

Nordic Genetic Evaluation of Feed Efficiency – Updated Model for Saved Feed in Nordic Dairy Cattle Breeds.

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Abstract

Since 2019, the Nordic Cattle Genetic Evaluation (NAV) has published breeding values for Saved Feed for Holstein (HOL), Jersey (JER), and Red Dairy Cattle (RDC). This trait is integrated into the Nordic Total Merit (NTM) index. Previously, the genetic evaluation of energy use for maintenance was based on body weight and indicator traits such as stature, body depth, and body width. Metabolic efficiency was genetically evaluated by using a two-step model, where the first step is a pre-correction of phenotypes that introduced challenges. This study developed a one-step genomic model for Saved Feed to both address these challenges and improve the use of research and Cattle Feed InTake (CFIT) data. The dataset comprised 741,491 weekly records from 4,541 JER, 5,377 RDC, and 8,030 HOL cows. SNP genotypes from NAV were used to create breed-specific single-step genomic evaluations. We fitted two-trait random regression models for each of the traits of dry matter intake (DMI), energy-corrected milk (ECM), and body weight (BW) where we treated the first and later lactations as separate traits. The breeding values for BW change (ΔBW) were derived from the BW model. Across lactation (2–44 weeks in milk), the heritabilities ranged from moderate to moderately high for DMI and ECM (0.22–0.50 & 0.47–0.52) and were moderately high for BW (0.46–0.61). The genetic correlations were strong across parities (≥ 0.82). These genetic parameters estimated with pedigree based BLUP, were used in three single-step GBLUP models, where lactation-wise breeding values for Saved Feed were calculated within each breed as:

$$GEBV_{\text{Saved Feed}} = 0.40 \times GEBV_{\text{ECM}} + 4.0 \times GEBV_{\Delta BW} - GEBV_{\text{DMI}}$$

One index unit of Saved Feed corresponds to 18.3 kg of dry matter saved per 305-day lactation, or 183 kg for 10 index units. Among for candidate bulls born in year 2022, the breeding values for Saved Feed had moderate index correlations with the NTM (0.20–0.30), weak to moderate index correlations with yield trait (0.07–0.26), and low index correlations with female fertility, udder health, and general health (–0.14 to 0.12). For HOL and RDC, the index correlations between Saved Feed and frame size were moderately negative (–0.19 to –0.29), while for JER, this correlation was close to zero. In conclusion, NTM has been updated with the new NAV one-step Saved Feed index which should promote genetic progress for feed efficiency in the Nordic Dairy Cattle breeds.

Key words: Saved Feed, Feed Efficiency, Genomic Prediction, Holstein, Jersey, Red Dairy Cattle.

Introduction

Feed is the largest operating expense on dairy farms (Stephansen et al., 2021a) and a major contributor to dairy farms' greenhouse gas emissions (Kristensen et al., 2015). Consequently, genetic evaluation centers worldwide have developed breeding values for feed efficiency. The Nordic Cattle Genetic Evaluation (NAV) has introduced breeding values for Saved Feed by first including breeding values for energy use related to maintenance in 2019 (Lidauer et al., 2019) and then including breeding values for metabolic efficiency in 2021 (Stephansen et al., 2021b). The Saved Feed index has been integrated into the Nordic Total Merit (NTM) index since 2020 to support selection for more feed-efficient cows in Holstein (HOL), Jersey (JER), and Red Dairy Cattle (RDC) populations.

Historically, the breeding values for energy use related to maintenance was calculated using body weight data collected from milking robots, heart girth collected with tape measurements, and indicator traits such as stature, body depth, and chest width. The breeding values for metabolic efficiency were calculated as residual feed intakes (RFI) using the data from both commercial farms from Cattle Feed InTake (CFIT) (Lassen et al., 2023) and research farms from AU-Foulum, Denmark and Luke, Finland. The breeding values for RFI were calculated using a two-step approach, where the first step was a pre-correction using a linear model, from which the residual was used in a single-step GBLUP. However, this two-step approach presented challenges with unrealistic regression coefficient of feed intake on milk energy, difficulty with handling of missing data, and poor correction of fixed effect when using multiple traits in regression models due to different means and variances in different levels of fixed effects. Such issues have previously been documented for this type of RFI model (Tempelman & Lu, 2020; Stephansen et al., 2024).

