

Genetic parameters for residual feed efficiency in three dairy cattle breeds in commercial farms using 3D cameras

C.I.V. Manzanilla-Pech¹, R.B. Stephansen¹, T. Andersen² and J. Lassen^{1,3}

¹ Center for Quantitative Genetics and Genomics, Aarhus University, Blichers Alle 20, 8830 Tjele, Denmark; ² SEGES Innovation P/S, Agro Food Park 15, DK 8200 Aarhus N, Denmark; ³ Viking Genetics, Ebeltoftvej 16, Assentoft, 8960 Randers, Denmark; *coralia.manzanilla@qgg.au.dk

Abstract

This is a preliminary study on estimating genetic parameters for dry matter intake (DMI), BW and residual feed intake (RFI) using 3D cameras in 4,069 cows from three dairy breeds. Weekly records of DMI and BW were recorded during 2019-2021 for 1,643 Holstein, 1,211 Jersey and 1,215 Red Dairy Cattle (RDC) cows at Danish commercial farms. Estimated heritabilities for DMI ranged from 0.23 to 0.34, whereas for BW ranged from 0.38 to 0.49. Estimated heritabilities for RFI were 0.19 for Holstein, 0.15 for Jersey and 0.16 for RDC. Genetic correlations between DMI and BW were moderate positive (0.23-0.57), whereas, the genetic correlations between RFI and DMI were highly positive (0.76-0.98) and between RFI and BW were low positive (0.28) to close to zero. With these results we conclude that feed efficiency (RFI) calculated using DMI and BW measured by 3D cameras (and ECM) is heritable for the three dairy breeds.

Introduction

In the last decade, several countries have included feed efficiency in their breeding goal (Veerkamp et al. 2014; Pryce et al. 2015, Holstein USA, 2021). The Saved feed index in the Nordic Total Merit Index (NTM; NAV, 2020) now includes the breeding value for metabolic efficiency and maintenance (Lidauer et al., 2019). Residual feed intake (RFI) has been proposed as proxy trait for feed efficiency in several species including cattle, pig and poultry (Martin et al. 2021). RFI is usually calculated as the partial regression of dry matter intake on energy sinks (energy-corrected milk; ECM, metabolic body weight; MBW, and BW change; Tempelman et al. 2015). As dry matter intake (DMI) and BW records are required to calculate RFI, new technologies are being developed to increase the number of individual records in an easier and more efficient way. In the last years, a 3D camera's technology to measure feed intake and body weight (BW) on individual cows at large scale has been developed. Using artificial intelligence and 3D cameras, the Cattle Feed InTake System (CFIT, Viking Genetics, 2020; Lassen et al. 2018) is an alternative tool to record individual feed intake and BW compared to scale based systems. The CFIT 3D cameras, located in barns, can identify individual cows and by using artificial intelligence algorithms, record individual DMI and BW for the entire herd. The squared correlation between traditional feed bins and 3D cameras is 0.9 (Lassen et al. manuscript submitted to WCGALP 2022). However, as with every new phenotype, the traits (DMI and BW) need to be quantified genetically. In this study, we estimated the genetic parameters including genetic correlations between DMI, BW (obtained by 3D cameras) and RFI from 4,069 Danish Holstein, Jersey and RDC commercial cows.

Materials & Methods

Data description. The data included weekly records of DMI and BW from 4,069 Danish cows. Only data from 1st to 6th parity from the first 330 days in milk was utilized. The cows were recorded for DMI and BW using 3D cameras technology on 12 (4 per breed) commercial farms

