Including second lactation data in Canadian feed efficiency evaluation

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Abstract

The Canadian 1st lactation genomic evaluation model for feed efficiency was expanded by inclusion of 2nd lactation phenotypes, which account for 30% of all available international data. The new model is a 12-trait (lactation by DIM interval by trait) animal model, with assumptions following the current official implementation. Feed Efficiency (FE) is defined as genetic Residual Feed Intake in 61- 305 DIM within each lactation, with Energy Corrected Milk and Metabolic Body Weight as energy sinks for Dry Matter Intake (DMI). Estimates of heritability for FE were 0.06 and 0.03 in 1st and 2nd lactation, respectively. Lactations were weakly genetically correlated ($r_g = 0.25$) for FE. Each sink was genetically uncorrelated with FE, by definition within each lactation, and genetic correlations between FE and DMI were around 0.4. There were 8,927 cows with DMI data in December 2021 test-run, of which 81% were genotyped. Inclusion of 2nd lactation data increased the Single-Step reference population size (N = 12,942) by 17%, compared with the 1st lactation only model. Average reliability of FE for a sample of 50,000 young, genotyped animals born in 2021 was around 50% for both within lactation traits and the FE Index, defined as an average of 1st and 2nd lactation FE. Reliability of 1st lactation FE was larger, on average, by 1.5 points compared with estimates using only 1st lactation data. Correlations between FE Index and within lactation FE were larger than 0.8. First lactation FE correlated well (r = 0.97) with the current official evaluations. A 5-point increase in RBV (mean = 100, SD = 5 for base bulls, reversed in sign) for FE Index is expected to result in a reduction in feed intake of bull's daughters by approximately 2%. The new Canadian FE model is scheduled for implementation in December 2022, with a simultaneous inclusion of FE in LPI and Pro$ indices.

Key words: Feed efficiency, single-step genomic evaluation, later lactations

Introduction

Several countries introduced genetic/ genomic selection for feed efficiency in dairy cattle during the last decade. In Australia, genomic selection for feed efficiency was launched in 2015 (Pryce et al., 2018). Feed efficiency evaluations were implemented in 2016 in the Netherlands (CRV, 2018), in December 2020 in US (Parker Gaddis et al. 2021), and in 2019 in Nordic (Denmark, Finland, Sweden) countries (Stephansen et al., 2021).

Dry Matter Intake (**DMI**) phenotypes are the foundation for feed efficiency evaluation. They are usually combined with 'Energy Sinks' to derive phenotypes for Residual Feed Intake (**RFI**), a measure of metabolic feed efficiency. This is typically done by fitting a phenotypic linear regression of DMI on the energy sinks, and then using phenotypic RFI as input for a genetic evaluation. Alternatively, genetic RFI (Kennedy et al., 1993) can be derived directly in a one-step approach, by using a linear function of multiple-trait evaluations for DMI and the sinks, Metabolic efficiency evaluations can be combined with several maintenance measures to form an overall feed efficiency index. For example, the US feed efficiency evaluation includes a genetic component for RFI combined with EBV for Live Weight derived from type traits. Feed Saved is then defined as the amount of feed saved through the

combination of improved metabolic efficiency and reduced maintenance requirements (Parker Gaddis et al., 2021).

The Canadian model for feed efficiency was implemented for the Holstein breed in 2021 (Jamrozik et al., 2021). The overall aim was to provide tools that would enable selection of cows that use less feed at the same level of production and body size after the peak of lactation. It was not aimed at reducing maintenance requirements by lowering body weight. A secondary objective was to not target a reduction of feed intake in early lactation, when animals usually have a negative energy balance. Consequently, all phenotypes are defined in two periods of first lactation: 5-60 days and 61-305 days in milk (**DIM**). Traits in the 6-trait multiple-trait linear animal model are:

- Metabolic Body Weight (**MBW**), calculated as (body weight)$^{0.75}$;
- Energy Corrected Milk (**ECM**), calculated as 0.25*Milk + 12.2*Fat + 7.7*Protein, and
- Dry Matter Intake (**DMI**).

All traits are weekly averages expressed in kg/day (ECM and DMI) or kg$^{0.75}$ (MBW).