To address these limitations, we propose a one-step Saved Feed model that was inspired by

the works of Khanal et al. (2022) and Abdalla et al. (2024). The objective of this study was to develop and implement a one-step Saved Feed evaluation model that enhanced the accuracy and robustness of breeding values for feed efficiency in the NAV evaluation.

Materials and Methods

Animal Care and Ethics Committee approval was not required for this study as data was collected using standard dairy herd management practices. Furthermore, no treatment or handling of animals were administered during the data collection for this study.

Phenotypic data

The analysis included phenotypic data on all breeds from 24 Danish CFIT farms that were obtained between January, 2019 and December, 2024, phenotypic data on HOL that were obtained from the Danish Cattle Research Center (DCRC) between January, 2003 and March, 2022 (Li et al., 2017; Stephansen et al., 2023), and phenotypic data on RDC from Natural Resources Institute Finland farms between September, 1998 and January, 2022 (Luke; Mehtiö et al., 2018). The phenotypic data was comprised of weekly averages of dry matter intake (DMI), weekly averages of body weight (BW), and monthly test-day records for energy-corrected milk (ECM). In total, the dataset included 741,491 DMI records from 4,541 JER cows, 5,377 RDC cows, and 8,030 HOL cows (Table 1).

Table 1: Numbers of records, cows, and cows with genotypes in the phenotypic data.

Breed	n records		n cows (genotyped)
	DMI	ECM	
HOL	361,412	202,360	8,030 (5,104)
RDC	233,867	108,255	5,377 (3,828)
JER	146,215	84,486	4,541 (3,040)
Total	741,491	395,101	17,948 (11,972)

HOL=Holstein, RDC=Red Dairy Cattle, JER=Jersey, DMI=Dry Matter Intake, ECM=Energy Corrected Milk

Pedigrees and genotypes

Both the initial breed-specific pedigrees and the genotypic data were provided by NAV using its standard operations from routine evaluations. The initial pedigree was pruned such that it only contained cows with either phenotypic or genotyped individuals and their ancestors within three generations. Afterwards, we added genetic groups for individuals with unknown parents. The genetic groups were defined based on the sex, breed, country of origin, and birth year class of the individual. The final pedigrees included 1,120,681 HOL, 488,855 RDC, and 256,551 JER animals. The genotypic data contained information on approximately 45,000 SNPs. The genotyping rates for animals in the pedigree were 58% for HOL, 66% for JER and 58% for RDC.

Statistical models

DMI, ECM, and BW were analyzed using breed-specific two-trait random regression models where primiparous and multiparous lactations were treated different traits:

$$\mathbf{y} = \mathbf{Xb} + \mathbf{Za} + \mathbf{Wpe} + \mathbf{Mp} + \mathbf{e},$$

where $\mathbf{y}$ is a vector of phenotypes for DMI, ECM, or BW across the two parity groups (primiparous or multiparous) and weeks in lactation (week 0-45); $\mathbf{b}$ is a vector of fixed effects for age at first calving (only primiparous), parity (only multiparous), calving herd $\times$ calving year $\times$ calving season, the regression on lactation curve (5th order Legendre polynomial terms nested within herd); $\mathbf{a}$ is a vector of additive genetic random regression coefficients (Legendre polynomials: intercept, linear); $\mathbf{pe}$ is a vector of permanent environmental random regression coefficients (Legendre polynomials: intercept, linear, quadratic); $\mathbf{p}$ is a vector of random effects for animal $\times$ parity (only multiparous); $\mathbf{e}$ is a vector of residuals nested within trait; and $\mathbf{X}$, $\mathbf{Z}$, $\mathbf{W}$, and $\mathbf{M}$ are design matrices. The parameters of the model were estimated using AI-REML in DMU (Madsen and Jensen, 2013) with a pedigree-based relationship matrix.

The estimated (co)variance components were used to predict lactation-wise genomic breeding values for DMI, ECM and BW using the ssGTaBLUP model in the MiX99 software (Mäntysaari et al., 2017). For RDC, we predicted genomic breeding values with (co)variance components from HOL. The genomic breeding values for BW change (ΔBW) were derived from the BW model as the difference between GEBVs at day 30 in milk and day 280 in milk.

