.0013, respectively. Individual PSD are given in Supplemental Table S2 (<https://cgil.shinyapps.io/correlations/>).

²BQ = bone quality, FAN = foot angle, HD = heel depth, RLRV = rear legs rear view, RLSV = rear legs side view, SRL = set of rear legs.

al. (2019) showed that the relative emphasis on fertility traits in selection indices globally was around 15%. One of the 2 current selection indexes in Canada (LPI) attributes 20% to the “health and fertility” component, which includes “daughter fertility” as a subindex weighted 67%, with the remaining 33% going toward “mastitis resistance” (Canadian Dairy Network, 2020). Therefore, the weight on fertility traits on LPI is about 13% and, given this low emphasis and low heritabilities of fertility traits, dairy producers should not expect rapid genetic improvements for these traits in the short term. Miglior et al. (2017) suggested that indicator traits, such as BCS, could be useful when selecting for fertility, given the low heritability and measurement difficulties of current fertility traits.

Calving. Selection for calving traits in Canada started in the yearly 2000s with calving ease (2006) and later calf survival (2007). Although these 2 traits are normally split in direct and maternal contribution, this study focused only on the direct effect. Low heritabilities were estimated for these traits, 0.03 for CE and 0.01 for CS (Table 9). Steinbock et al. (2003) also reported low heritabilities for direct calf survival and calving ease, with values of 0.04 and 0.06, respectively. Although calving difficulties are costly to dairy produc-

ers, the Canadian Dairy Network reported that unassisted calving represented 69 and 74% of progeny born from heifers and cows, respectively, from 2016 to 2020. Moreover, the phenotypic trend of having an unassisted calving has increased since 2003 (Fleming et al., 2020).

Gestation length in both heifers and cows had the highest heritability within calving traits, at 0.17 and 0.13, respectively. Norman et al. (2011) found that an intermediate gestation length was desirable for productive life, calving ease, stillbirth, culling, and days open. In contrast, Jenkins et al., (2016) concluded that the net effect of shortened gestation length is likely to be economically positive for the seasonal calving dairy system of New Zealand.

Health. A national dairy cattle health and disease data management system was implemented in 2007 by the Canadian DHI associations. Recording of disease incidence is done by producers using on-farm herd management software or record books. These records are later collected by the DHI milk-recording technicians at each test-day herd visit and then provided to the region’s DHI association. Additionally, health data from producers participating in the Dossier Santé Animale/Animal Health Record program is collected and forwarded to the DHI database by veterinarians.

Table 6. The posterior mean¹ of the genetic correlation (above diagonal), heritability (diagonal), and phenotypic correlation (below diagonal) for dairy strength traits²

Item	BCS	BD	CW	DC	HFE	ST ³
BCS	0.23	0.09	0.72	-0.71	-0.01	-0.04
BD	0.05	0.31	0.57	0.45	0.30	0.16
CW	0.24	0.26	0.20	-0.06	0.29	0.36
DC	-0.22	0.29	0.06	0.19	0.11	0.46
HFE	0.01	0.07	0.12	0.25	0.24	0.27
ST ³	0.07	0.32	0.70	0.40	0.33	0.47

¹Posterior standard deviations (PSD) for heritability estimates varied from 0.0019 to 0.0027, whereas for genetic and phenotypic correlations, they varied from 0.0040 to 0.0064 and 0.0008 to 0.0035, respectively. Individual PSD are given in Supplemental Table S2 (<https://cgil.shinyapps.io/correlations/>).

²BD = body depth, CW = chest width, DC = dairy capacity, HFE = height at front end, ST = stature.

³Measured trait.

Table 7. The posterior mean¹ of the genetic correlation (above diagonal), heritability (diagonal), and phenotypic correlation (below diagonal) for rump traits²

Item	LS	PS	PW ³	RA ³	THP
LS	0.20	0.53	0.10	0.42	0.38
PS	0.15	0.07	0.07	0.69	0.69
PW ³	0.07	0.05	0.32	-0.03	0.00
RA ³	0.19	0.15	-0.02	0.36	-0.95
THP	0.22	0.18	0.10	-0.87	0.22

¹Posterior standard deviations (PSD) for heritability estimates varied from 0.0015 to 0.0030, whereas for genetic and phenotypic correlations, they varied from 0.0022 to 0.0108 and 0.0010 to 0.0022, respectively. Individual PSD are given in Supplemental Table S2 (<https://cgil.shinyapps.io/correlations/>).