The final outcome is a Canadian genetic evaluation for Feed Efficiency (**FE**), defined as genetic RFI in the second part of lactation (61 – 305 DIM), and derived through linear re-parameterization of the multiple-trait evaluations for DMI and energy sinks (i.e. ECM and MBW).

Only 1st lactation data are currently used for genetic evaluation of FE in Canada. Including later lactations might better reflect genetic aspects of feed efficiency through animal's lifetime. The majority of current genetic evaluation models for feed efficiency use data from all available lactations in a repeatability model. A multiple-trait approach, defining feed efficiency traits as similar but not identical in different lactations, is theoretically better than a repeatability model, but it is more difficult to apply due to limited feed efficiency data. Estimates of genetic parameters for feed efficiency traits in different lactations (especially RFI) are scarce, and they differ vastly depending on the population and the definition of RFI (phenotypic vs. genetic, and one-step vs. two-step approaches).

The objective of this paper was to present an extension of the Canadian feed efficiency model to include 2nd lactation data. The official implementation of this model for routine genetic evaluation of Holsteins in Canada is scheduled for December 2022.

Material and Methods

Data

The feed efficiency data used by Lactanet includes data from fourteen herds in five countries, within the Efficient Dairy Genome Project (https://genomedairy.ualberta.ca) and the Resilient Dairy Genome Project (http://www.resilientdairy.ca).

The data are organized in several files including: **Pedigree**, **Calving**, **Production** (milk, fat, protein), and **Event** (body weight, DMI). After merging Pedigree file with the official Lactanet counterparts, the August 2021 Holstein extract included 23,637,765 Pedigree records; 19,099 Calving records; 1,080,919 Production records, and 1,410,523 event records.

First lactation constitutes about half of all DMI data available at Lactanet, with 2nd, 3rd and later lactations contributing 30, 16 and 7%, respectively. Altogether, the first 2 lactations included 77%, and the first 3 contained 93% of the total data. The data from lactations greater than 3rd were of relatively little value for genetic evaluation purposes, but it was unclear if we should use the first 3 lactations or if using the first 2 would suffice? After testing different options we decided to use lactations 1 and 2 only, in a multiple-trait manner. Reasons for this (results not shown) were: more reasonable and simpler modelling, relatively few data benefits from the 3rd lactation data, more acceptable genetic parameters from the 2-lactation model, and good agreement between FE EBV from using 2nd only vs. combined 2nd and 3rd lactation data.

Model

The linear animal model for genomic evaluation is the same for each of the 12 feed efficiency traits (ECM, MBW and DMI, in 2 DIM intervals in the first 2 lactations), as in Chud et al. (2019). The phenotypes for MBW and DMI are standardised within herds to the mean and SD of one selected Canadian herd (Elora Research Station, affiliated with University of Guelph, Guelph, ON).

Factors in the model, for a single trait, are:
AGEC = Age at calving (6 classes),
weeklact = Lactation week,
YS = Year-Season of calving (4 seasons),
HY = Herd-Year of calving,
a = Additive genetic effect,
pe = Permanent Environmental (**PE**) effect
e = Residual.

All effects except *a*, *pe* and *e* are treated as fixed in the model. In matrix notation, the model can be written as:
$y = X\,b + Z_1\,a + Z_2\,p + e$, where
y is a vector of observations (traits within cows within DIM interval), **b** is a vector of all fixed effects, **a** is a vector of animal additive genetic effects, **p** is a vector of PE effects, **e** is a vector of residuals, **X** and Z_i (i =1, 2) are respective incidence matrices.

Assumptions are that:
$V(a) = H \otimes G$, **H** is a combined pedigree-genotypes relationship matrix, **G** is the additive genetic covariance (12x12) matrix;
$V(p) = I \otimes P$, **P** is the covariance (12x12) matrix for the PE effect;

$$V(e) = \sum_{i=1}^{N}{}^{+} E_i,\ E_i \text{ is a residual covariance}$$

matrix (3x3) for either first or second DIM interval within each lactation, N is the total number of weekly phenotypic records. Residuals for traits collected in the same week of lactation were assumed correlated, and uncorrelated otherwise.