The new Saved Feed calculation

We used the GEBVs of the traits to calculate breeding values for Saved Feed within each combination of parity group and breed:

$$\text{GEBV}_{\text{Saved Feed}} = 0.40 \times \text{GEBV}_{\text{ECM}} + 4.0 \times \text{GEBV}_{\Delta\text{BW}} - \text{GEBV}_{\text{DMI}}$$

Instead of estimating the regression coefficients for ECM and ΔBW in the equation above from genetic parameters, we obtained the regression coefficient for ECM from Abdalla et al. (2024), while the regression coefficient for ΔBW was based on Lidauer et al. (2023). Parity-specific $\text{GEBV}_{\text{Saved Feed}}$ values were weighted with 1/3 emphasis on primiparous lactation and 2/3 emphasis on multiparous lactations.

The breeding values for Saved Feed were standardized to have a mean of 100 and a standard deviation (SD) of 10 for base animals, defined as three to five years old (rolling base) cows with phenotypes. One index unit represents 18.3 kg of dry matter feed saved in the first 305 days of lactation.

Results & Discussion

Covariance parameters

Lactation-wise (2 to 44 weeks in milk) heritabilities were moderate for DMI ($\text{HOL}_{\text{primi}}$:0.43; $\text{HOL}_{\text{multi}}$:0.49; $\text{JER}_{\text{primi}}$:0.22; $\text{JER}_{\text{multi}}$:0.50), moderate for ECM ($\text{HOL}_{\text{primi}}$:0.50; $\text{HOL}_{\text{multi}}$:0.48; $\text{JER}_{\text{primi}}$:0.47; $\text{JER}_{\text{multi}}$:0.52), and moderately high for BW ($\text{HOL}_{\text{primi}}$:0.52;

$HOL_{multi}:0.58$; $JER_{primi}:0.46$; $JER_{multi}:0.61$). The heritabilities were in accordance with those reported using a CFIT dataset (Stephansen et al., 2025) and research data for HOL in US (Khanal et al., 2022). The genetic correlations between parity groups were high for DMI (HOL: 0.90; JER: 0.82), high for ECM (HOL: 0.89; JER: 0.94), and high for BW (HOL: 0.95; JER: 0.90). This is also in accordance with previous studies (de Jong et al., 2019; Jamrozik et al., 2022; Stephansen et al., 2025).

Index correlations and genetic trends

The new index for Saved Feed had correlations with the previous index of 0.30, 0.50, and 0.25 for HOL, RDC and JER respectively. The levels of these correlations were expected because the model changed to a one-step Saved Feed approach instead of the previous two-step RFI model with challenges observed in the pre-correction step, and because we thereby omitted BW phenotypes from cows without DMI and ECM information. The NAV Saved Feed index has been weighted fully into NTM since February 2025 using the economic weights proposed by Sørensen et al., (2018). This has resulted in moderate index correlations between Saved Feed and NTM at 0.30, 0.26, and 0.20 for HOL, RDC and JER, respectively, among candidate bulls born in 2022 (Table 2).

There has been a positive genetic trend for Saved Feed among bulls with genotype information between 2010 and 2023 with an average increase of 4 Saved Feed index units over the past decade (Figure 1).

The correlations between predicted breeding values for Saved Feed and DMI were moderately high and negative (-0.55 to -0.75), which means that selection for enhanced Saved Feed applies selection pressure against feed intake (Table 2). The correlations between predicted breeding values for Saved Feed and the Yield index were low to moderate (0.07 to 0.26), which indicates that feed efficient cows

