Genetic Evaluations for Energy Balance
A Real Possibility?

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1. INTRODUCTION

Energy balance, the difference between energy intake and expenditure, is indicative of health and fertility in dairy cattle. To date no country directly includes energy balance in their national genetic evaluations chiefly due to the difficulty of collating energy intake data on sufficiently large numbers of animals. The mid-infrared (**MIR**) spectrum of milk is the method of choice worldwide for quantification of milk fat and protein content during routine milk testing. Recently the MIR of milk was shown to be a good indicator of energy balance in Holstein cows (McParland et al., 2011) although equations were developed and tested on one research herd only. The objective of this study was validate the prediction equations of McParland et al. (2011) for energy balance from MIR on an independent data set from cows in Ireland and to estimate genetic parameters for this new measure of energy balance.

2. MATERIALS AND METHODS

2.1 Data

Two separate data sets were used in this study: 1) data from the Scottish Agricultural College Langhill herd (**SAC**) and 2) data from the Teagasc Moorepark dairy research herd (**MPK**) in Ireland. The SAC herd comprised 1,218 cows divided into two dietary treatments, high concentrate and low concentrate. The MPK data set comprised 1,586 animals of differing strains of Holstein-Friesian (Coleman et al., 2010) on a predominantly grazed grass diet with periodic concentrate supplementation.

Weekly average milk yield (SAC cows were milked thrice daily and MPK cows were milked twice daily), together with weekly fat and protein content, body condition score (**BCS**) and live weight (**LWT**) performance data were available for all animals between the years 1990 and 2010. Individual dry matter intake (**DMI**) data was recorded for 3 successive days per week for SAC animals, while individual DMI of MPK cows was periodically recorded at grass using the *n*-alkane technique and faecal grab samples up to 12 times across lactation.

2.2. Computing Energy Balance

Random regression models were fitted in ASReml (Gilmour et al., 2009), within parity, through the routine measures of milk yield, milk fat and protein content, LWT and BCS. Each country was handled separately. Random regression models were fitted through routine measures of DMI in the SAC data set only. Thus energy balance was computed for MPK animals only during periods of lactation where true DMI was recorded. All random regression models included the fixed effects year of calving-by-season of calving, age at calving, year of record-by-month of record, a fourth order orthogonal polynomial on days post-calving and the random effect of the interaction of cow by a fourth order orthogonal polynomial on days post-calving. Random regression models fitted to the SAC data included the additional fixed effects of genetic line and feeding group. Random regression models fitted to the MPK data included the additional fixed effect of research herd (n=2).

Energy balance (MJ/d), was computed as a function of milk yield, fat and protein content, DMI, LWT and BCS (Banos and Coffey, 2010).

2.3. Mid-Infrared Spectrum Data

From June 2008 to August 2011, individual morning (**MPK(am)**) and evening (**MPK(pm)**) milk samples from all MPK animals were analysed weekly using an MIR spectrometer (Foss MilkoScan FT6000, Hillerod, Denmark) and the resulting spectrum was stored. The Foss MIR spectrum contains 1,060 data points which represent the absorption of infrared light by the milk sample at wavelengths in the 900 cm^{-1} to 5,000 cm^{-1} region. Between September 2008 and December 2010, monthly milk samples from the morning (**SAC(am)**), midday (**SAC(md)**) and evening (**SAC(pm)**) milking on a given day for all SAC cows were sent to Teagasc Moorepark in Ireland for analysis using the same MIR spectrometer. A total of 820 MPK(pm) and 844 MPK(am) spectral records across 338 lactations from 244 MPK cows with true DMI data were available and 2,989 SAC(pm), 2,992 SAC(am) and 2,742 SAC(md) spectral records across 564 lactations from 337 SAC cows were available.

