Genetic Evaluation for Maintenance – Towards Genomic Breeding Values for Saved Feed in Nordic Dairy Cattle

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Abstract

Nordic Cattle Genetic Evaluation NAV (Denmark, Finland, Sweden) is developing an index for Saved Feed, which comprises maintenance and metabolic efficiency. In the launching phase, the index contains maintenance, which is based on breeding values for metabolic body weight (MBW). Therefore, we developed breed-specific genetic evaluations for MBW in Holstein (HOL), Nordic Red Dairy Cattle (RDC) and Jersey (JER). Included data reaches back to the year 1990 and comprise 0.8 million cows with body weight (BW) observations, complemented with first parity conformation observations from 2.9 million cows. BW observations are either based on heart girth measurements (90%) or scale and are used to model MBW in first, second and third parity. Differences in accuracy of measurements and in the number of BW observations per cow are dealt by weighting MBW observations in the statistical models. The applied multiple-trait animal models include six traits: first, second and third parity MBW, and first parity stature, chest width and body depth. Estimated genetic correlations among MBW traits were high (>0.96) and genetic correlations between MBW and conformation traits ranged from 0.65 to 0.68, from 0.53 to 0.58 and from 0.48 to 0.51 for stature, chest width and body depth, respectively. Heritability for combined MBW across the first three parities in HOL and RDC was 0.65 and in JER 0.58. Estimated breeding values for MBW increased on average by 0.8 SD_g over the last 25 years in the HOL breed, whereas in the RDC and JER breeds the increase was only 0.4 SD_g. We also developed genomic predictions for MBW for which validation reliabilities for genomic breeding values for candidate bulls were 0.59, 0.74 and 0.65 for HOL, RDC and Jersey respectively. The developed index for MBW is negatively correlated with frame, almost uncorrelated with milk production traits, and positively correlated with claw health, calving traits and longevity.

Keywords: feed efficiency, metabolic body weight, genomic prediction, Holstein, Red Dairy Cattle, Jersey

Introduction

Improving feed efficiency in dairy cattle requires several traits to be included into selection. The trait residual feed intake models the metabolic efficiency and its applicability for dairy cattle has been studied intensively (Berry & Crowley, 2013). In order to improve the gross efficiency of milk production not only the residual feed intake is important, but also to which shares feed energy is allocated by the cow towards milk production and body maintenance. The latter accounts for about one third of the energy intake of a cow (Mehtiö et al., 2018). The maintenance requirement is a function of the metabolic body weight (MBW) of the cow. Establishing genetic evaluations for MBW allows to account for maintenance in a selection index for feed efficiency.

Nordic Cattle Genetic Evaluation (NAV) in Denmark, Finland, and Sweden is developing an index for Saved Feed (Pryce et al., 2015), which comprises maintenance and metabolic efficiency. Maintenance is the first trait to start with. In Finland, body weight (BW) of cows is measured voluntary for feeding management reasons. More recently, BW is measured on a daily basis at herds equipped with scales. The available MBW data is of sufficient size to establish genetic evaluations. The objective of this study was to develop genetic and genomic evaluations for MBW in Danish, Finnish and Swedish dairy breeds.

Materials and Methods

The BW data built the foundation for the genetic evaluations. In order to increase the accuracy of the breed-specific evaluations for Holstein (HOL), Nordic Red Dairy Cattle (RDC) and Jersey (JER), also correlated information was utilized. Based on a literature review and the available data, it was decided to include the observations from first parity stature (ST), chest width (CW) and body depth (BD) as correlated traits by fitting multiple-trait models.

Metabolic body weight observations

Over 800 000 RDC and HOL cows of the cows born after 1990 had tape-measured BW observations (heart girt) and from more recent years over 90 000 cows from all three breeds had scale-measured BW observations. When BW was measured by tape, typically only one observation per cow and parity was available. On the contrary, in herds with scales up to several hundred BW observations within a cow's parity may have been recorded.

