Genomic Evaluations for Body Maintenance Requirements in Canadian Holsteins

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Abstract

A genomic evaluation was developed for Body Maintenance Requirements (BMR) in Canadian Holsteins, with the first official publication in April 2023. The BMR index characterizes feed requirements for maintenance based on the metabolic body weight of the animal. Body weights of lactating cows recorded through feed advisory services in Quebec since 2002 are used in the genetic evaluation. Metabolic body weight (MBW), calculated as body weight$^{0.75}$, in first, second, and third lactations are analyzed in a three-trait linear animal model as separate but correlated traits with repeated records within a lactation. Genetic parameters were estimated by MC EM REML method using a subset of the data including 373 219 records from 195 198 cows. Heritabilities for MBW in first, second, and third lactation were 0.34, 0.43, and 0.47, respectively, and repeatabilities were 0.53, 0.61, and 0.64, respectively. Genetic correlations between different lactations were strong, ranging from 0.78 to 0.86. A Single-Step genomic evaluation was implemented using the MiX99 software. The April 2023 official evaluation run had records from 540 619 cows of which 28 263 were genotyped and a total of 47 967 genotyped animals in the model. The BMR index combines genomic estimated breeding values (GEBVs) for MBW in the three lactations at equal weightings. This index is published as a relative breeding value, with a mean of 100 and standard deviation of 5 for base bulls, where the sign is reversed such that higher values represent a lower MBW and thus lower body maintenance requirements. The average reliability of BMR for young, genotyped bulls was approximately 68%. Observed phenotypic and genetic trends demonstrated that animal size has been steadily increasing over time. The BMR evaluations can be considered by producers looking to reduce or maintain cow body size in their herd as another way to reduce feed costs.

Key words: Body maintenance requirements, metabolic body weight, single-step, genomic evaluation

Introduction

While genetic selection has historically focused on increasing performance and revenue, it also has great value in reducing inputs and expenses. Feed represents the greatest expense for dairy farms and as prices continue to rise, there is increasing interest and need to improve the efficiency of feed use on dairy farms through genetic selection.

Feed efficiency can be defined in many ways, but broadly is used to describe how efficiently animals convert feed into product. Energy from the feed eaten by cows is used for milk production but also maintenance, growth, reproduction, and activity. Feed efficiency is a complex trait and there are many different expressions and indicators that can be targeted for genomic selection. Residual Feed Intake (RFI) is a popular measure of feed efficiency and can be estimated in dairy cattle by the linear regression of Dry Matter Intake (DMI) on factors representing various energy sinks, such as milk energy and body weight (Koch et al., 1963; Connor et al. 2015). Genomic selection for RFI has been shown to be feasible to breed for cows that convert feed gross energy to net energy more efficiently without impacting production.

The other route to improve feed efficiency is to reduce maintenance requirements for a cow by decreasing body weight. Small cows will have lower maintenance requirements and require less feed to meet those needs, which is a financial benefit for producers. Breeding values for feed saved, proposed by Pryce et al. (2015), combine the reductions in feed eaten associated with RFI and the effect of body weight on feed intake as required for maintenance. Performing multi-trait selection for improved metabolic efficiency through RFI and reduced maintenance requirement can target cows that have the genetic ability to use a greater proportion of their feed intake for milk production.

In April 2021, Canada released genomic evaluations for feed efficiency which is a genetic RFI derived by using a linear function of multiple-trait evaluations for DMI and the energy sinks of energy corrected milk and Metabolic Body Weight (MBW) (Jamrozik et al., 2021, 2022). The overall aim of the Canadian feed efficiency evaluations is to enable selection of cows that use less feed at the same level of production and body size after the peak of lactation (metabolic feed efficiency).

Not included in Canadian feed efficiency is the second component for selection for reduced feed requirements, i.e. maintenance requirements. The net energy needed for maintenance is a function of MBW and establishing genetic evaluations for MBW would allow for selection for less feed required for maintenance to be used alongside feed efficiency evaluations. The focus of this paper is to describe the implementation of a routine genomic evaluation for Body Maintenance Requirements (BMR), which was launched in Canada for the Holstein breed in April 2023.

