Contributed paper

GENETIC PARAMETERS FOR FEED EFFICIENCY AND WEIGHT IN JERSEY COWS USING 3D CAMERAS IN COMMERCIAL DANISH FARMS

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SUMMARY

A challenge of including feed intake in a breeding goal is to have sufficient phenotypic records of feed intake, given how difficult it is to measure on an individual cow basis. With new tools available, such as 3D cameras, this problem might be overcome. This is a preliminary study on estimating genetic parameters for dry matter intake (DMI) and body weight (BW) measured using 3D cameras to posteriorly calculate residual feed intake (RFI). A total of 24,746 weekly records of DMI and BW recorded from 3D cameras during 2019-2021 were available from 963 commercial Danish Jersey cows. These weekly records were complemented with milk and milk content records for the same period, and energy corrected milk (ECM) was calculated. Residual feed intake was calculated as the partial regression of dry matter intake on energy sinks (Tempelman et al., 2015). Estimated heritabilities were 0.08 (RFI), 0.18 (DMI), 0.35 (BW) and 0.29 (ECM). Genetic correlations between DMI with ECM (0.69) were highly positive and DMI with BW (0.37) were moderate positive. Genetic correlations of RFI and DMI were highly positive (0.90), whereas between RFI and BW (0.12) and ECM (0.39) were low to moderate with large standard errors. Phenotypic correlations of RFI with ECM and RFI with BW were close to zero as expected, whereas, between RFI and DMI were close to one. With these results, we conclude that feed efficiency (RFI) calculated using DMI and BW measured by 3D cameras is heritable. Given that DMI and BW were measured only on 963 animals in four commercial farms, adding more farms, animals and records may change the genetic parameters for DMI, BW and RFI.

INTRODUCTION

In the last decade, several countries have included feed efficiency in their breeding goal (Veerkamp *et al.* 2014; Pryce *et al.* 2015). The Saved feed index in the Nordic Total Merit Index (NTM; NAV, 2020) now includes the breeding value for feed efficiency (also called 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). Residual feed intake is commonly defined as the difference between the actual measured feed intake and the expected feed intake, and is a measure of how efficiently a cow utilizes the feed consumed. One way to calculate RFI is as the partial regression of dry matter intake on energy sinks (energy-corrected milk; ECM, metabolic body weight; BW, 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 fulfil the demand of individual records in an easy way. Using artificial intelligence and 3D cameras, the Cattle Feed InTake System (CFIT, Viking Genetics, 2020; Lassen *et al.* 2018) is one of the latest alternative tools to record feed intake and BW. Through CFIT 3D cameras located in barns can identify individual cows and using artificial intelligence algorithms, record individual DMI and BW for the entire herd. However, as with every new phenotype, the traits (DMI and BW) need to be quantified genetically and determine its associations with other traits (such as ECM). The first CFIT data are now available for Jersey cows. In this study, we estimated the genetic parameters including genetic correlations between DMI, BW (obtained by 3D cameras) and ECM in 963 Danish Jersey commercial cows, to posteriorly, calculate RFI.

MATERIALS AND METHODS

Data. The data included 24,746 weekly records of DMI and BW from 963 Danish Jersey cows. Only data from 1st to 6th parity from the first 330 days in milk was utilized in the genetic evaluation of RFI. The Jersey cows were recorded for DMI and BW using 3D cameras technology on four 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 complete description of the 3D cameras methodology to measure DMI. Body weight is also predicted using 3D images of the back of the cow (paper in preparation). From these images, couvertures of the back were obtained. Using a PLS method, a prediction model was developed based on scale measures of the cows. The prediction was done with high accuracy (0.9) and RMSE of 18 kilo. Posteriorly DMI and BW weekly averages were calculated. Weekly milk yield and content were available through the national milk recording system. Energy corrected milk was calculated using the following formula (Sjaunja *et al.* 1991), ECM (kg) = 0.25 Milk (kg) + 12.2 Fat content (kg) + 7.7 Protein content (kg). Residual feed intake (RFI) was the residual of the partial regression of DMI on metabolic BW (MBW), ECM and body weight change (ΔBW) (according to the two-steps RFI from Tempelman *et al.* 2015), along with fixed effects described posteriorly in the model. Metabolic BW (MBW) was defined as $BW^{0.75}$. Body weight change (ΔBW) is described as change in kg per day.

