Genetic Evaluations for Energy Balance A Real Possibility?

Sinéad McParland,
G. Banos, M. O’Donovan, M. P. Coffey,
B. McCarthy, B. O’Neill, E. Wall & D. P. Berry

[Logos]
Develop innovative and practical breeding tools for improved dairy products from more robust dairy cows.

www.robustmilk.eu
Introduction

- **Energy balance** (output-input) is an indicator of health & fertility in dairy cows

- Useful for multi-trait breeding programme

- **BUT**
  - Measurement not feasible on commercial herds
  - Little data available

- *Milk mid-infrared spectrum* accurate predictor of energy balance
Example of Energy Balance Prediction

Milk fat content

Milk protein content

Predicted Energy Balance
Objective

- Validate prediction equations on independent data
- Determine genetic parameters of predicted energy balance
Materials and Methods

1. 2 Data Sets

- Langhill experimental herd (SAC, Scotland)
  - 2 genetically divergent lines * 2 feeding systems
- Teagasc Moorepark (Ireland)
  - Different strains of Holstein-Friesian
- Routinely recorded phenotypic traits
  - Milk, fat, protein, live weight, BCS & (DMI)
- Random regressions fit to data separately
  - Models fit within parity
  - Data retained between 1990-2011

- Energy balance (MJ/d) = inputs - outputs
  - Incl. milk, fat, protein, LWT, BCS, DMI
Materials and Methods

2. Mid Infrared Spectral (MIR) data

- MPK samples (AM & PM) analysed weekly
- SAC samples (AM, MD & PM) analysed monthly
  - June / September 2008 – January 2011
  - Light shone through each milk sample
  - 1,060 wavelength readings for each sample
Materials and Methods

2. Mid Infrared Spectral (MIR) data

- MPK samples (AM & PM) analysed weekly
- SAC samples (AM, MD & PM) analysed monthly
  - June / September 2008 – January 2011
  - Light shone through each milk sample
  - 1,060 wavelength readings for each sample
Materials and Methods

3. Prediction equations

- Partial least squares analysis (PROC PLS, SAS)
- Predictors - MIR spectrum + milk yield
- AM, PM & (MD) samples handled separately
- SAC samples (n ≤ 2,989)
- MPK samples (n ≤ 844)
- 3 sets of analyses
  - Calibration - develop equations
  - Validation - independent test of equations
## Calibration & Validation Data

<table>
<thead>
<tr>
<th>Calibration</th>
<th>Validation</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>1. Within Research data set</td>
<td>SAC → SAC</td>
<td>(4 iterations)</td>
</tr>
<tr>
<td></td>
<td>MPK → MPK</td>
<td>(4 iterations)</td>
</tr>
<tr>
<td>2. Across Research data set</td>
<td>SAC → MPK</td>
<td></td>
</tr>
<tr>
<td>3. Pooled data sets</td>
<td>SAC &amp; MPK → SAC &amp; MPK</td>
<td></td>
</tr>
</tbody>
</table>
RESULTS
### Within Research Data Set

<table>
<thead>
<tr>
<th>Data Sets</th>
<th>Cross Val</th>
<th>External Validation</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>RMSE</td>
<td>R</td>
</tr>
<tr>
<td>SAC</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PM PM</td>
<td>24</td>
<td>0.70</td>
</tr>
<tr>
<td>AM AM</td>
<td>24</td>
<td>0.70</td>
</tr>
<tr>
<td>MD MD</td>
<td>24</td>
<td>0.72</td>
</tr>
<tr>
<td>MPK</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PM PM</td>
<td>19</td>
<td>0.74</td>
</tr>
<tr>
<td>AM AM</td>
<td>19</td>
<td>0.74</td>
</tr>
</tbody>
</table>
## Across Research Data Set

<table>
<thead>
<tr>
<th>Data Sets</th>
<th>Cross Val</th>
<th>External Validation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cal</td>
<td>Val</td>
<td>RMSE</td>
</tr>
<tr>
<td>SAC</td>
<td>MPK</td>
<td></td>
</tr>
<tr>
<td>PM</td>
<td>PM</td>
<td>24</td>
</tr>
<tr>
<td>AM</td>
<td>PM</td>
<td>25</td>
</tr>
<tr>
<td>MD</td>
<td>PM</td>
<td>24</td>
</tr>
<tr>
<td>PM</td>
<td>AM</td>
<td>24</td>
</tr>
<tr>
<td>AM</td>
<td>AM</td>
<td>25</td>
</tr>
<tr>
<td>MD</td>
<td>AM</td>
<td>24</td>
</tr>
</tbody>
</table>
Energy Balance - SAC & MPK

Days in milk

Energy Balance (MJ/d)

MPK  SAC

RobustMilk

Agriculture and Food Development Authority
PCA of spectra - SAC & MPK
Pooled Research Data Sets

**SAC (MD) and MPK (PM)**

- **Cross Validation**
  - RMSE = 27 MJ
  - $R = 0.69$

- **External Validation**
  - Slope = 0.98 (0.03)
  - Bias = 1.12 (0.88)
  - $R = 0.69$
Genetic parameters

Heritability of energy balance
- True: 0.07 (se = 0.05)
- Predicted: 0.28 (se = 0.08)

Repeatability of energy balance
- True: 0.29 (se = 0.03)
- Predicted: 0.43 (se = 0.03)

Correlations - true and predicted energy balance
- Genetic: 0.05 (0.42)
Conclusion

- The mid-infrared spectrum is useful as a predictor of energy balance
- Not useful to predict energy balance across systems
- Pooled data across systems gives a robust equation
- Low heritability and low genetic correlation between true and predicted energy balance reported
  - Small data set
- MIR spectrometry is a useful method to routinely collect large volumes of data on energy balance
Acknowledgements

This work was carried out as part of the RobustMilk project that is financially supported by the European Commission under the Seventh Research Framework Programme, Grant Agreement KBBE-211708

http://www.robustmilk.eu