For each Lactation - DIM interval, let $a = [a_1, a_2, a_3]'$ represent the GEBV for ECM, MBW and DMI, respectively. A linear re-parameterization of these GEBV is defined as (following Jamrozik et al., 2021):

$$a^* = \Lambda\,a,$$

with

$$\Lambda = \begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ -L_{31} & -L_{32} & 1 \end{bmatrix}$$

such that $v(a^*) = G^* = \Lambda G \Lambda'$ with a_3^* being uncorrelated with a_1^* and a_2^*. Non-zero elements of Λ, L_{31} and L_{32} can be expressed as functions of elements of genetic covariance matrix **G** as:

$L_{31} = (g_{12}{}^*g_{23} - g_{13}{}^*g_{22})/(g_{12}{}^*g_{12} - g_{11}{}^*g_{22})$
$L_{32} = (g_{12}{}^*g_{13} - g_{11}{}^*g_{23})/(g_{12}{}^*g_{12} - g_{11}{}^*g_{22})$,

and they are partial (genetic) regression coefficients of DMI on ECM and MBW.

The re-parameterized EBV of DMI are equivalent to genetic RFI, as discussed in Kennedy et al. (1993). The re-parameterization as above can also be derived using a recursive model approach (Jamrozik et al., 2017).

Co-variance components and related genetic parameters involving RFI can be obtained as:

$$G^* = \Lambda G \Lambda',$$
$$P^* = \Lambda P \Lambda',$$
$$R^* = \Lambda R \Lambda'.$$

The derivations of proxies for RFI were presented in a 'within Lactation - DIM interval' framework. This can be easy generalized for the newly proposed 2 lactation FE model (involving multiple traits for 2 DIM intervals within each lactation) by defining Λ as $\sum^{+}\Lambda_{ij}$, where Λ_i refers to the j-th DIM interval in the i-th lactation.

Estimation of genetic parameters

The final data after edits, for co-variance component estimation using the August 2021 extract, consisted of 208,432 weekly records on 7,302 cows. The phenotypes, within two DIM classes (5 – 60 DIM and 61 – 305 DIM) of 1st and 2nd lactations, are described in Table 1. Pedigree file was created by tracing the ancestry of cows with phenotypes 4 generations back. It resulted in 21,465 animals to be included for covariance component estimation.

Co-variance components of the model for ECM, MBW and DMI were estimated with the

Monte Carlo-Expectation Maximization-Restricted Maximum Likelihood- (**MC-EM-REML**) algorithm (Matilainen et al., 2012) implemented in the Mix99 software package (MiX99 Development Team, 2017). The same model as above was used, with the **H** relationship matrix replaced by the additive relationships matrix (**A**).

Genomic Evaluation

The Single-Step method is used to fit the multiple-trait linear animal model for 12 traits, with genotypic information via MiX99 software (MiX99 Development Team, 2017). Details of the methods are presented in Jamrozik et al. (2021).

The sign of evaluations for DMI and RFI is reversed, thus the higher values indicate a better (more desirable) feed efficiency of an animal. All evaluations are expressed as Relative Breeding Values (**RBV**) with a mean of 100 and SD = 5 for base bulls (born 2006 – 2015, with an official GEBV for FE. Similarly to the current model, FE is defined as genetic RFI in 61- 305 DIM within each lactation. The Feed Efficiency Index (**FE Index**) is created as the average across both lactations, of RBVs for FE in 61 – 305 DIM. Sire evaluation for all traits is declared as 'Official' when the bull has at least 5 daughters with DMI data and a minimum reliability for FE Index of 50%.

Results and Discussion

Genetic Parameters

Estimates of the co-variance components were obtained with 498 iterations of the MC-EC-REML algorithm, assuming the convergence criterion of 1.e-8.

Estimates of genetic regression coefficients of DMI on energy sinks are in Table 2. Since those are not directly comparable between sinks and specific RFIs, standardized regression coefficients and the relative impact (%) of energy sinks on DMI are also provided. There was a positive relationship among DMI and both energy sink traits across all lactations and DIM intervals. ECM and MBW contributed to

RFI at the ratio of 60 to 40% in 61 – 305 DIM in both lactations, indicating stronger impact of ECM on energy requirement after the peak of lactation. This proportion was different in the first part of lactation and varied a little between lactations.