RFI calculation. 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):

$$y_{ijklmn} = \mu + HTYS_i + LW_j + ACC_k(P) + ACC^2{}_l(P) + \mathrm{YSLACP}_m + ECM + MBW + \Delta BW + e_{ijklmn}$$

where y_{ijklmn} is the phenotype for RFI; μ is the mean; HTYS is the fixed effect *i* for herd-trial-year-season; LW is the fixed effect *j* for week of lactation; ACC (P) is the fixed effect of the *k* age of cow at calving with parity nested, ACC2 (P) is the fixed effect of the *l* age of cow at calving squared with parity nested; YSLACP is the fixed effect *m* for year-season-lactation period, ECM is the regression on energy corrected milk, MBW is the regression of metabolic body weight, ΔBW is the regression of body weight change.

Statistical analyses. A univariate animal model for repeated measures was performed to estimate the variance and covariance components using DMU software (Madsen and Jensen 2014). The model used to estimate the variance components for DMI, BW, and ECM was:

$$y_{ijklmnop} = \mu + HTYS_i + LW_j + ACC_k(P) + ACC^2{}_l(P) + \mathrm{YSLACP}_m + a_n + pe_o + e_{ijklmnop}$$

where $y_{ijklmnop}$ is the phenotype for DMI, BW, ECM; μ is the mean; HTYS is the fixed effect *i* for herd-trial-year-season; LW is the fixed effect *j* for week of lactation; ACC (P) is the fixed effect of the *k* age of cow at calving with parity nested, ACC^2 (P) is the fixed effect of the *l* age of cow at calving squared with parity nested; YSLACP is the fixed effect *m* for year-season-lactation period. Random effects are as follows: a is the additive genetic effect *n* distributed as N (0, $A\sigma^2a$), in which A is the pedigree relationship matrix and σ^2a is the genetic variance, pe the permanent environmental effect o (within and across parities) distributed as N (0, $I\sigma^2pe$), in which I is an identity matrix and σ^2pe is the permanent environmental variance and e is the residual effect *p* of $y_{ijklmno}$. To estimate the genetic correlations, pairwise bivariate models between all four traits were fitted. The pedigree included 6,903 animals up to 5 generations. The model to estimate variance components for RFI only included the additive genetic effect, the permanent environmental effect and the residual as RFI has been previously adjusted by fixed effects.

RESULTS AND DISCUSSION

Descriptive statistics. Descriptive statistics for DMI, BW, ECM and RFI in Danish Jersey cows are presented in Table 1. The mean DMI was 21.88 kg with a phenotypic standard deviation of 3.87 kg, whereas, the mean BW was 467.98 kg with standard deviation of 41.73 kg. Both were slightly higher than averages reported previously in literature for Jersey cows by Li *et al.* (2018; primiparous cows) and Halachmi *et al.* (2011).

Table 1. Descriptive statistics for dry matter intake (DMI), body weight (BW), energy corrected milk (ECM), residual feed intake (RFI) in Danish Jersey cows

Trait	No. of records	No. of animals	Mean	SD	Min	Max	CV (%)
DMI	24,746	963	21.88	3.87	8.21	36.55	18
BW	24,746	963	467.98	41.73	312.0	603.0	9
ECM	24,746	963	33.99	6.97	4.05	55.88	20
RFI	24,746	963	0.00	3.10	-14.64	14.45	--

SD=standard deviation, CV= coefficient of variation.

Genetic parameters. There are few studies available reporting genetic parameters for feed intake and feed efficiency in Jersey cows. Genetic and permanent environmental variances, heritabilities, genetic correlations, and phenotypic correlations of DMI, BW, ECM and RFI in Danish Jersey cows are shown in Table 2**.** The genetic variance for DMI in this study was slightly higher (2.11) than previously reported by Li *et al.* (2016) who reported a range from 0.6 to 1.8 (depending on the lactation stage of Jersey cows), however DMI heritability (0.18) was within the range reported (0.17 to 0.52). Likewise, heritability for ECM was within the range of values (0.14-0.53) previously reported by Ulutas *et al.* (2008), Sabedo *et al.* (2018) and Li *et al.* (2018) in primiparous Jersey cows. Estimated heritability for BW was slightly lower than the values (0.46-0.61) reported by Li *et al.* (2018) across lactation stages. Genetic variance for RFI was in the range (0.4-1.4) reported by Li *et al.* (2017) in Holstein cows, same than the permanent environmental variance reported values (1-3.5). However, heritabilities were higher (0.10-0.23) than the reported in this study (0.08).