Materials and Methods

Data

Body weight (BW) data on lactating cows is collected voluntarily for feed advisory services offered by Lactanet for herds in the province of Québec. The BW measurements are estimated using a tape measuring heart girth circumference. Holstein data recorded since 2002 was considered for use in genomic evaluations. Herds determined to be consistently recording individual animal BW as a continuous measure were selected for inclusion. Body weights recorded between 0 and 305 DIM in first, second, and third lactation were converted to MBW kg$^{0.75}$. Multiple MBW measures in a lactation for an individual animal were kept if available. The average number of records per lactation per cow was 1.15. Approximately 7% of lactations in the April 2023 genetic evaluation data had multiple records (up to 11 records per lactation) and records were on average 48 days apart. Most weights were recorded within the first 60 DIM. After all, editing data used in the April 2023 evaluation for BMR consisted of 387 037, 296 604, and 198 719 records for first, second, and third lactation, respectively, from 540 619 cows.

Model

The model is a three-trait linear animal model for MBW in first, second, and third lactation with repeated records within each lactation. The same model is used for MBW in each lactation, considering the fixed effects of herd, age at calving in monthly classes, DIM class (daily DIM classes for first lactation up to 98 DIM and then weekly classes; weekly DIM classes for second and third lactation), and month of weighing (12 classes), and random effects of herd-year of calving (HY), animal additive genetic, permanent environmental (PE), and residual. In matrix notation, the model can be written as:

$$y = Xb + Z_1hy + Z_2a + Z_3p + e$$

where y is a vector of observations (MBW in first, second, or third lactation), **b** is a vector of all fixed effects, **h** is a vector of HY effects, **a** is a vector of animal additive genetic effects, **p** is a vector of PE effects, **e** is a vector of residuals, and **X**, $\mathbf{Z_1}$, $\mathbf{Z_2}$, and $\mathbf{Z_3}$ are the respective incidence matrices. Random effects were assumed to be normally distributed, with means equal to zero. Model assumptions are that: v(**h**) = $\mathbf{I} \otimes \mathbf{HY}$, **I** is an identity matrix and **HY** is the covariance (3x3) matrix for HY effects, v(**a**) = $\mathbf{H} \otimes \mathbf{G}$, **H** is a combined pedigree-genotype relationship matrix, **G** is the additive genetic covariance matrix, v(**p**)= $\mathbf{I} \otimes \mathbf{P}$, **P** is the covariance matrix for the PE effects, v(**e**) = **E, E** 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 subset of the data including 373 219 records from 195 198 cows. This subset of the data only included herds still recording BW within the last five years and with multiple years of recorded BW. Cows with a record in second or third lactation were required to have a record in all preceding lactations. Summary statistics for the data used for genetic parameter estimation are presented in Table 1. 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 three-trait Single-Step genomic evaluation was implemented at Lactanet Canada using MiX99 and related software (MiX99 Development Team, 2017). The April 2023 data included 47 967 genotyped animals, with 28 263 genotyped cows with records and 8 635 genotyped sires. Animals are genotyped either with 50K SNP panel or a low-density panel and imputed to 50K using F-Impute (Sargolzaei al., 2014). The genomic relationship matrix (**G**) is constructed by VanRaden Method I. (VanRaden, 2008), and **G** is blended with the additive relationship matrix (**A**) assuming that 80% of the total genetic variance was explained by SNP effects. Scaling of **G** and **A** is performed using the Christensen (2014) method. The APY algorithm for Proven and Young (Misztal et al., 2014) is applied for inversion of **G**, with the core population of 20 000 (the oldest genotyped animals in the Lactanet database). 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

Table 1. Descriptive statistics of the dataset used for parameter estimation.

Lactation	Records	Cows	BW (kg)		MBW (kg$^{0.75}$)	
			Ave.	SD	Ave.	SD
1	234 498	195 198	620.3	63.2	124.2	9.5
2	97 661	73 253	674.1	67.4	132.2	9.9
3	41 060	28 170	708.3	70.8	137.2	10.3

BW = body weight, MBW = metabolic body weight calculated using SNP prediction error co-variances with the SNP-BLUP-REL software (Luke, Finland). Animal model reliabilities are calculated based on Effective Daughter Contributions (EDC). The EDC and reliability software of Sullivan (2023) is used.

