

# Novel genetic parameters to improve gRFI in dairy cattle using big data from multiple lactations and countries

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## Abstract

To optimize breeding for feed efficiency, dry matter intake data from 3,967 Holstein cows with 131,234 weekly records from Denmark, France, The Netherlands, and Canada were combined. A random regression model was fitted to 1<sup>st</sup> and 2<sup>nd</sup> parity data for dry matter intake, energy corrected milk and body weight. Results showed that genetic residual feed intake is heritable in both parities, with an average heritability of 0.21. Genetic correlations across lactation and parities showed moderate to high estimates between mid and late lactation within parity. Early lactation had low genetic correlation with mid and late lactation. The genetic correlations between parities were around zero at all lactation stages. These findings show the importance of data collection and modelling at all lactation stages and parities.

## Introduction

Genetic improvement of feed efficiency (FE) is a hot research topic to increase the environmental and economical sustainability in the dairy cattle industry. However, expensive recording schemes for large-scale feed intake registration and appropriate trait definition for FE in the breeding goal are main limitations to implement effective genetic evaluation of FE. We address the trait definition by studying genetic parameters for genetic residual feed intake (gRFI) and lack of feed intake data by international collaboration. Most evaluation centers use the Feed saved definition (Pryce et al., 2015), where residual feed intake (RFI) is an important part. Residual feed intake is typically seen as an output of phenotypic regression of an animal's feed intake on energy sinks (yield, maintenance, etc.). Kennedy et al. (1993) proposed gRFI, assuming that the genetic correlations between feed intake and energy sinks are zero, which is important to avoid double counting in breeding goals. To overcome limited data size, collaboration on feed intake data around the world is crucial to achieve genetic progress for the economical important gRFI trait. Martin et al. (2021b) proposed a RFI model that was able to better describe the dynamic nature of the lactation, but this model did not include a genetic part. The aim of this study was to estimate variance components for a dynamic RFI model using time series data from multiple lactations and countries.

## Material and methods

**Phenotypes, data editing & pedigree.** Data from 870 Danish Holstein cows were collected from 2003-2019, at the Danish Cattle Research Center (DKC; Foulum, Denmark). Feeding data were described by Martin et al. (2021b). Data from 329 French Holstein cows were collected from 2014-2020, at the Le Pin and Méjusseaume research herds (Martin et al. (2021a); Lefebvre et al. submitted to WCGALP 2022). Data from 1,953 Dutch Holstein cows were collected from 1991-2019, in different research herds at Wageningen University (Heida et al., 2021). The Danish, French and Dutch data were shared as a part of the Gentore project (<https://www.gentore.eu>). Additionally, data from 815 Canadian Holstein cows were collected from 2015-2020, at the Sunalta, DRTC and Elora research farms (<https://genomedairy.ualberta.ca/>; <http://www.resilientdairy.ca/>).

The combined dataset consisted of 5,470 lactations and 131,234 weekly records for feed intake. Various editing and plausibility checks were undertaken to ensure high-quality data, and requirements to cohesive lactations with a length of minimum 100 days in milk. All traits had their variance standardized to the average variance across herd, year, parity, and week of lactation. The pedigree obtained from the collaborators was pruned for eight generations. Missing parents were assigned to genetic groups with effects of country, breed, and birth year. Data editing were performed in the SAS software version 9.4.

**Statistical analysis.** The statistical software DMU (Madsen and Jensen, 2013) was used for variance component estimation, using the AI-REML algorithm. The random regression models were as follows:

$$y_{ijkclmnop} = \mu + HYS_i + WOL_j + ACC_k + ACC_k^2 + \sum_{l=0}^m a_{cl} \Phi_{cjl} + \sum_{l=0}^m pe_{cl} \Phi_{cjl} + EXP_n + YM_o + e_{ijkclnop}$$

where  $y$  were the phenotype DMI, energy corrected milk (ECM; Sjaunja (1990)) or BW for cow  $c$  on week of lactation  $j$  ( $j=1, 2, \dots, 44$ ),  $\mu$  were the intercepts,  $HYS$  were the fixed effects of herd x year x season  $i$  (670 levels; season were defined as quarters from date of calving),  $WOL$  were the fixed effects for week of lactation  $j$ ,  $ACC$  and  $ACC^2$  were the fixed regressions on age at calving and age at calving squared,  $a$  were the random additive effects with the  $l^{\text{th}}$  order of Legendre polynomials with  $a \sim N(0, A\sigma_a^2)$ ,  $pe$  were the random permanent environmental effects with the  $l^{\text{th}}$  order of Legendre polynomials with  $pe \sim N(0, I\sigma_{pe}^2)$ ,  $EXP$  were the random effects on trial  $n$  (376 levels),  $YM$  were the random effects of year x month defined from the record date  $o$  (320 levels) and  $e$  were the residuals  $p$  (11 levels, one every 4 weeks assuming residual covariance to be 0)  $e \sim N(0, I\sigma_e^2)$ . The order of  $l$  was 1<sup>st</sup> for DMI and ECM, and 2<sup>nd</sup> order for BW. To derive genetic and phenotypic output, the notation by Islam et al. (2020) and Martin et al. (2021b) was followed. The final variance component matrix was made positive definite using the bending method of Schaeffer (2014).