²LS = loin strength, PS = pin setting, PW = pin width, RA = rump angle, THP = thurl placement.

³Measured trait.

All data are stored in the national database at the Canadian Dairy Network (Koeck et al., 2012b). In 2016, approximately 40% of all herds enrolled on DHI milk-recording programs participated in the voluntary health-recording system (Beavers and Van Doormaal, 2016). These records provide a means of tracking health information for dairy producers and their veterinarians to improve herd management and are used in the national genetic evaluation system for genetic selection of disease resistance.

Among the 9 health-related traits, BHB had the highest heritability (0.21), followed by SCS (0.13) and displaced abomasum (**DA**; 0.04). The lowest heritabilities (0.01) were observed for cystic ovaries (**CO**), metritis (**METR**), and lameness (**LAM**; Table 10). The heritabilities were similar to the literature (Koeck et al., 2012a,b, 2014; Guarini et al., 2019). However, given the categorical outcome of disease traits, heritability estimates on the linear scale are frequency dependent, making direct comparison of values from different studies impossible. Mean incidences of clinical mas-

titis (**MAST**), **METR**, retained placenta (**RP**), **CO**, clinical ketosis (**CK**), **DA**, and **LAM** were 10.3, 8.4, 5.4, 7.1, 5.1, 2.5, and 7.9%, respectively. Even though metabolic diseases are heavily influenced by management, Lactanet has been publishing genetic evaluation for metabolic disease resistance since 2016. It is worth highlighting that traits such as **CK** are only measured on visibly ill cows and have a low recording rate (Beavers and Van Doormaal, 2016).

Hoof Health. Hoof health-related traits had heritability estimates ranging from 0.01 [toe ulcer (**TU**) and interdigital dermatitis (**ID**)] to 0.11 digital dermatitis (**DD**; Table 11) and followed values reported in the literature (Malchiodi et al., 2017, 2020; Heringstad et al., 2018). Genetic evaluation for hoof health traits started in 2018 in Canada, after a successful research project that spanned from 2014 to 2017. The most prevalent lesion in the data set was **DD** (30.2%), followed by sole hemorrhage (8.3%), sole ulcer (**SU**; 6.2%), white line disease (4.2%), **ID** (3.4%), heel horn erosion (2.8%), interdigital hyperplasia (**IH**; 2.1%), and **TU** (1.1%). Malchiodi et al. (2017) noted that these lesion frequencies may be overestimated because they are only based on cows presented to the hoof trimmers, where some animals might be preferentially chosen for trimming.

Workability. In the workability group of traits, milking speed and milking temperament had heritability estimates of 0.16 ± 0.01 and 0.07 ± 0.01 , respectively. Previously reported heritability estimates of milking speed ranged between 0.11 and 0.42 (Meyer and Burnside, 1987; Boettcher et al., 1998; Hayes, 1998; Lassen and Mark, 2008; Sewalem et al., 2011; Kramer et al., 2013), and between 0.04 and 0.18 for milking temperament (Sewalem et al., 2002, 2011; Lassen and Mark, 2008; Kramer et al., 2013).

Milking temperament is subjectively recorded by producers, where the relative temperament of each cow

Table 8. The posterior mean¹ of the genetic correlation (above diagonal), heritability (diagonal), and phenotypic correlation (below diagonal) for fertility traits²

Item	AFS	CTFS	DO	FSTC	FSTCh	NRR	NRRh	NSC	NSCh
AFS	0.05	0.39	0.22	0.08	0.17	0.21	0.11	-0.03	0.05
CTFS	0.15	0.06	0.88	0.60	0.15	0.07	0.08	0.20	0.10
DO	0.01	0.45	0.06	0.88	0.35	-0.43	-0.12	0.72	0.25
FSTC	-0.03	-0.07	0.66	0.03	0.62	-0.85	-0.48	0.97	0.62
FSTCh	-0.04	-0.05	-0.01	0.02	0.01	-0.65	-0.84	0.71	0.97
NRR	0.05	0.08	-0.33	-0.50	-0.03	0.01	0.66	-0.94	-0.68
NRRh	0.06	0.02	0.01	-0.01	-0.53	0.03	0.01	-0.57	-0.94
NSC	-0.04	-0.08	0.73	0.87	0.03	-0.62	-0.02	0.03	0.66
NSCh	-0.05	-0.04	-0.02	0.02	0.87	-0.04	-0.65	0.04	0.01