in Denmark during 2019-2021. The cows were fed with a total mixed ration diet that mainly consisted of maize silage, grass silage and concentrates. The cameras were located above the feeding area floor, and the cows were recorded when eating. An algorithm based on artificial intelligence identify the cows and translate their 3D images into phenotypes (DMI and BW). Lassen et al. (2018) have presented a description of the 3D cameras methodology to measure feed intake. Body weight is also predicted using 3D images of the back of the cow, from these images, contours of the back were obtained. Using a PLS method, a prediction model was developed based on scale measures of the cows. Posteriorly DMI and BW weekly averages were calculated. Residual feed intake (RFI; Tempelman et al., 2015) was the residual of the partial regression of DMI on metabolic BW (MBW), energy corrected milk (ECM) and body weight change (Δ BW). The model used to calculate RFI is the one used to calculate the breeding values for RFI by the Nordic Cattle Genetic Evaluation (NAV; Stephansen et al. 2021). Milk yield and content were available through the national milk recording system. Metabolic BW (MBW) was defined as $BW^{0.75}$. Body weight change (Δ BW) is described as change in kg per day. As the recording cameras were installed at different times at the different farms, there is a great variation in the number of records available per animal. These records are also at different times of the lactation. For this reason, a repeatability model was not considered at this time. Instead, averages per animal per lactation for DMI, BW and RFI were calculated. Given that only quarter of the animals have more than one lactation, only one lactation per animal was considered.

Statistical analyses. A univariate animal model was performed to estimate the variance and covariance components using DMU software (Madsen and Jensen 2014) for each trait. To estimate the genetic correlations, pairwise bivariate models between the three traits were fitted. The general model used to estimate the variance components for DMI, BW, and RFI was:

$$y = Xb + Z_1a + e \quad [2]$$

Where y is the vector of phenotypes (DMI, BW, RFI); b represent the vector of fixed effects (herd-year; parity and age of cow); X is the incidence matrix relating observations with fixed effects; a is the vector of direct additive genetic effects; Z_1 is the incidence matrix relating observations with random genetic effects; and e is the vector of residual effects. Distributions of the random effects are $\text{var}(a) = A\sigma^2a$ where A is the pedigree relationship matrix, and $\text{var}(e) = I\sigma^2e$, where I is an identity matrix of an order equal to the number of observations and σ^2e is the residual variance. The pedigree for Holstein included 8,349 cows, whereas, for Jersey 5,405 cows and for RDC 7,963 cows.

Results

Descriptive statistics for DMI, BW, and RFI in Danish Holstein, Jersey and RDC cows are presented in Table 1. DM content was assumed to be 40%. The mean DMI was 27.9 kg/d in Holstein, 22.1 kg/d in Jersey and 27.6 kg/d in RDC. While, the mean BW was 680.6 kg for Holstein, 454.4 for Jersey and 658.2 for RDC. Genetic variances, heritabilities, genetic correlations, and phenotypic correlations of DMI, BW, ECM and RFI in Danish Holstein cows are shown in Table 2. Estimated heritabilities for DMI were 0.34, 0.23 and 0.30, for Holstein, Jersey and RDC. Whereas, for BW were 0.42, 0.38 and 0.49; and for RFI were 0.19, 0.15 and 0.16 for Holstein, Jersey and RDC respectively. Genetic correlations between DMI and BW ranged from 0.23 to 0.57 for the three breeds. RFI and BW showed low correlations (0.06 to 0.26) with large standard errors. Additionally, genetic correlations between DMI and RFI were highly positive for the three breeds (0.76 to 0.98).

Table 1. Descriptive statistics for dry matter intake (DMI), body weight (BW), energy corrected milk (ECM), residual feed intake (RFI) in Danish Holstein, Jersey and Red Danish (RDC) cows with number of animals in parenthesis.

Trait	Holstein (n=1,643)				Jersey (n=1,211)				RDC (n=1,215)			
	Mean	SD	Min	Max	Mean	SD ¹	Min	Max	Mean	SD	Min	Max
DMI	27.9	4.0	17.9	39.8	22.1	3.5	12.3	33.9	27.6	3.4	14.1	36.3
BW	680.6	76.3	449.9	907.3	454.4	40.6	351.3	568.2	658.2	76.0	428.0	889.2
RFI	0.0	1.2	-4.4	4.8	-0.1	2.0	-6.5	6.5	0.0	1.4	-5.3	4.8

Table 2. Genetic and phenotypic variances, heritabilities (diagonal), genetic correlations (lower diagonal) and phenotypic correlations (upper diagonal) of dry matter intake (DMI, g/d), body weight (BW, kg), residual feed intake (RFI, g/d) in Danish Holstein, Jersey and Red Danish (RDC) cows with standard errors in parenthesis.