The available BW observations were used to model each cow's average MBW in the first, second and third parity. We analysed data from 284 research cows that had both tape and scale measurements, and found that both of them yielded high genetic correlations with the lactation average MBW. Therefore, we considered tape and scale measurements as the same trait.

In the first step each single BW observation was transformed to MBW by MBW = $BW^{0.75}$ and the observations were cleaned from outliers. When more than one observation per parity was available, an average observation and the corresponding average days in milk (DIM) were formed.

Single MBW observations that came from scales implemented in automatic milking systems were pre-corrected for the scale × season and stage of lactation effects based on a linear model fitted to the raw MBW data. The pre-corrected BW observations were used to form MBW averages that were then used as the observations for the evaluation.

In a second step, weights (w_{ij}) were calculated for each MBW observations to account for the type of measurement and the number of observations behind the MBW observation:

$$w_{ij} = 1 \Big/ \left(r_{jk} + \frac{1-r_{jk}}{n_{ij}} \right) - s_k \, , \qquad [1]$$

where r_{jk} is the repeatability of observations in parity j under measurement method k (tape, scale), n_{ij} is the number of observations for animal i in parity j, and s_k accounts for the difference in accuracy of one single MBW observation made either by tape or by scale.

Conformation observations

Conformation observations for all three breeds were acquired from the existing NAV conformation evaluation routine. For the first parity traits ST (linear), CW (linear score 1 to 9) and BD (linear score 1 to 9) that were included, the same data editing was applied as in the routine conformation evaluation (NAV, 2019).

Statistical model

For each breed a multiple-trait animal model that included six traits was solved to obtain estimated breeding values (EBV). For Finland, observations from HOL and RDC cows were included in both the HOL and RDC evaluations to increase contemporary group sizes. The linear model for the first (1), second (2) and third (3) parity MBW was:

$$y_{td:ijmnopqr} = ca_{t:i} \propto_r + \sum_{k=1}^{3} lt_{t:ijmk}\varphi(d)_k + YM_{t:jno} + H5Y_{t:pq} + hy_{t:pn} + a_{t:r} + e_{td:ijmnopqr} \text{ ,} \qquad [2]$$

were $y_{td:ijmnopqr}$ is a weighted observation of trait *t* (MBW1, MBW2 or MBW3) measured at DIM d on cow *r* which belongs to breed *i* and performs in herd p of country *j*; $ca_{t:i} \propto_r$ is a linear regression on calving age $\propto$ of cow *r* nested within breed *i*; $\sum_{k=1}^{3} lt_{t:ijmk}\varphi(d)_k$ is the fixed regression function on DIM d nested within breed *i* × country *j* × time period *m*, where $\boldsymbol{\varphi}(d)$ is a vector containing the covariates of the linear and quadratic term of a Legendre polynomial for DIM d plus the exponential $e^{-0.1d}$; $YM_{t:jno}$ is the fixed effect of year *n* × month *o* nested within country *j*; $H5Y_{t:pq}$ is the fixed effect of herd *p* × 5-years-period *q*; $hy_{t:pn}$ is the random effect of herd *p* × year *n*; $a_{t:r}$ is the random additive genetic effect of animal *r* and $e_{td:ijmnopqr}$ is the random residual.

The linear model for first parity traits ST, CW and BD was:

$$y_{tw:ijmnopqr} = ca_{t:i} \propto_r + lt_{t:ij}\beta(w) + C_{t:m} + YM_{t:jno} + H5Y_{t:pq} + hy_{t:pn} + a_{t:r} + e_{tw:ijmnopqr} \text{ ,} \qquad [3]$$

where $y_{tk:ijmnopqr}$ is an observation of trait *t* (ST, CW or BD) measured in lactation week *w* on cow *r* which belongs to breed *i* and performs in herd *p* of country *j*; the model effects are otherwise the same as in [2] but instead of a lactation trajectory a linear regression on lactation week ($lt_{t:ij}\beta(w)$) is fitted and a fixed classifier effect is added ($C_{t:m}$).