¹Posterior standard deviations (PSD) for heritability estimates varied from 0.0005 to 0.0016, whereas for genetic and phenotypic correlations, they varied from 0.0020 to 0.0379 and 0.0001 to 0.0260, respectively. Individual PSD are given in Supplemental Table S2 (<https://cgil.shinyapps.io/correlations/>).

²AFS = age at first service, CTFS = calving to first service, DO = days open, FSTC = first service to conception, NRR = nonreturn rate, NSC = number of services per conception, h = trait measured on heifers.

Table 9. The posterior mean¹ of the genetic correlation (above diagonal), heritability (diagonal), and phenotypic correlation (below diagonal) for calving traits²

Item	CZ	CZh	CE	CEh	GL	GLh	CS	CSH
CZ	0.05	1.00	0.62	0.56	0.14	0.49	-0.15	-0.01
CZh	1.00	0.08	0.56	0.57	0.48	0.45	-0.01	-0.06
CE	0.15	0.15	0.03	1.00	0.05	0.04	-0.49	-0.54
CEh	0.15	0.26	1.00	0.10	0.22	0.19	-0.54	-0.55
GL	0.23	0.22	0.04	0.04	0.13	1.00	-0.09	-0.03
GLh	0.22	0.20	0.03	0.06	1.00	0.17	0.03	-0.01
CS	0.05	0.05	-0.10	-0.10	0.13	0.12	0.01	0.74
CSH	0.05	-0.05	-0.10	-0.17	0.12	0.06	0.03	0.07

¹Posterior standard deviations (PSD) for heritability estimates varied from 0.0005 to 0.0029, whereas for genetic and phenotypic correlations, they varied from 0.0001 to 0.0465 and 0.0001 to 0.0009, respectively. Individual PSD are given in Supplemental Table S2 (<https://cgil.shinyapps.io/correlations/>).

²CZ = calf size, CE = calving ease, GL = gestation length, CS = calving survival, h = trait measured on heifers.

during milking is usually observed during the first 6 mo of their first lactation. Animals are classified in 5 categories, with 1.3% classified as “very nervous,” 9.7% “nervous,” 51.5% “average,” 33.6% “calm,” and 3.9% “very calm” in the data set. Milking speed is recorded similarly, and showed frequencies of 2.0, 10.7, 62.7, 22.5, and 2.1% for “very slow,” “slow,” “average,” “fast,” and “very fast,” respectively.

Genetic Correlation Within Trait Groups

Regarding production traits, the 5 highest genetic correlations were observed for MY and PY (0.86 ± 0.01), Fat% and Protein% (0.66 ± 0.01), FY and PY (0.64 ± 0.01), MY and Protein% (-0.57 ± 0.01), and FY and Fat% (0.49 ± 0.01 ; Table 3). Cai et al. (2020) also reported high genetic correlations between MY and PY (0.78), FY and MY (0.40), and FY and PY (0.56). Likewise, Kadarmideen et al. (2003) and Martin et al. (2019) reported similar results as in this study.

Among the 26 conformation traits, the highest genetic correlations were observed for RA and thurl

placement (**THP**; 0.95 ± 0.01), FAN and HD (0.83 ± 0.01), UT and MSL (0.72 ± 0.01), BCS and CW (0.72 ± 0.01), BCS and DC (-0.71 ± 0.01). Rump angle measures the height of pin bones relative to the height of hip bones, whereas THP measures the position of the thurl between the hook and pin bones. Therefore, the high negative correlation between them (-0.95 ± 0.01) was expected, whereby a thurl placed too far back would increase the rump angle (lower pin bones). A positive correlation (0.83 ± 0.01) between FAN and HD was also expected given the nature of the traits, because the lower the angle of the hairline, the shallower the depth of heel will be. Interestingly, RLSV was moderately correlated with both FAN (-0.35 ± 0.01) and HD (-0.34 ± 0.01), suggesting that a curved leg would contribute to a deeper FAN and shallower HD. Median suspensory ligament was positively correlated with UT (0.73 ± 0.01), indicating that a softer and more expandable udder is expected in cows with a stronger MSL. Body condition score had similar correlations values with CW (0.72 ± 0.01) and DC (-0.71 ± 0.01), suggesting that animals with higher BCS would