Estimates of heritability, genetic and phenotypic correlations for all traits are in Tables 3 and 4, for 1st and 2nd lactation, respectively. Table 5 gives genetic correlations among traits in 1st and 2nd lactation. Heritability estimates for DMI and energy sinks were in line with other literature estimates. Heritability of RFI was lower, 6 and 3% for 61 – 305 DIM in 1st and 2nd lactation, respectively. A significant portion of genetic variability caused by ECM and MBW was removed by the genetic adjustment of DMI. By definition, RFI and the energy sink traits were genetically uncorrelated.

Genetic correlations between DMI and ECM were larger than between DMI and MBW, in the second part of both lactations. DMI was correlated with RFI at the level of 40%, indicating that DMI and RFI are genetically different traits. Genetic correlations for traits between lactation were high for DMI, ECM and MBW, and much smaller for RFI (25% in 61 – 305 DIM). Phenotypically, RFI was less correlated with energy sinks compared to DMI, as expected.

Our estimates of heritability for RFI were generally smaller than other published values for this trait. Hardie et al. (2017) reported heritability of RFI equal to 0.14 and 0.13 for primiparous and multiparous US Holstein cows, respectively. Genomic heritabilities of RFI in Australian Holsteins ranged between 0.18 for cows and 0.36 for heifers (Bolormaa et al., 2022). The principal reason for our lower heritability estimates seems to be the definition of RFI (genetic vs. phenotypic), confirming Kennedy et al. (1993) observations. Similarly, genetic correlations for RFI between lactation obtained in this study were smaller than estimates for other populations, although there is a relatively limited literature on this subject. Estimates from other sources are also difficult

to compare directly, given differences in RFI definitions, estimation models, and other factors. Bolormaa et al. (2022) reported a genetic correlation of 0.47 between RFI for Australian Holstein heifers and cows. US Holstein estimate of genetic correlation between 1st and later lactation cows was 0.76 (Hardie et al., 2017). On the contrary, Stephansen et al. (2022) estimated genetic correlation of 0.0 between 1st and 2nd lactation for genetic RFI using international Holstein data. This latter result supports our lower estimates of between lactation genetic correlations for RFI, and further illustrates important differences between genetic and phenotypic RFI (Kennedy et al., 1993).

Genomic Evaluations

A December 2021 test-run of the new model included 8,927 cows with phenotypic data, of which 8,247 had DMI and 7,218 were genotyped (Table 6). These phenotyped cows were represented by 1,775 sires, of which 1,465 were genotyped. In total, there were 27,203 animals in the 4-generation pedigree, and the genomic reference population included 12,942 genotyped animals. Adding 2nd lactation data to the model increased the number of genotyped cows with phenotypes by 28%, sires of those cows by 12%, and finally, the size of the reference population, which are all genotyped animals in the pedigree, by 17%.

Two groups of animals were selected for comparison purposes, in terms of RBV and respective reliabilities: 479 sires with official status (**PROVEN**), and a sample of 50,000 young, genotyped animals born in 2021 (**YOUNG**). RBVs for YOUNG animals were derived indirectly, using the SNP solutions (Jamrozik et al., 2021).

Reliabilities for YOUNG animals were 50 – 51%, with similar distributions for all FE characteristics. PROVEN sires had higher levels of reliability for all traits (75 – 79%). Adding 2nd lactation data increased reliability of FE in 1st lactation by 1 or 2 points for the majority of YOUNG animals. Correlations

between FE in 1st and 2nd lactation were 0.47 and 0.34 for YOUNG and PROVEN, respectively, and were larger than the corresponding genetic correlations (0.25). The FE Index was correlated with FE in each of 1st and 2nd lactations at the level of 80% for both groups of animals. The FE evaluations in 1st lactation, when estimated using only 1st lactation data, were highly correlated with proofs based on data from both lactations (0.97 for both PROVEN and YOUNG). The 2-lactaions FE Index had a correlations of 80% with FE in 1st lactation based only on 1st lactation data, for both the YOUNG and PROVEN animals.

Relationships Between sire RBV and Daughter Phenotypes

Sire daughter averages for DMI in 1st and 2nd lactations were regressed on sire RBV for FE Index, to translate RBV expressions to an equivalent expected reduction in DMI of daughters (Figures 1 and 2). Sires with higher FE Index values had daughters with lower DMI intake in both lactations, indicating better feed efficiency for the high-ranking sires. A 5-point increase in FE Index (1 SD) has the expected effect of decreasing DMI in daughters by 80 and 120 kg between 61-305 DIM in 1st and 2nd lactation, respectively, which is equivalent to approximately 2% reduction in DMI per lactation.

