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 1st and 2nd 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:

$$y_{ijclmnop} = \mu + HYS_i + WOL_j + \beta_1 ACC_c + \beta_2 ACC_c^2 + \sum_{l=0}^{m} a_{cl}\Phi_{cjl} + \sum_{l=0}^{m} pe_{cl}\Phi_{cjl} + EXP_n + YM_o + e_{ijclnop}$$

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,…, 44), μ 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, β_1 and β_2 were the regressions on age at calving (ACC) and ACC^2 for cow c respectively, a were the random additive effects with the m^{th} order of Legendre polynomials (LP), pe were the random permanent environmental effects with the m^{th} order of LP, EXP were the random effects of 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). It is assumed that var(a) = $\mathbf{A}\otimes\mathbf{m}$, var($pe$)=$\mathbf{I}\otimes\mathbf{m}$ and var(e)=$\mathbf{I}\sigma_e^2$=$\mathbf{R}$, where $\mathbf{A}$ is the numerator relationship matrix, $\otimes$ is the Kronecker product and $\mathbf{m}$ is the order of LP fitted for a and pe effects (m was 1st order for DMI and ECM, and 2nd 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. 1st parity: 0.18, 2nd parity: 0.24) with additive variance ranging between 0.2 and 2.8 in 1st parity and between 0.6 and 3.5 in 2nd 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 1st and 2nd parity, gRFI in early lactation was not correlated to gRFI in mid and late lactation. The genetic correlation between gRFI in mid and late lactation was moderate to high. The genetic correlation between 1st and 2 parity was around zero.

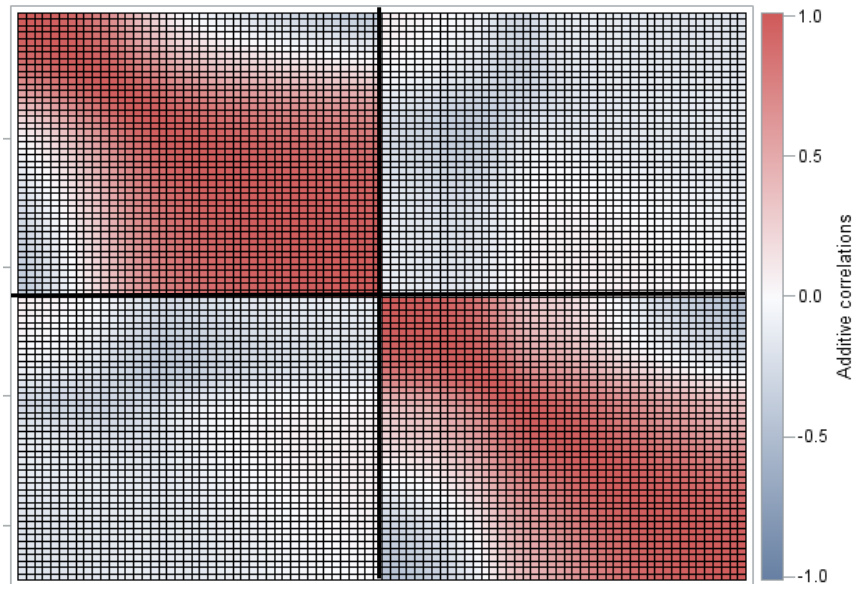

Figure 1. Genetic correlations across lactation in the first two parities. 1st parity is seen in upper left box and 2nd parity in lower right box. The genetic correlations between parities are in the off-diagonal boxes. Each pixel represents one week of lactation, with a total of 88 weeks of lactation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

Absence of correlation between 1st and 2nd parity could be expected in early lactation due to higher mobilization of body reserve in 2nd parity animals compared with 1st 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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References

Heida M., Schopen G.C., Te Pas M.F., Gredler-Grandl B., and Verkamp R.F. (2021) J. Dairy Sci. 104(8): 8966-8982. https://doi.org/10.3168/jds.2020-19533
Islam M., Jensen J., Løvendahl P., Karlskov-Mortensen P., and Shirali M. (2020) J. Dairy Sci. 103(10): 9150-9166. https://doi.org/10.3168/jds.2019-17137
Kennedy B.W., van der Werf J.H., and Meuwissen T.H. (1993) J. Ani. Sci. 71(12):3239-3250. https://doi.org/10.2527/1993.71123239x
Lefebvre R., Faverdin P., Barbey S., Jurquet J. and Tribout T. *et al.* (2022) WCGALP 2022
Li B., Berglund B., Fikse W.F., Lassen J., and Lidauer M.H. *et al.* (2017) J. Dairy Sci. 100(11):9076-9084. https://doi.org/10.3168/jds.2017-12775
Madsen P., and Jensen J. (2013) Aarhus Res Cent. Foulum Box 50, 8830 Tjele Denmark.
Martin P., Ducrocq V., Fischer A., and Friggens N.C. (2021a) Animal 15(12):100412. https://doi.org/10.1016/j.animal.2021.100412
Martin P., Ducrocq V., Gordo D.G.M., and Friggens N.C. (2021b) Animal 15(2):100101. https://doi.org/10.1016/j.animal.2020.100101
Pryce J.E., Gonzalez-Recio O., Nieuwhof G., Wales W.J., and Coffey M.P. *et al* (2015) J. Dairy Sci. 98(10):7340-7350. https://doi.org/10.3168/jds.2015-9621
Schaeffer, L. 2014. Making covariance matrices positive definite. Available at: https://animalbiosciences.uoguelph.ca/~lrs/ELARES/PDforce.pdf
Sjaunja, L. (1990) Proc. of the 27th Session International Committee for Recording and Productivity of Milk Animals; 2-6 July 1990, Paris, France.