Table 10. The posterior mean¹ of the genetic correlation (above diagonal), heritability (diagonal), and phenotypic correlation (below diagonal) for health traits²

Item	BHB	CK	MAST	CO	DA	LAM	METR	RP	SCS
BHB	0.21	0.58	0.23	0.02	0.17	0.09	0.11	-0.02	0.14
CK	0.12	0.02	0.22	0.14	0.61	0.27	0.14	0.13	0.34
MAST	0.01	0.01	0.02	0.17	0.20	0.25	0.28	0.14	0.76
CO	0.01	0.01	0.01	0.01	0.05	0.16	0.22	0.23	0.04
DA	0.05	0.21	0.01	0.01	0.04	0.14	0.31	0.12	0.18
LAM	0.01	0.01	0.02	0.00	0.01	0.01	0.10	0.09	0.27
METR	0.01	0.07	0.01	0.02	0.06	0.01	0.01	0.81	0.28
RP	-0.01	0.03	0.01	0.01	0.02	0.00	0.10	0.03	0.09
SCS	0.09	0.01	0.20	-0.01	-0.01	0.01	0.00	-0.02	0.13

¹Posterior standard deviations (PSD) for heritability estimates varied from 0.0006 to 0.0021, whereas for genetic and phenotypic correlations, they varied from 0.0067 to 0.0575 and 0.0006 to 0.0024, respectively. Individual PSD are given in Supplemental Table S2 (<https://cgil.shinyapps.io/correlations/>).

²CK = clinical ketosis, MAST = clinical mastitis, CO = cystic ovaries, DA = displaced abomasum, LAM = lameness, METR = clinical metritis, RP = retained placenta.

Table 11. The posterior mean¹ of the genetic correlation (above diagonal), heritability (diagonal), and phenotypic correlation (below diagonal) for hoof health traits²

Item	DD	HHE	ID	IH	SH	SU	TU	WL
DD	0.11	0.43	0.81	0.67	0.05	0.16	-0.18	0.06
HHE	0.06	0.02	0.42	0.32	0.03	0.04	-0.19	-0.03
ID	0.05	0.10	0.01	0.65	-0.02	0.02	-0.08	-0.07
IH	0.11	0.02	0.05	0.04	0.05	0.14	-0.31	0.01
SH	0.00	0.03	0.00	0.01	0.03	0.83	0.16	0.46
SU	0.00	0.06	0.02	0.00	0.09	0.04	0.35	0.60
TU	-0.03	0.00	0.00	-0.01	0.02	0.05	0.01	0.41
WL	-0.02	0.01	-0.01	0.00	0.07	0.04	0.05	0.02

¹Posterior standard deviations (PSD) for heritability estimates varied from 0.0010 to 0.0039, whereas for genetic and phenotypic correlations, they varied from 0.0200 to 0.0790 and 0.0020 to 0.0020, respectively. Individual PSD are given in Supplemental Table S2 (<https://cgil.shinyapps.io/correlations/>).

²DD = digital dermatitis, HHE = heel horn erosion, ID = interdigital dermatitis, IH = interdigital hyperplasia, SH = sole hemorrhage, SU = sole ulcer, TU = toe ulcer, WL = white line disease.

have a wider chest, and less angular and sprung ribs. It is interesting to note that each of these correlations are between traits from the same scorecard, and all 4 (scorecards) are represented within the 5 highest genetic correlated traits, reinforcing the importance of balanced conformation in dairy cows.