Conclusions

A new model for feed efficiency evaluation, using data from 1st and 2nd lactations in a multiple-trait, one-step approach, was developed for Canadian Holsteins. Feed efficiency measures, derived as genetic RFI in 61 – 305 DIM, separately by lactation, had relatively low heritabilities and weak genetic correlations between lactations. Adding 2nd lactation data increased the reliabilities of feed efficiency for young, genotyped animals. There was good agreement between evaluation results from the current, 1st lactation only model and the new model. Routine implementation of the

new model is planned for December 2022, with simultaneous inclusion of FE in LPI and Pro$ indices.

Acknowledgements

References

Bolormaa, S., MacLeod, I.M., Khansefid, M., Marett, L.C., Wales, W.J., Nieuwhof, G.J., Baes, C.F., Schenkel, F.S., Goddard, M.E., Pryce, J.E., 2022. Evaluation of updated Feed Saved breeding values developed in Australian Holstein dairy cattle. J. Dairy Sci. Comm., 3: 114-119.

Chud, T.C.S., Miglior, F., Seymour, D.J., Houlahan, K., Hailemariam, D., Jamrozik, J., Kistemaker, G.J., Baes, C., Schenkel, F.S, 2019. Genetic parameters for dry matter intake. body weight, and energy corrected milk in Holstein cattle. Research Report to GEB, September 2019, pp.5.

CRV, 2018. Breeding value dry matter intake. E40.https://cooperatiecrv-e6.kxcdn.com/wp-content/uploads/2018/12/E_40-Feed-intake-dec-2018-1.pdf

Hardie, L.C., VandeHaar, M.J., Tempelman, R.J., Weigel, K.A., Armentano, L.E., Wiggans, G.R., Veerkamp, R.F., de Haas, Y., Coffey, M.P., Connors, E.E., Hanigan, M.D., Staples, C., Wang, Z., Dekkers, J.C.M., Spurlock, D.M., 2017. The genetic and biological basis of feed efficiency in mid-lactation Holstein cows. J. Dairy Sci., 100: 9061-9075.

Jamrozik, J., Johnston, J., Sullivan, P.G., Miglior, F., 2017. Recursive model approach to traits defined as ratios: genetic parameters and breeding values. J. Dairy Sci., 100: 3767-3772.

Jamrozik, J., Kistemaker, G.J., Sullivan, P.G., Van Doormaal, B.J, Chud, T.C.S., Baes, C.F., Schenkel, F.S., Miglior, F., 2021. Genomic evaluation for feed efficiency in Canadian Holsteins. Int. Bull. 56: 153-161.

Kennedy, B.W., van der Werf, J.H.J., Meuwissen, T.H.E., 1993. Genetic and statistical properties of residual feed intake. J. Anim. Sci., 71: 3239-3250.

Matilainen, K., E.A. Mäntysaari, M. Lidauer, I. Strandén, I., R. Thompson. 2012. Employing a Monte Carlo algorithm in expectation maximization restricted maximum likelihood estimation of the linear mixed model. J. Anim. Breed. Genet. 129(6): 457–468.

MiX99 Development Team. 2017. MiX99: A software package for solving large mixed model equations. Release XI/2017. Natural Resources Institute Finland (Luke). Jokioinen, Finland. URL: http:///www/luke.fi/mix99.

Parker Gaddis, K.L., Van Raden, P.M., Tempelman, R.J., Weigel, K.A., White, H.M., Penagaricano, F., Koltes, J.E., Santos, J.P.E., Baldwin, R.L., Burchard, J.F., Durr, J.W., VandeHaar, M.J., 2021. Implementation of feed saved evaluation in the US. Int. Bull. 56: 147-152.

Pryce, J.E., Nguyen, T.T.T., Axford, M., Nieuwhof, G. and Shaffer, M., 2018. Symposium review: Building a better cow - The Australian experience and future perspectives. J. Dairy Sci., 101(4): 3702-3713.