Relative Breeding Values

Genetic evaluations for BMR combine the three individual MBW evaluations for first, second, and third lactation at equal weighting and it is the only value published. The sign of the combined BMR evaluation is reversed, such that the higher values represent the more desirable, lower body maintenance requirements (lower MBW). The BMR evaluation is expressed as Relative Breeding Values (RBV) with a mean of 100 and SD of 5 for base bulls that for April 2023 are those born 2008-2017 and with an 'official' status. Sire evaluations are defined as 'official' for bulls with at least 20 daughters from 5 herds with MBW data and a minimum reliability of 70%.

Results & Discussion

Phenotypic Trends

The average body weight of Holstein females in the dataset available have been increasing over time. Figure 1 shows the phenotypic trend for average BW (kg) by year of birth by lactation number, including only those weights occurring in the first seven weeks of lactations. The overall increasing trend was similar for each of the lactations. The average BW of third lactation cows has gone from roughly 671 kg for cows born in 2000 to 735 kg for 2017-born cows. Since 2010, third lactation body weights have increased 4.3 kg/year. At the same time, the age at calving for each lactation presented has been slowly decreasing.

Genetic Parameters

Heritability and genetic and phenotypic correlation estimates for MBW in first, second, and third lactation are shown in Table 2. Heritability estimates for MBW were moderately high and ranged from 0.34 for first lactation to 0.47 for third lactation. These heritabilities were slightly lower than the 0.46, 0.51, and 0.60 found by Lidauer et al. (2019) for MBW in first, second, and third lactations, respectively, but showed the same trend of increased heritability with higher lactations. The within lactation repeatability

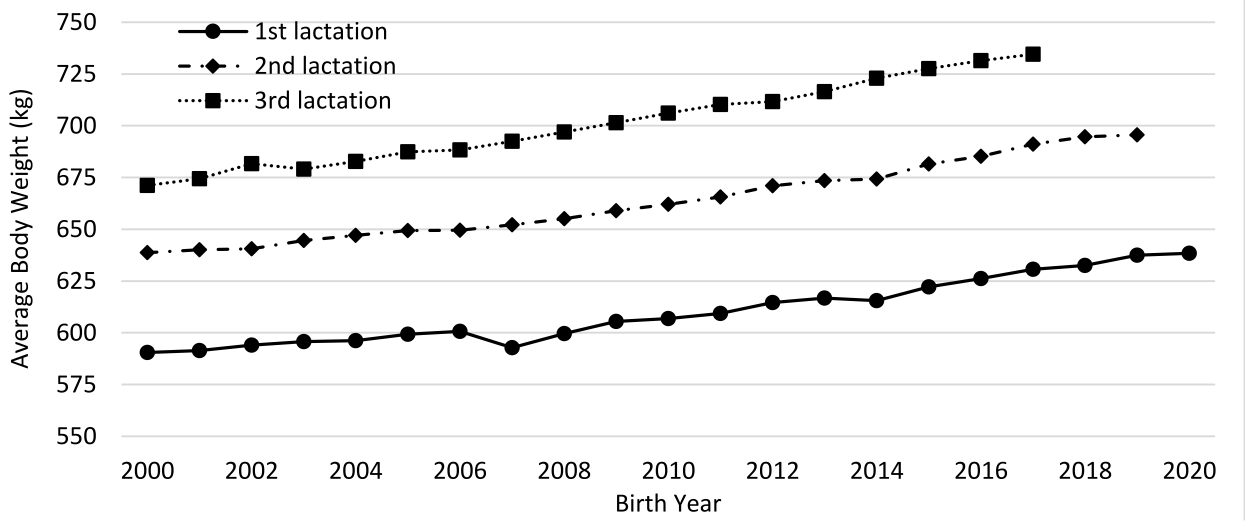

Figure 1. Phenotypic trend by year of birth for average body weight (kg) for cows in first, second and third lactation with weights recorded within the first seven weeks of the lactation.

estimates increased as parity number increased, going from 0.53 for MBW for first lactation, 0.61 for second, and 0.63 for third.