Applied variance components were estimated by a multiple-trait REML analyses that included observations from 23 158 RDC and HOL cows from 119 herds, where each MBW observation was based on one single BW measurement within parity. For JER an own set of variance components was estimated. Furthermore, additional REML analyses were performed to assess the heritabilities for MBW observations, which are based on the average of all BW measurements made within parity. These estimates were used to develop proper weights [1] for the different types of MBW observations.

The EBVs for MBW were used to form for each animal a MBW index by weighting first, second and third parity EBVs with the weights 0.30, 0.25 and 0.45, respectively, and changing the sign of the index values so that a higher index value refers to a lower MBW.

Genomic Predictions

Genomic prediction equations for MBW were developed by applying a SNP BLUP model of the following form:

$$\boldsymbol{y} = \mu\mathbf{1} + \boldsymbol{Wa} + \boldsymbol{Zg} + \boldsymbol{e} \text{ ,} \qquad [4]$$

where $\boldsymbol{y}$ is a vector of de-regressed proofs (DRP) based on the combined EBVs for MBW across parity 1, 2 and 3, where $\boldsymbol{y}$ includes all genotyped bulls that have an EBV reliability above 0.5 and all genotyped cows that have observations (Table 1); $\boldsymbol{Wa}$ accounts for the random polygenic effect (a 10% proportion); $\boldsymbol{Z}$ is the matrix coding the genotypes of the animals where low density SNP information for cows was imputed to 50k; $\boldsymbol{g}$ is a vector of SNP solutions; and $\boldsymbol{e}$ is a vector of random residuals.

Forward prediction validation was carried out by excluding the observations of the bulls from the five most recent birth year classes (candidate bulls) and the observations of their progenies. Validation reliability was calculated as the squared correlation between DRPs and direct genomic breeding values weighted by the average reliability of their DRPs.

Table 1. Number of genotyped animals included in the reference population.

	HOL	RDC	JER
Bulls	7 268	5 487	1 556
Cows	39 630	38 737	18 799

HOL=Holstein; RDC=Nordic Red Dairy Cattle; JER=Jersey.

Results & Discussion

The included data span back to the beginning of 1990, though variation in the starting dates exists because of the multitude of traits, breeds and countries. Comparison of MBW and ST of cows born after 2012 shows that HOL cows are somewhat larger and heavier than RDC cows and JER cows are smallest (Table 2).

Table 2. Phenotypic means and standard deviations (sd) of observations from cows born after 2012 by trait and breed.

	HOL		RDC		JER	
	mean	sd	mean	sd	mean	sd
MBW1	114.1	10.2	115.9	10.6	86.1	5.4
MBW2	125.0	9.9	122.2	10.9	96.7	5.7
MBW3	130.4	10.1	126.5	11.6	101.3	6.3
ST	147.8	3.6	141.1	3.6	128.2	2.9
CW	5.0	0.9	5.0	0.9	5.0	0.9
BD	5.5	0.9	5.1	0.9	5.7	0.9

HOL=Holstein; RDC=Nordic Red Dairy Cattle; JER=Jersey; MBW=metabolic body weight [$kg^{0.75}$] in parity 1, 2 & 3; ST=stature [cm]; CW=chest width [1 – 9]: BD=body depth [1 – 9].

Estimated heritabilities for HOL and RDC were 0.46, 0.51, 0.56, 0.60, 0.18 and 0.26 for MBW1, MBW2, MBW3, ST, CW and BD, respectively and estimated correlations between MBW traits and conformation traits were highest for ST (Table 3). For the HOL and RDC breeds the heritability and genetic standard deviation (SD_g) for the combined MBW EBV was 0.65 and 6.2 $kg^{0.75}$, respectively. The corresponding values for the JER breed were smaller, i.e., 0.58 and 4.0 $kg^{0.75}$, respectively.

Reliabilities of MBW EBVs for bulls with at least 20 daughters ranged from 0.50 to 0.99 and were on average 0.79, 0.86, and 0.62 for HOL, RDC and JER, respectively.

Table 3. Estimated genetic correlations applied for each of the breed-specific evaluations.