Stephansen, R.B., Lidauer, M.H., Nielsen, U.S., Poso, J., Fikse, F., Manzanilla-Pech, C.I.V., Aamand, G.P., 2021. Genomic prediction of residual feed intake in the Nordic breeds using data from research herds and 3D cameras in commercial herds. Int. Bull. 56: 162-166.

Stephansen, R.B., Martin, P., Gredler-Grandl, B., Manzanilla Pech, C.I.V., Sahana, G., Ducrocq, V., Baes, C., Veerkamp, R.F., Lassen, J., 2022. Novel genetic parameters to improve gRFI in dairy cattle using big data from multiple lactations and countries. In: Proceedings of the World Congress on Genetics Applied to Livestock Production (WCGALP) 2022 Rotterdam, The Netherlands.

Table 1: August 2021 data after edits, for estimation of co-variance components by lactation and DIM class.

Lactation	Trait[1]/DIM interval	5 – 60 DIM			61 – 305 DIM		
		# Records	Mean	SD	# Records	Mean	SD
First	ECM	22,829	32.4	6.6	79,861	32.5	6.2
	MBW	17,743	115.4	9.2	60,221	122.3	10.6
	DMI	24,629	17.6	3.5	75,124	21.5	3.3
Second	ECM	16,456	42.9	7.6	54,764	37.6	8.3
	MBW	12,869	126.8	9.8	43,253	132.6	11.4
	DMI	16,409	21.8	4.4	47,789	25.0	4.3

[1]ECM = Energy Corrected Milk, MBW = Metabolic Body Weight, DMI = Dry Matter Intake

Table 2: Estimates of regression and standardized genetic regression coefficients (Energy Sink → DMI), and relative impact (%) of energy sinks on DMI, by lactation and DIM class

Lactation	Sink[1]/ DIM	Regression coefficients		Standardized regression coefficients		Relative impact	
		5 - 60	61 - 305	5 - 60	61 - 305	5 - 60	61 – 305
First	ECM	0.179	0.463	0.387	0.782	37	64
	MBW	0.177	0.123	0.651	0.440	63	36
Second	ECM	0.421	0.595	0.594	0.762	55	60
	MBW	0.158	0.162	0.488	0.510	45	40

[1]ECM = Energy Corrected Milk, MBW = Metabolic Body Weight

Table 3: First lactation heritability (diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations (all values x100)

DIM Interval/ Trait[1]		5 - 60				61 – 305			
		ECM	MBW	DMI	RFI	ECM	MBW	DMI	RFI
5 – 60	ECM	**32**	13	47	0	94	-4	74	4
	MBW	12	**52**	70	0	16	96	50	-10
	DMI	36	40	**26**	60	55	65	87	37
	RFI	5	-13	79	**13**	13	7	44	70
61 – 305	ECM	54	9	26	3	**28**	0	78	0
	MBW	-3	77	32	-3	3	**53**	44	0
	DMI	31	25	41	22	50	30	**24**	44
	RFI	-9	-5	15	24	-27	-2	65	**6**

[1]ECM = Energy Corrected Milk, MBW = Metabolic Body Weight, DMI = Dry Matter Intake, RFI = Residual Feed Intake

Table 4: Second lactation heritability (diagonal), genetic (above diagonal) and phenotypic (below diagonal) correlations (all values x100)

DIM Interval/ Trait[1]		5 - 60				61 – 305			
		ECM	MBW	DMI	RFI	ECM	MBW	DMI	RFI
5 – 60	ECM	**16**	19	69	0	91	10	80	14
	MBW	17	**49**	60	0	7	98	54	-3
	DMI	44	33	**15**	55	65	55	95	41
	RFI	-22	-4	74	**6**	14	3	38	63
61 – 305	ECM	45	4	28	1	**16**	-2	75	0
	MBW	3	82	26	-2	-1	**50**	50	0
	DMI	28	24	46	27	48	30	**15**	42
	RFI	-7	-1	22	30	-29	3	66	**3**

[1]ECM = Energy Corrected Milk, MBW = Metabolic Body Weight, DMI = Dry Matter Intake, RFI = Residual Feed Intake

Table 5: First (row) vs. second (column) lactation genetic correlations (all values x100)