Among the fertility traits, DO had a correlation of 0.88 ± 0.01 with both CTFS and FSTC. The high correlation between NS and FSTC (0.97 ± 0.01) was expected because lower NS will reduce the FSTC interval for both heifers and cows. Similarly, NRR and FSTC also showed a high correlation of -0.85 ± 0.01 and -0.84 ± 0.01 for cows and heifers, respectively. It is important to highlight that the current fertility traits are highly influenced by management decisions and human errors, such as: voluntary waiting periods, data-recording errors or failure to record events, failure to detect estrus, mismanagement (e.g., inseminating animals at an inappropriate time of the estrous cycle), and unrecorded management decisions (e.g., unrecorded hormonal synchronization treatments; Berry et al., 2016; Oliveira Junior et al., 2021).

With the exception of calf survival, no genetic difference was observed between calving traits measured on heifers and cows (i.e., correlation equal to one). Haile-Mariam and Pryce (2019) also reported a high correlation of gestation length measured in heifers and cows. The authors concluded that given the limited data on heifers, a repeatability animal model that uses both heifer and cow data is preferred. Given the moderate correlation between CZ and CE, and the negative correlation between CE and CS, it can be concluded that larger calves have a harder birth process and, in turn, poor survival. Calving ease in heifers was highly correlated with both CZh (0.57 ± 0.01) and CSh (-0.55 ± 0.01), suggesting again that larger calves have harder birth processes and, in turn, reduced survival.

Somatic cell score and MAST showed a high genetic correlation (0.76 ± 0.01), reinforcing the use of SCS as an indirect means of selection for mastitis resistance. Mastitis was also moderately correlated with METR (0.28 ± 0.05) and LAM (0.25 ± 0.02). Retained placenta and METR had an estimated correlation of 0.81 ± 0.02 , the highest value among health-related traits. Koeck et al. (2012b) also reported high correlation between these 2 traits (0.62 ± 0.11).

Among hoof health traits, DD was the trait with highest genetic correlation values, specifically with ID (0.81 ± 0.03) and IH (0.67 ± 0.04). Other notable genetic correlations (≥ 0.60) were observed between SH and SU (0.83 ± 0.02), ID and IH (0.65 ± 0.03), and SU and WL (0.60 ± 0.03). Malchiodi et al. (2017, 2020) also estimated high correlations between the mentioned traits, but with smaller values than the ones reported by this study.

Correlations Among Trait Groups

Production–Conformation. Not surprisingly, conformation traits in the dairy strength and mammary system scorecards had the highest genetic correlation with production, such as MY and DC (0.54 ± 0.01), PY and DC (0.52 ± 0.01), MY and UD (-0.45 ± 0.01), FY and DC (0.45 ± 0.01), and PY and UD (-0.45 ± 0.01). Dairy capacity, which is related to the angle, openness and spring of ribs, was highly positively correlated with MY, FY, and PY. In contrast, UD was negatively correlated with the 3 yield production traits, with FY and UD (-0.33 ± 0.01) being the strongest correlation.

Production–Fertility. The 10 strongest correlations among production and fertility traits were unfavorable. For example, the correlation between MY and DO was 0.43 ± 0.01 ; therefore, higher breeding values

for MY are associated with high values for DO, which is not desired. Milk yield was also unfavorably correlated with CTFS (0.38 ± 0.01), FSTC (0.38 ± 0.01), and NS (0.37 ± 0.01). The correlation between PY and DO (0.41 ± 0.01) was the second highest between these 2 groups of traits.

Production–Health. In general, an unfavorable correlation between production and health traits was observed, with the 5 highest correlations found between: Protein% and CK (-0.33 ± 0.03), MY – LAM (0.30 ± 0.03), FY and CO (0.30 ± 0.02), MY and BHB (0.30 ± 0.01), and FY and CK (0.30 ± 0.03). The correlation between MY and MAST was 0.29 ± 0.01 , which is within the literature range of 0.21 to 0.55 (Heringstad et al., 2000), suggesting a higher probability of mastitis in high-production cows.

Production–Hoof Health, Calving, and Workability. The 2 highest genetic correlations estimated between production and hoof health, calving and workability traits were MY and TU (0.26 ± 0.05), MY and SU (0.26 ± 0.02), PY and CZh (0.18 ± 0.01), MY and CZh (0.17 ± 0.01), MY and MT (0.14 ± 0.01), and PY and MT (0.12 ± 0.01). Similar to fertility, positive genetic correlations between production and such traits are unfavorable, such that higher MY is associated with higher cases of TU and SU, and consequently with LAM, a health trait also positively correlated with MY (0.30 ± 0.03).