2.4. Development of Prediction Equations

Partial least squares regression (Proc PLS; SAS Institute Inc., Cary, NC) was used to predict energy balance from the MIR linear absorbance data. Predictor variables included a subset of wavelengths from the spectrum of 1,060 correlated wavelengths, together with milk yield. All prediction equations were undertaken using AM, MD (where available), and PM samples, separately. Accuracy of all equations was tested using both split sample cross-validation and external validation.

Three types of analyses were undertaken: 1) prediction equations were calibrated and validated within a research data set, 2) prediction equations were calibrated within one research data set and externally validated on the other research data set, and 3) the two research data sets were combined and equations calibrated and validated using the combined data set.

When equations were developed and calibrated with the same research data set, data was stratified according to feeding treatment, genetic line and season of calving for SAC animals and by experimental farm, stage of lactation (<100 days or >=100 days in milk) and season of calving for MPK animals. Equations were calibrated using 75% of the data set within strata for each research data set and externally validated on the remaining 25%. This procedure was iterated four times, each time using a different 25% of the data until all data had been externally validated at least once. No animal was ever present in both the calibration and validation data sets.

When equations were calibrated and externally validated using combined data from MPK and SAC animals, the combined data set was sorted according to energy balance, and every fourth record removed from the calibration data set for inclusion in the external validation data set. This was done to optimise the robustness of a prediction equation, since samples contained in the calibration data set should represent the variation observed in the phenotype to be predicted (McParland et al., 2011).

2.5. Energy Balance Genetic Parameters

Variance components of both true energy balance, (i.e. energy balance computed using daily solutions), and energy balance predicted using the MIR of milk were undertaken using an animal model in ASReml (Gilmour et al., 2009). MIR predictions of energy balance were obtained from a one-out cross validation model using all SAC(md) samples available (n=2,713). The genetic correlation between true and predicted energy balance was also estimated. Univariate and bivariate models were similar to models used for the random regression analyses, however were undertaken across parities, thus parity was also included as a fixed effect and a random permanent environmental effect was also fitted. An animal pedigree file, four generations deep was generated and contained 1,415 individuals.

3. RESULTS and DISCUSSION

3.1 Animal Performance

Mean performance of SAC and MPK animals for true energy balance and its component variables of milk (kg), fat and protein content (%), BCS (units), LWT (kg) and DMI (kg DM) are presented in Table 1 for days where the MIR spectrum was recorded. Despite the higher DMI of SAC animals relative to MPK animals, SAC animals were on average in negative energy balance, whilst MPK animals were on average in positive energy balance. This may be explained by the higher milk yield, and LWT and lower BCS of SAC cows compared to MPK cows.

Table 1. *Mean performance of SAC and MPK animals*

Variable	SAC	MPK
Cows (n)	337	244
Records (n)	3269	844
Milk (kg)	31.4(8.8)	20.8(6.1)
Fat Percent	3.8(0.7)	4.1(0.6)
Protein Percent	3.3(0.4)	3.5(0.3)
DMI (kg DM)	16.6(4.6)	15.7(2.7)
BCS (units)	2.1(0.3)	2.3(0.3)
Live Weight (kg)	589.4(79.3)	502.6(62.6)
EB[1] (MJ/d)	-10.1(34)	27.9(28)

[1]EB=Energy Balance

3.2 Prediction of energy balance

3.2.1. Within each research data set. The average accuracy (R) of predicting energy balance using milk yield and the MIR spectrum of milk from different calibration and validation data sets is presented in Table 2. When equations were calibrated and validated using data from SAC, the average external prediction accuracy across the four external validation data sets was 0.69 from using MD milk samples to predict energy balance. In general, when predictions were undertaken using either SAC(pm) or SAC(md) samples the slope from the regression of true energy balance on predicted energy balance was close to 1. The poorest slope across the 4 external validations is reported in Table 2. Similarly, the average bias was generally closer to 0 than the absolute maximum average which is reported in Table 2.

The accuracy of predicting energy balance when equations were calibrated and validated using data from MPK were similar to the accuracy obtained from equations using SAC data only with an average accuracy of 0.66 and 0.67, when MPK(pm) and MPK(am) milk samples were used, respectively.