Breed	Trait	σ_a^2	σ_e^2	DMI	BW	RFI
Holstein	DMI	1.6	3.0	0.34 (0.06)	0.49 (0.01)	0.72 (0.01)
	BW	1,352.7	1,857.8	0.57 (0.09)	0.42 (0.06)	0.07 (0.01)
	RFI	0.3	1.2	0.76 (0.07)	0.12 (0.15)	0.19 (0.05)
Jersey	DMI	1.8	5.9	0.23 (0.07)	0.24(0.02)	0.84 (0.01)
	BW	304.6	488.5	0.23 (0.17)	0.38 (0.07)	0.24 (0.02)
	RFI	0.6	3.5	0.98 (0.02)	0.06 (0.15)	0.15 (0.05)
RDC	DMI	1.8	4.1	0.30 (0.07)	0.42 (0.03)	0.67 (0.02)
	BW	1,732.4	1,782.1	0.50 (0.12)	0.49 (0.07)	0.06 (0.03)
	RFI	0.3	1.6	0.80 (0.09)	0.26 (0.18)	0.16 (0.06)

Discussion

The average DMI for Holstein were slightly higher than previously reported (19.5 kg/d and 607 kg) for Danish Holstein cows by Difford et al. (2020). Additionally, Li et al. (2018) reported lower DMI and BW averages for the three breeds in primiparous Nordic cows measured within 32 weeks of lactation (Holstein= 19.4 kg/d and 601.2 kg; Jersey= 15.8 kg/d and 433.0 kg; RDC=18.5 kg/d and 575.1kg, respectively).

Genetic parameters and correlations. Estimated heritabilities for DMI (Table 2) using 3D cameras were within the range (depending on the lactation week) reported by Li et al. (2016, 2018) for the 3 breeds (0.30-0.55 for Holstein; 0.17-0.52 for Jersey; and 0.20-0.48 for RDC) in primiparous Nordic cows. Likewise, estimated heritabilities for BW were within the range reported by Li et al. (2018) for the 3 breeds, ranging from 0.49 to 0.63 in Holsteins, and from 0.46 to 0.61 in Jersey cows, whereas in RDC was from 0.32 to 0.53. Additionally, NAV (2021) reported heritabilities between 0.51 and 0.53 for second and third lactation Holsteins and Jersey cows. Furthermore, Difford et al. (2020) reported higher heritabilities for DMI (0.43), BW (0.52) and RFI (0.21) for Danish Holstein cows measured with conventional methods. Finally, heritabilities for RFI reported by Li et al. (2017) were similar (0.10-0.23) than the reported in this study (0.19) for Holstein. Moderate to high genetic correlations were estimated between DMI and BW, these values were within the range of values previously reported (0.3-0.7) for Danish Holstein and RDC cows across lactation stages with traditional methods (Li et al. 2018). Furthermore, Manzanilla-Pech et al. (2017) reported lower genetic correlations (0.43) between

DMI and BW in Dutch Holstein cows. Genetic and phenotypic correlations between RFI and DMI were large and positive as expected given that RFI is the residual of DMI after been corrected by energy sinks. Thus, genetic and phenotypic correlations between RFI and BW were between low positive and close to zero (with large standard errors) as expected, as RFI has been corrected by BW. This study has showed that 3D phenotypes (DMI and BW) are heritable and their heritability is comparable to the heritabilities reported with conventional measuring methods. Furthermore, feed efficiency (RFI) calculated using DMI and BW measured by 3D cameras is also heritable. The results of this study are promising, endorsing a new technique of recording feed intake and body weight that has been implemented in commercial farms. We conclude that feed intake, efficiency and body weight measured by 3D cameras are heritable traits, endorsing a new technology of recording feed intake and weight that has been implemented in commercial farms allowing to measure feed intake in a larger and efficient way.