	MBW2	MBW3	ST	CW	BD
MBW1	0.98	0.96	0.65	0.58	0.51
MBW2		0.99	0.68	0.55	0.49
MBW3			0.68	0.53	0.48
ST				0.17	0.21
CW					0.55

MBW=metabolic body weight in parity 1, 2 & 3; ST=stature; CW=chest width; BD=body depth.

The estimated genetic trend for combined MBW EBVs increased on average by 0.8 SD_g over the last 25 years in HOL cows, whereas in RDC and JER cows the increase was only 0.4 SD_g (Figure 1). The stronger increase in HOL may be due to the significant use of foreign sires from countries where a greater selection emphasis is given to ST.

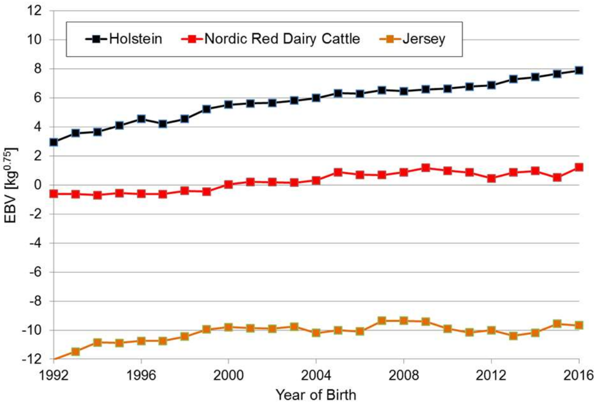

Figure 1. Genetic trend of combined estimated breeding value (EBV) for metabolic body weight in cows given by year of birth and breed.

To validate the genomic predictions for MBW we assessed 584 HOL, 516 RDC and 188 JER candidate bulls. The validation reliabilities for these bull groups were 0.59, 0.74 and 0.65 for HOL, RDC and JER, respectively. RDC obtained the highest validation reliability among the breeds which was due to a larger share of cows with MBW observations in the RDC breed. Overall, validation reliabilities were even higher than those for the production traits, giving support that the quality of the MBW index is high enough to be included into the Nordic Total Merit (NTM) index. The benefit of including MBW into the NTM index will depend on the correlations between MBW and the other index traits. Table 4 shows that the MBW index is negatively correlated with frame and beef traits, almost uncorrelated with milk traits, and positively correlated with claw health, calving traits and longevity. The MBW index showed only a small positive correlation with the NTM index, and therefore it can be expected that inclusion of this new information will further improve the net merit of the NTM.

Table 4. Correlations between MBW index and other index traits calculated for 729 Holstein (HOL) and 568 Nordic Red Dairy Cattle (RDC) bulls born in 2005 to 2010 that have a MBW index with a reliability above 0.8.

Trait	HOL	RDC
Frame	-0.78	-0.72
Milk production	-0.01	0.05
Beef production	-0.12	-0.29
Mastitis	0.06	0.06
Female fertility	0.06	0.03
Claw health	0.14	0.18
Calving traits	0.10	0.35
Longevity	0.18	0.20
Nordic Total Merit	0.04	0.11

Under the consideration that maintaining one kg MBW requires 0.515 MJ metabolizable energy (ME) and that the average energy density of the feed is 11.7 MJ ME / kg dry matter (Luke 2015; Mäntysaari et al., 2012), a difference in the MBW index of HOL and RDC cows of one SD_g corresponds on average to a difference of 104 kg dry matter feed intake per cow and year. For JER cows one SD_g corresponds to a difference of 67 kg.

Conclusions

The NAV countries Denmark, Finland and Sweden have introduced for the three main breeds Holstein, Nordic Red Dairy Cattle and Jersey genetic and genomic evaluations for metabolic body weight. The evaluation models utilize body weight measurements and correlated conformation trait information. The achieved genomic validation reliabilities for metabolic body weight were even higher than those for production traits. Results show that metabolic body weight can be considered for inclusion into the Nordic Total Merit index to enhance resource efficiency in dairy cattle.

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