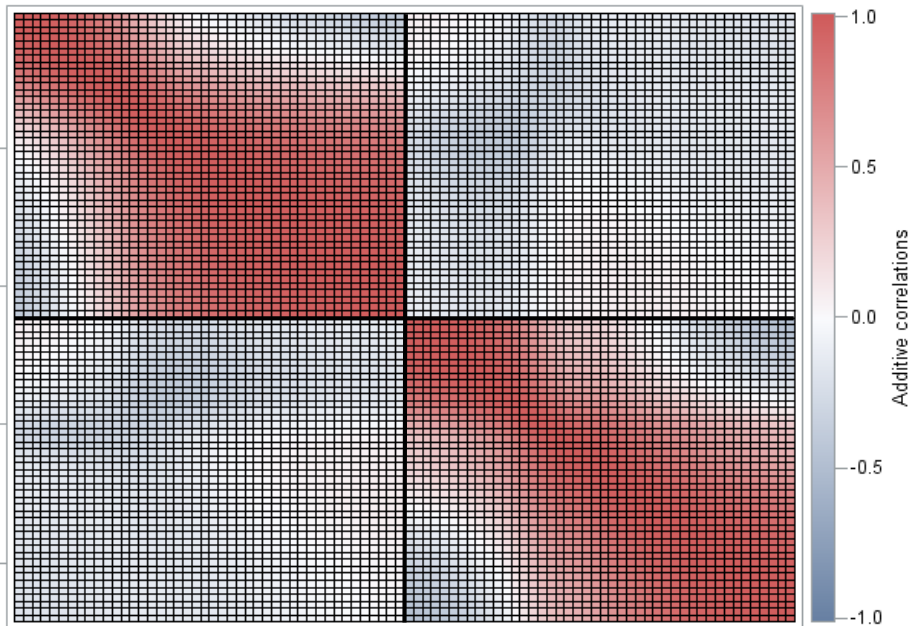
## Results

The descriptive statistics show small differences in mean and variance levels between the countries (Table 1).

**Table 1. Descriptive statistics for phenotypes by the different countries.**

	Denmark	France	The Netherlands	Canada
No. DMI records	65,793	14,370	52,869	26,741
Avg. DMI (SD)	21.5 (3.7)	21.2 (3.7)	20.7 (3.8)	22.1 (5.0)
Avg. ECM (SD)	34.3 (7.8)	30.4 (6.7)	31.3 (7.2)	35.3 (7.5)
Avg. BW (SD)	653.4 (73.3)	626.4 (71.8)	593.3 (76.8)	667.7 (80.0)
Avg. WOL (SD)	20.7 (12.0)	20.0 (11.7)	17.0 (10.5)	20.8 (11.8)
Avg. Parity (SD)	1.7 (0.8)	1.5 (0.7)	1.6 (0.8)	1.6 (0.7)

Genetic RFI is heritable (avg. 1<sup>st</sup> parity: 0.18, 2<sup>nd</sup> parity: 0.24) with additive variance ranging between 0.2 and 2.8 in 1<sup>st</sup> parity and between 0.6 and 3.5 in 2<sup>nd</sup> parity. The highest levels of additive variance were seen during early and late lactation. The genetic correlations across lactation are presented in Figure 1. For 1<sup>st</sup> and 2<sup>nd</sup> parity, gRFI in early lactation is not correlated to gRFI in mid and late lactation. The genetic correlation between gRFI in mid and late lactation is moderate to high. The genetic correlation between 1<sup>st</sup> and 2 parity is around zero.



**Figure 1. Genetic correlations across lactation in the first two parities. 1<sup>st</sup> parity is seen in upper left box and 2<sup>nd</sup> parity in lower right box. The genetic correlations between parities are in the off-diagonal boxes. Each pixel represents one week of lactation, with a total of 88 weeks of lactation when combining 1<sup>st</sup> and 2<sup>nd</sup> parity.**

## Discussion

Within parity, it is expected that gRFI in early lactation is different from the rest of the lactation, because of mobilization not properly accounted for. This was also seen in Li et al. (2017) using Danish data from 1<sup>st</sup> parity Holstein cows.

Absence of correlation between 1<sup>st</sup> and 2<sup>nd</sup> parity could be expected in early lactation due to higher mobilization of body reserve in 2<sup>nd</sup> parity animals compared with 1<sup>st</sup> parity; however, a higher correlation could be expected between parities in mid and late lactation. This could be

an artifact of bending the variance component matrix. These results suggest it is important to register phenotypes for DMI, ECM and BW through the whole lactation and in multiple lactations. This is necessary to achieve the highest possible genetic improvement for feed efficiency. Furthermore, it is important to avoid that selection for gRFI leads to an increased level of metabolic disorders in dairy cattle. The low correlation between early lactation and the rest of the lactation, indicates that selection for gRFI possibly leads to an increased degree of mobilization. Future research should focus on ensuring that selection for gRFI do not lead to increased mobilization in dairy cattle. A possibility is to include body condition scores in the gRFI equation, to account for the change in adipose tissue.

## Conclusions

We demonstrated that gRFI is heritable and the genetic correlation structure shows that within parity, mid and late lactations are moderately to highly correlated. However, the genetic correlation between parities is around zero at all lactation stages. These results suggest that collection of data in all lactation stages and parities is important for genetic gain in feed efficiency.

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