The genetic correlation between MBW in sequential lactations were similar at 0.86 for first and second and 0.85 for second and third, and a slightly lower genetic correlation of 0.78 was found between MBW in first and third lactations. The correlation between MBW in different lactations was strong but there was some variation which could be related to growth and maturity rate.

Table 2. Heritabilities with standard error in parentheses, genetic correlations (above diagonal), and phenotypic correlations (below) diagonal for metabolic body weight in first (MBW-1st), second (MBW-2nd), and third (MBW-3rd) lactation.

	MBW-1st	MBW-2nd	MBW-3rd
MBW-1st	0.34 (0.02)	0.86	0.78
MBW-2nd	0.57	0.43 (0.03)	0.85
MBW-3rd	0.60	0.61	0.47 (0.04)

Genomic Evaluations

In April 2023 there were 3 728 Holstein sires with an official BMR evaluation. The RBV for the combined BMR evaluation ranged from 85 to 121 for this group and averaged 104 as the average birth year of this group was older than the base bull group. The average reliability was 91% and ranged from 72 to 99% for official sires. The average reliability of genotyped Holstein bulls born in 2021 that were identified as being controlled by an AI organization (N=2 182) was 68%.

There has not been direct genetic selection on MBW or BW in Canada, but through indirect selection there has been a strong genetic trend observed. The genetic trend for BMR in bulls with official evaluations, as shown in Figure 2, has been in steady decline for the last 2 decades, demonstrating that genetic component for MBW and thus maintenance requirements has been increasing. In the most recent birth years, it appears that the trend may be lessening, which may be related to more awareness and a shift in selection away from larger animals and high stature. A similar genetic trend was also observed for cows, although not quite as steep.

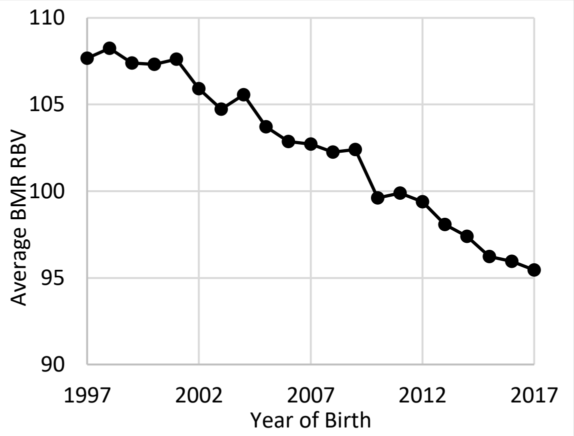

Figure 2. Genetic trend for bulls with an official body maintenance requirements (BMR) relative breeding value (RBV).

Relationships with Other Traits

Proof correlations were estimated between BMR and other routinely evaluated traits in Canada using 1 323 Holstein sires born since 2008 with an official LPI and BMR. In general, BMR had the strongest negative proof correlations with conformation traits. The major type traits of conformation, dairy strength, rump, mammary system, and feet and legs had proof correlations with BMR of -0.40, -0.49, -0.27, -0.26, and -0.06, respectively. The individual traits with the strongest proof correlation with BMR were stature (-0.73) and chest width (-0.55). Many conformation traits, especially dairy strength traits, describe various aspects of the cow's body size and structure and are often used to create proxy traits for body weight (e.g. Body Weight Composite Index, Holstein Association USA). A non-conformation trait strongly correlated with BMR was age at first service, with a negative correlation of -0.51. The group of proven sires used to estimate proof correlations spanned ten birth years. Therefore, due to the negative genetic trend for BMR, some negative correlations that were found with traits displaying genetic improvement over this period may largely be a result of the opposite genetic trends over time. This is likely for the observed correlation of -0.29 and -0.24 with LPI and Pro$, respectively, which become slightly positive when correlations are averaged within birth year. A slight positive correlation with calving ability was also observed (0.21). As expected, no correlation was observed between BMR and Feed Efficiency evaluations.