Conformation–Fertility. In terms of correlations between conformation and fertility traits, DC was positively correlated with DO (0.48 ± 0.01), FSTC (0.42 ± 0.01), and NS (0.41 ± 0.01), which suggests that more capacious animals need more services to conceive, therefore having more days between first service to conception and consequently having more open days. These moderate correlations suggest that DC could be a good indicator of fertility performance. A moderately high negative correlation between ST and AFS (-0.45 ± 0.01) suggests that animals with faster growth rate are likely to reach puberty early in life (Moore et al., 1990; Bastin and Gengler, 2013). Correlation between BCS and CTFS (-0.39 ± 0.01) were among the 5 highest correlations found between BCS and other fertility traits, which is in agreement with previously published work by Pryce et al. (2001), who observed genetic correlation between BCS and days to first service ranging from -0.18 to -0.54 . This unfavorable correlation suggests that thinner cows, or cows in greater negative energy balance, tend to have worse fertility performance (Veerkamp and Thompson, 1999; Pryce et al., 2000).

Conformation–Health. High genetic correlations were observed between conformation and health traits, such as BCS and KET (-0.56 ± 0.03), set of rear legs and LAM (-0.45 ± 0.02), DC and KET (0.44 ± 0.03),

BCS and BHB (-0.37 ± 0.01), and UD and KET (-0.36 ± 0.03). It is well known that cows with low BCS are more susceptible to metabolic diseases, such as KET (Shin et al., 2015). This agrees with the moderate negative correlation observed between these traits. Dairy capacity and UD also showed moderate genetic correlation with KET, suggesting that higher DC and deeper UD could lead to animals more susceptible to KET. The set of rear legs had a moderate negative correlation with LAM, suggesting that straight legs (side view) could be an indicator of LAM problems.

Conformation–Calving. Estimated correlations between conformation and calving traits also showed interesting results. The 5 highest values were ST and CZ (0.52 ± 0.01), ST and CZh (0.44 ± 0.01), CW and CZ (0.37 ± 0.01), THP and CS (0.33 ± 0.03), and PW and CZ (0.29 ± 0.01). Stature, CW, and PW appeared to be positively correlated with CZ. These 3 conformation traits (ST, CW, and PW) also showed positive correlation with calving ease (0.16 ± 0.02 , 0.09 ± 0.01 , 0.14 ± 0.02 , respectively). This suggests that larger animals are more likely to have calving difficulties. On the other hand, THP was positively correlated with CS, suggesting that higher THP scores could facilitate the calving process.

Conformation–Hoof Health. Feet and leg traits had the highest correlations with hoof health traits. Foot angle and TU were the highest correlated traits (0.42 ± 0.06), followed by RLRV and ID (-0.31 ± 0.02). Heel depth had a correlation of -0.28 ± 0.03 with IH, SU, and ID. These correlations suggest that indirect selection on hoof health can be done by selection on traits included in the “feet and legs” scorecard.

Fertility–Calving. Calf size on both cows and heifers were negatively correlated with AFS (-0.50 ± 0.02 , -0.45 ± 0.02 , respectively), suggesting that younger heifers are likely to have bigger calves in comparison with their own size. A negative correlation was found between CS and DO (-0.29 ± 0.03), suggesting that cows with calving problems leading to stillborn calves are likely to have longer days open intervals. Calf survival in both cows and heifers was also negatively correlated with NS (-0.30 ± 0.02 and -0.28 ± 0.02 , respectively), which is in line with the previously mentioned results.

Fertility–Health. Among fertility and health traits, CO had a correlation of 0.54 ± 0.03 with both FSTC and DO. Likewise, METR was also unfavorably correlated with NRR (-0.47 ± 0.03), FSTC (0.45 ± 0.05), and NS (0.45 ± 0.04). This is in agreement with previous research, highlighting that cows affected by any disease are more likely to have problems starting a new estrous cycle, thus requiring more inseminations (Pryce et al., 1997; Pritchard et al., 2013).