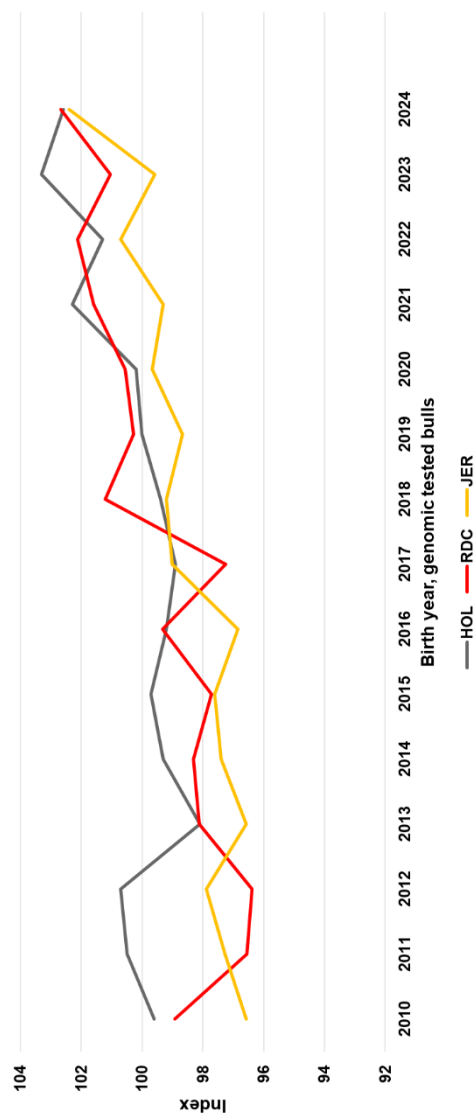


Figure 1: Genetic trends for Saved Feed among bulls with genotype information from Holstein (HOL), Red Dairy Cattle (RDC), and Jersey (JER).

tend to produce more solids and less fluids. The correlations between predicted breeding values for Saved Feed and Female fertility, Udder health, and General health were low and ranged from -0.14 to 0.12 (Table 2). HOL and RDC had moderately negative correlations between predicted breeding values for Saved Feed and frame size (-0.19 to -0.29), whereas for JER this correlation was approximately zero. For JER, the correlation between predicted breeding values for Saved Feed and Longevity was slightly negative (-0.09; Table 2). Lastly, the correlations between predicted breeding values for

Longevity and BW were low and negative in JER and HOL (Table 3).

Table 2: Index correlations for 2022 candidate bulls from Saved Feed to other breeding goals traits.

	Saved Feed		
	HOL (3,267)	RDC (2,592)	JER (488)
DMI	-0.55	-0.75	-0.55
NTM	0.30	0.26	0.20
Yield	0.26	0.07	0.23
FERT	-0.02	0.12	-0.14
MAST	-0.11	0.06	-0.11
GH	-0.11	-0.14	-0.08
Frame	-0.19	-0.29	0.01
Udder	-0.15	-0.08	-0.22
YSS	0.11	0.14	NA
LONG	0.01	0.17	-0.09

HOL=Holstein, RDC=Red Dairy Cattle, JER=Jersey, DMI=Dry Matter Intake, NTM=Nordic Total Merit, FERT=Female Fertility, MAST=Mastitis, GH=General Health, YSS=Young Stock Survival, LONG=Longevity, NA=Not available.

The slightly negative correlations between predicted breeding values for Saved Feed and functional traits may originate from the correlations between DMI and ECM, and the functional traits, since these have mostly negative correlations (Table 3) to female fertility (DMI: -0.05 to -0.30; ECM: -0.20 to -0.30), udder health (DMI: -0.05 to -0.15; ECM: -0.15 to -0.20), and general health (DMI: 0.00 to -0.15; ECM: -0.20 to -0.30).

Conclusions

The updated NAV Saved Feed evaluation has improved utilization of data, and it provides more enhanced feed efficiency selection indices to Nordic dairy farmers. The updated Saved Feed index has been fully weighed into the Nordic breeding goal NTM since February 2025. This has resulted in moderate correlations between the new NTM and the updated Saved Feed index which indicates that selection for NTM leads to genetic progress for feed efficient and profitable Nordic Dairy Cattle.

Table 3: Index correlations among 2022 candidate bulls between component traits for Saved Feed component traits and functional traits in the Nordic breeding goal.

	JER			RDC			HOL		
	DMI	ECM	BW	DMI	ECM	BW	DMI	ECM	BW
FERT	-0.05	-0.30	0.00	-0.05	-0.20	0.00	-0.10	-0.20	-0.05
MAST	-0.05	-0.20	0.00	-0.15	-0.15	0.00	-0.05	-0.15	-0.20
GH	-0.15	-0.20	0.00	0.00	-0.20	0.00	-0.15	-0.30	0.00
YSS	-0.20	0.05	-0.20	-0.15	0.05	-0.20	-0.20	0.10	-0.20
LONG	0.00	0.00	0.20	-0.20	0.05	-0.20	0.00	0.00	-0.05

HOL=Holstein, RDC=Red Dairy Cattle, JER=Jersey, DMI=Dry Matter Intake, ECM=Energy Corrected Milk, BW=Body Weight, FERT=Female Fertility, MAST=Mastitis, GH=General Health, YSS=Young Stock Survival, LONG=Longevity.

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