Table 2. Genetic and phenotypic variances, heritabilities (diagonal), genetic correlations (lower diagonal) and phenotypic correlations (upper diagonal) of dry matter intake (DMI), body weight (BW), energy corrected milk (ECM), residual feed intake (RFI) in Danish Jersey cows

Trait (unit)	σ^2_a	σ^2_{pe}	DMI	BW	ECM	RFI
DMI (g/d)	2.11	3.69	**0.18 (0.05)**	0.19 (0.02)	0.35 (0.02)	0.93 (0.00)
BW (kg)	338.20	387.74	0.37 (0.15)	**0.35 (0.07)**	0.02 (0.02)	0.02 (0.02)
ECM (kg/d)	9.55	12.12	0.68 (0.10)	0.12 (0.15)	**0.29 (0.06)**	0.03 (0.02)
RFI (g/d)	0.76	2.70	0.90 (0.03)	0.12 (0.18)	0.39 (0.16)	**0.08 (0.03)**

Correlations between traits. Moderate to high genetic correlations were estimated between DMI and BW, and DMI and ECM, these values were within the range of values previously reported in Danish Jersey cows across lactation stages (Li *et al.* 2018). Furthermore, Manzanilla *et al.* (2017)

reported lower genetic correlations (0.59) for DMI and ECM and higher (0.43) between DMI and BW in Dutch Holstein cows. Genetic and phenotypic correlations between RFI and DMI were large and positive (0.90 and 0.96, respectively) as expected given that RFI is the residual of DMI after been corrected by ECM, MBW and ΔBW. Phenotypic correlations between RFI and its regressors (BW and ECM) were close to zero as expected, whereas genetic correlations were low (0.12) for RFI-BW and moderate positive (0.39) for RFI-ECM, however, due to the large standard errors, the values between RFI and BW are not significantly different from zero. The correlations between DMI and BW-ECM show the importance of having a trait as RFI that is phenotypically independent of economically important traits as ECM and BW.

CONCLUSIONS

This study shows that feed efficiency calculated using DMI and BW measured by 3D cameras is heritable. Despite the slightly low heritability of DMI, which could be influenced by the small number of farms, animals and records, the results of this study appear promising, endorsing a new technique of recording feed intake and weight that can be implemented in commercial farms. Measuring larger number of animals in more commercial farms, extending the period of measuring and making adjustments in the algorithm and the editing procedure might help to get better quality data and consequently more accurate estimates for genetic parameters.

REFERENCES

Lassen J., Thomasen J.R., Hansen R.H., Nielsen G.G.B., Olsen E., Stentebjerg P.R.B., Hansen N.W., Borchersen S.. (2018) *Proceedings of the 11th WCGALP*. Auckland, New Zeland. 613.

Li, B., Fikse W.F., Løvendahl P., Lassen J., Lidauer M.H., Mäntysaari P., Berglund B. (2016) *J. Dairy Sci.* **99**: 7232.

Li, B., Fikse W.F., Løvendahl P., Lassen J., Lidauer M.H., Mäntysaari P., Berglund B.. (2018) *J. Dairy Sci.* **101**: 10011.

Lidauer, M.H., Leino A.M., Stephansen R.S., Poso J., Nielsen U.S., Fikse W.F., Aamand G.P.(2019) Proceedings 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., Veerkamp R., de Haas Y., Calus M. and J. tenNapel. (2017) *J. Dairy Sci.* **100**:9103.

Martin, P., Ducrocq V., Faverdin P., Friggens N.C. (2021) *J. Dairy Sci*. **106**: 6329.

NAV. (2020). https://www.nordicebv.info/wp-content/uploads/2020/11/Metabolic-efficiency-included-in-the-Saved-feed-index.pdf

Pryce J., Gonzalez-Recio O., Nieuwhof G., Wales W.J., Coffey M.P., Hayes B.J. and Goddard M.E. (2015) *J. Dairy Sci.* **98**: 7340.

Veerkamp, R.F., Calus M.P.L., de Jong G., van der Linde R., De Haas Y. (2014) *Proceedings of the 10th WCGALP,* Vancouver, Canada.

Sabedot, M., Romano G.S., Pedrosa V.B. and L.F.B. Pinto. (2018) *R. Bras. Zootec.* **47**:1806.

Sjaunja, L.O., Baevre L., Junkkarinen L., Pedersen J. and J. Setala. (1991) *Centre for Agricultural Publishing and Documentation (PUDOC),* Wageningen, the Netherlands.

Stephansen, R.V., Lidauer M. H., Nielsen U.S., Pösö J., Fikse F., Manzanilla-Pech C.I.V. and. Aamand G.P. (2021) Proceedings of the 2021 Interbull meeting.

Tempelman, R., Spurlock D., Coffey M. P., Veerkamp R. F., Armentano L., Weigel K., de Haas Y., Staples C., Connor E. E., Lu Y. and VandeHaar M. (2015) *J. Dairy Sci.* **98**: 2013.

Ulutas, Z., A. Sahin, and M. Saatci. (2008). *J. Appl. Anim. Res*. **34**:29.

Viking Genetics. (2020). https://www.vikinggenetics.com/about-us/innovative-breeding/ntm/saved-feed