3.2.2. Across research data sets. Prediction equations calibrated using data from SAC only, were not useful to predict the energy balance of MPK animals (Table 2). External validation accuracies ranged from 0 to a maximum of 0.15 when equations developed using SAC(md) milk were validated on MPK(pm) milk. SAC(md) and MPK(pm) samples were taken at similar times of the day.

3.2.3. Using a combined research data set. Prediction equations developed using pooled data from SAC and MPK research data sets were the most robust of all prediction equations developed in this study. Combined prediction equations had an accuracy of prediction of 0.69, had the lowest mean bias of predicted values when compared to other prediction equations, and had a slope (se) from the regression of true on predicted values of EB of 0.98 (0.03).

3.3 Genetics of energy balance

The heritability (se) of true and predicted energy balance was 0.07 (0.05) and 0.28 (0.08), respectively. Respective repeatabilities (se) were 0.29 (0.03) and 0.43 (0.03) These heritability estimates of true energy balance are lower than those reported in the literature (Banos and Coffey, 2010), however were computed here using a limited data set of 337 animals. The genetic, residual and permanent environmental correlations (se) between true and predicted energy balance were 0.05(0.42), 0.46(0.02) and 0.92(0.11), respectively.

4. CONCLUSION

Equations have been developed which give accurate predictions of energy balance across lactation using the MIR spectrum of milk. Although equations developed on one production system are not robust to predict energy balance of animals on a different production system, when a combined data set across production systems was used, results were satisfactory. To date, the chief factor which precluded national genetic evaluations for energy balance was the infeasibility of calculating energy balance for large numbers of animals. This study provides a solution to that problem.

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Table 2. *Root mean square error (RMSE), correlation coefficient, number of records included in the external validation (Recs), bias (SE in parentheses) and slope (b, SE in parentheses) from predicting energy balance using mid-infrared spectra and milk yield in different data sets*

Data Sets		Cross-Validation		External Validation				
Calibration	External	RMSE	R	Recs	Bias(se)	b(se)	RMSE	R
SAC (pm)	SAC (pm)	23.97†	0.70†	738†	2.18(0.85)‡	0.71(0.04)Δ	25.35†	0.65†
SAC (am)	SAC (am)	24.34†	0.70†	738†	1.57(0.90)‡	0.87(0.04)Δ	25.15†	0.67†
SAC (md)	SAC (md)	23.78†	0.72†	678†	-2.35(0.90)‡	0.87(0.04)Δ	24.75†	0.69†
MPK(pm)	MPK(pm)	18.91†	0.74†	214†	3.63(1.70)‡	0.80(0.06)Δ	20.74†	0.66†
MPK(am)	MPK(am)	18.90†	0.74†	220†	-1.99(1.23)‡	0.81(0.06)Δ	20.66†	0.67†
SAC (pm)	MPK(pm)	23.74	0.70	837	62.84(1.19)	0.11(0.04)	27.77	0.09
SAC (am)	MPK(pm)	24.50	0.69	837	69.92(1.32)	0.08(0.03)	27.79	0.09
SAC (md)	MPK(pm)	24.01	0.71	837	70.49(1.32)	0.14(0.03)	27.58	0.15
SAC (pm)	MPK(am)	23.74	0.70	862	40.53(1.17)	-0.05(0.05)	28.05	0.03
SAC (am)	MPK(am)	24.50	0.69	862	49.87(1.24)	0.00(0.04)	28.07	0.00
SAC (md)	MPK(am)	24.01	0.71	862	45.52(1.21)	0.08(0.04)	28.00	0.07
SAC+MPK	SAC+MPK	26.64	0.69	893	1.12(0.88)	0.98(0.03)	26.40	0.69

†Average value across 4 calibrations or validations; ‡Largest average difference between true and predicted values in any external validation data set ; ΔPoorest linear regression coefficient of true energy balance on predicted energy balance across 4 validations