DIM Interval/ Trait[1]		5 - 60				61 – 305			
		ECM	MBW	DMI	RFI	ECM	MBW	DMI	RFI
5 – 60	**ECM**	65	5	56	29	65	0	61	28
	MBW	19	90	57	4	8	89	52	0
	DMI	43	65	76	34	42	63	72	21
	RFI	10	7	28	34	18	9	25	17
61 – 305	**ECM**	66	7	62	36	70	2	66	29
	MBW	8	92	49	-1	-2	92	43	-4
	DMI	58	46	78	39	57	43	79	26
	RFI	7	0	18	25	7	3	26	25

[1]ECM = Energy Corrected Milk, MBW = Metabolic Body Weight, DMI = Dry Matter Intake, RFI = Residual Feed Intake

Table 6: Data statistics for December 2021 test-run

No. of		Lactation		Total
		First	Second	
	Records	132,438	89,444	221,882
	DMI Records	110,094	68,498	178,592
	Cows with data	6,777	4,885	8,927
	Cows with DMI	6,020	4,179	8,247
	Sires of cows	1,475	1,330	1,775
Genotyped	Cows	5,643	3,868	7,218
	Cows with DMI	5,161	3,390	6,953
	Sires of cows	1,248	1,095	1,465

Figure 1: Relationship between sire proof for FE Index and daughter average daily DMI in 61 – 305 DIM of 1st lactation

$$y = -0.0701x + 29.121$$
$$R^2 = 0.31$$
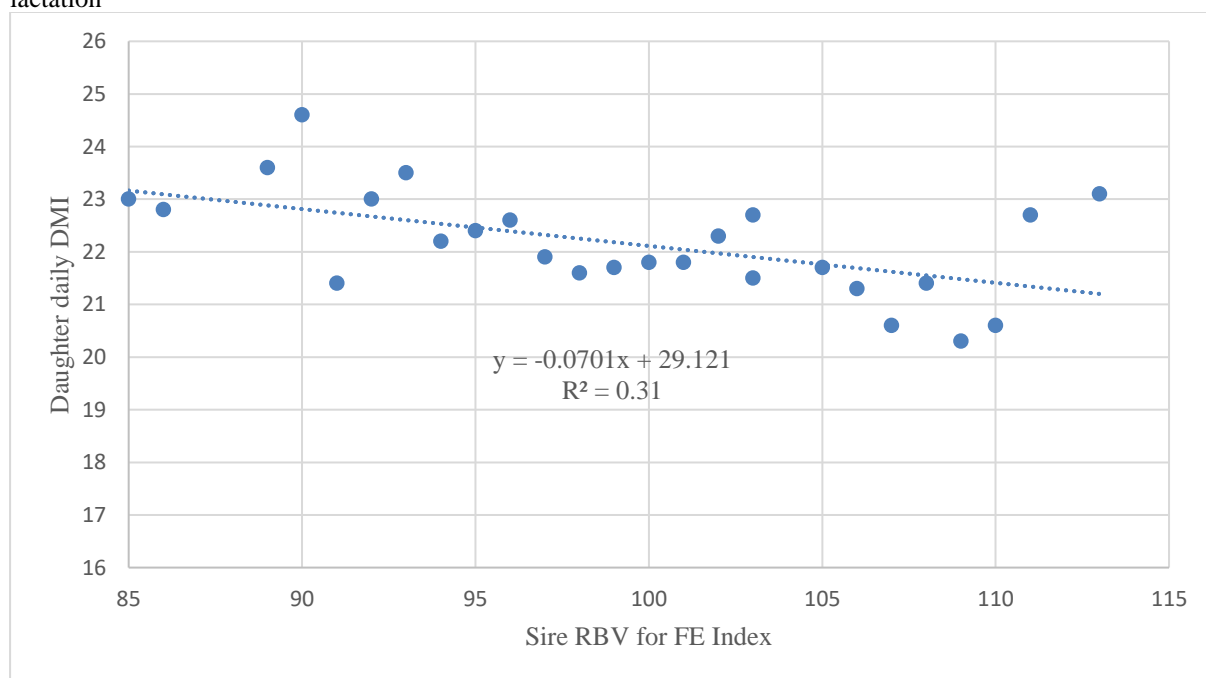
Figure 2: Relationship between sire proof for FE Index and daughter average daily DMI in 61 – 305 DIM of 2nd lactation