References

- Difford, G.F., P.Løvendahl, R.F.Veerkamp, H.Bovenhuis, M.H.P.W.Visker, *et al.* (2020). 103(3):2442-2459. <https://doi.org/10.3168/jds.2019-16966>
- Lassen, J., J. R. Thomasen, R. H. Hansen, G. G. B. Nielsen, E. Olsen, P. R. B. Stentebjerg, *et al.* (2018). Proc. of the 11th WCGALP. Auckland, New Zealand.
- Lassen J., Thomasen JR and S Borchersen (2022) WCGALP 2022
- Li, B., W.F.Fikse, P.Løvendahl, J.Lassen, M.H.Lidauer, *et al.* (2016). J. Dairy Sci. 99(9): 7232-77239. <https://doi.org/10.3168/jds.2015-10669>
- Li, B., W.F.Fikse, P.Løvendahl, J.Lassen, M.H.Lidauer, P.Mäntysaari, B.Berglund. (2018). J. Dairy Sci. 101(11): 10011-10021. <https://doi.org/10.3168/jds.2018-14611>
- Li, B., B.Berglund, W.F.Fikse, J.Lassen, M.H.Lidauer, P.Mäntysaari, P.Løvendahl. (2017). J. Dairy Sci. 100(11): 9076-9084. <https://doi.org/10.3168/jds.2017-12775>
- Lidauer, M.H., A. M. Leino, R. S. Stephansen, J. Poso, J. U. S. Nielsen, *et al.* 2019. Proc. of the 2019 Interbull meeting, Cincinnati, Ohio, USA June 22-24.
- Madsen, P., and Jensen. (2014). Aarhus Res Cent. Foulum Box 50, 8830 Tjele Denmark.
- Manzanilla-Pech, C.I.V., R. Veerkamp, Y. de Haas, M. Calus, and J. tenNapel. (2017). J. Dairy Sci. 100(11):9103-91014. <https://doi.org/10.3168/jds.2017-12741>
- Martin, P., V. Ducrocq, P. Faverdin, N. C. Friggens. 2021. J. Dairy Sci. 106: 6329-6342.
- NAV. (2020). <https://www.nordicebv.info/wp-content/uploads/2020/11/Metabolic-efficiency-included-in-the-Saved-feed-index.pdf>
- NAV. (2021). https://nordicebv.info/wp-content/uploads/2021/10/NAV-routine-genetic-evaluation_EDITYSS-08102021.pdf
- Stephansen, R.V., M. H. Lidauer, U.S. Nielsen, J. Pösö, F. Fikse, *et al.* Proc. of the 2021 Interbull meeting.
- Tempelman, R., D. Spurlock, M. P. Coffey, R. F. Veerkamp, L. Armentano, *et al.* (2015). J. Dairy Sci. 98(3):2013-2026. <https://doi.org/10.3168/jds.2014.8510>
- Viking Genetics. (2020). <https://www.vikinggenetics.com/about-us/innovative-breeding/ntm/saved-feed>
- Pryce, J., O. Gonzalez-Recio, G. Nieuwhof, W.J. Wales, M.P. Coffey, *et al.* (2015) J. Dairy Sci. 98(10): 7340-73450. <https://doi.org/10.3168/jds.2015-9621>
- Veerkamp, R.F., M.P.L. Calus, G. de Jong, R. van der Linde, Y. De Haas. (2014). Proc. of the 10th WCGALP, Vancouver, Canada.
- Holstein USA, 2021. TPI Formula.
- https://www.holsteinusa.com/genetic_evaluations/ss_tpi_formula.html