Relationships Between Sire RBV and Daughter Phenotypes

The average daughter MBW of sires with an official BMR were averaged by sire RBV for BMR by lactation. Sires were required to have at least ten daughter records in a lactation to be included. A regression of average daughter MBW on sire RBV was conducted to determine the relationship between the observed daughter phenotype and sire RBV. The average daughter MBW and regression is shown in Figure 3. Bulls with a higher BMR evaluation have daughters with lower MBW and body maintenance requirements in all lactations compared to bulls with low BMR evaluations. The regression coefficients were similar for each of the lactations, ranging from -0.51 to -0.57 kg$^{0.75}$ per sire RBV point. As they were approximately equal, regression coefficients were averaged to form one interpretation value for interpreting BMR. For each plus five RBV points for BMR (one standard deviation) the MBW of daughters are approximately 2.75 kg$^{0.75}$ lower.

Conclusions

The genomic evaluation for BMR was first implemented in April 2023 by Lactanet for the Holstein breed. Producers can utilize BMR in their selection decisions to help reduce feed costs by decreasing cow MBW and the feed required for body maintenance. Cow size has been increasing over time and BMR can be used to help cease this trend and either maintain or decrease body size in a herd. The BMR evaluations are not correlated to genetic evaluations for Feed Efficiency, which is calculated to be genetically independent of MBW. The Canadian Feed Efficiency and BMR evaluations are published separately and not together in an index. Producers can therefore use these two tools in combination or choose to

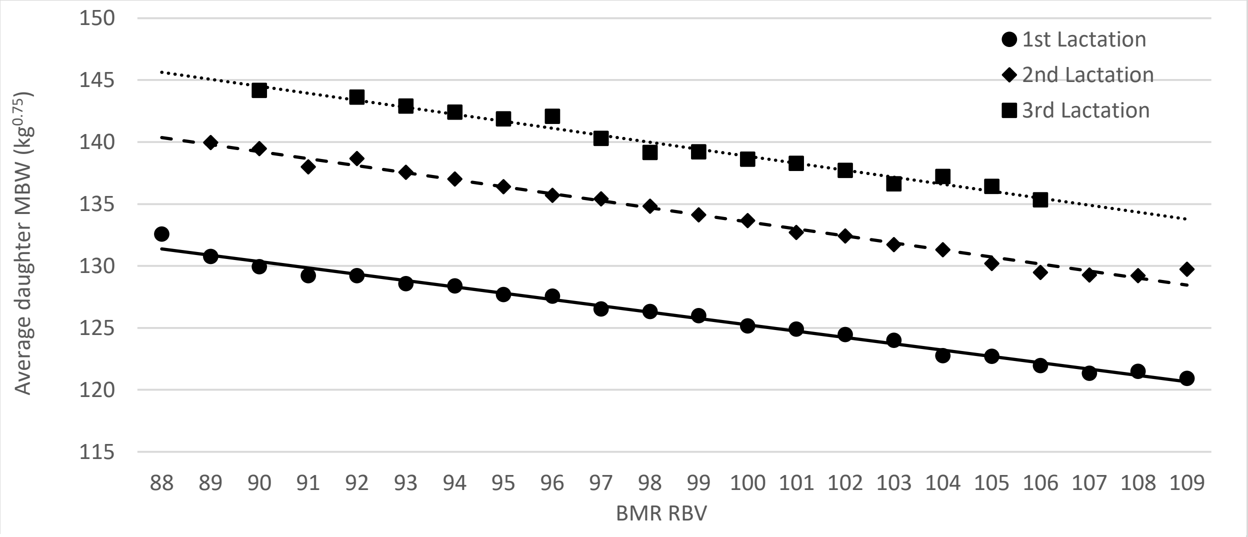

Figure 3. Average daughter metabolic body weight (MBW) in first, second, and third lactation averaged by sire Body Maintenance Requirements (BMR) RBV.

concentrate more on one to help reduce their overall feed costs.

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