Fertility–Hoof Health. Considering fertility and hoof health traits, TU was positively correlated with NS (0.35 ± 0.04), DO (0.31 ± 0.05), and FSTC (0.28 ± 0.05), whereas SU was positively correlated with CTFS (0.32 ± 0.04), and DO (0.28 ± 0.04). These unfavorable correlations were expected, because injured animals would allocate additional energy into the recovery process, reducing energy available for reproductive activities.

Workability. The genetic correlation between MSP and MT was 0.18 ± 0.01 . This estimated correlation is within the literature range, with values ranging from -0.04 (Kramer et al., 2013) to 0.25 (Sewalem et al., 2011). In regard to their correlation with other trait groups, a cow with a calmer temperament would also have less heel horn erosion (0.27 ± 0.03), easier calving (0.19 ± 0.03), smaller calf size (0.19 ± 0.02), less lame (0.18 ± 0.04), and better dairy capacity (0.17 ± 0.01). On the other hand, cows that milk more quickly likely have higher SCS (0.27 ± 0.01), shorter teats (-0.21 ± 0.01), a deeper udder (0.20 ± 0.01), better udder texture (0.18 ± 0.01), and fewer toe ulcer problems (-0.17 ± 0.05).

Genetic Trends

The Canadian Dairy Network works closely with breed associations when updating their selection index formula emphasizing conformation traits (LPI). In the latest Holstein LPI update (March 2020) weights were kept as 40% production, 40% durability, and 20% health and fertility (www.lactanet.ca). In general, national indexes are updated every few years as market conditions or breed goals evolve. However, if important changes occur in the industry, for example, to favor fat production to an even greater extent, indexes are updated more frequently to reflect such changes.

All production traits showed considerable genetic gain in the whole period of time considered in this study (1980 to 2019). Interestingly, Fat% had a decrease in its genetic mean from 1993 to 2003, which then returned to an increasing trend. Fertility traits showed an unfavorable genetic trend for all 9 measured traits for several years; however, the trend for DO, CTFS, and FSTC started to flatten around 2002. The NS had a sharp drop in 2011, whereas AFS started to decrease around 1994.

Mammary system conformation traits generally showed positive genetic trends, except for a slight decrease in TL, which was considered favorable, and a more pronounced decrease in rear attachment height since 1990. In the “feet and legs” scorecard, all traits showed a positive genetic trend, highlighting bone quality, which has increased since 1988. Among dairy

strength traits, ST had a more pronounced gain, with a positive trend since 1984. Around the same year, a positive trend for DC and a decreasing trend in BCS was observed. Loin strength was the trait with greatest gain among rump traits. Pin setting and THP trends became positive around 1988, whereas RA showed an inconsistent trend, with ups and downs during the analyzed period.

Given the high correlation between GL and GLh, their genetic trends followed similar a pattern, with higher values in 2005 and a decreasing tendency since then. Calf size and CE trends followed a similar pattern of decrease (around 2005), whereas CS values started to increase around 2007. Fleming et al. (2020) observed the phenotypic trend of having an unassisted calving has increased since 2003. It is worth noting that genetic selection on these traits officially started in 2008 with the introduction of “Daughter Calving Ability” and “Calving Ability” selection indexes (Van Doormaal, 2007).

Health traits MAST, CK, METR, and DA showed a decreased trend starting around 2007. Lameness had an increasing trend between 1995 and 2007, with a slight decrease after 2013. On the other hand, CO and BHB had positive trends for the whole studied period. Somatic cell score trend started decreasing around 2003. It is worth mentioning that these health-related traits have a recent selection history, with selection for mastitis resistance starting in 2013 and, later in 2016, for other health-related traits.

Heel horn erosion, ID, and TU trends spiked in 2005, with other hoof health traits trends slightly decreasing after 2008. These trends are a consequence of indirect selection (genetic correlations), given that selection on hoof health traits officially started in 2018. In the group of workability traits, both MSP and MT showed positive trends since around 1986.

CONCLUSIONS

In this study, we estimated population genetic parameters for 67 currently evaluated traits on heifers and first-lactation Canadian Holstein cows. We report genetic parameters that have not been previously estimated for Canadian Holsteins and update those that have been previously estimated. These estimates are useful for building new indexes, updating existing selection indexes, and for predicting correlated responses due to inclusion of novel traits in the breeding programs.

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