Genomic selection for feed efficiency in dairy cattle: a complex objective

Jennie Pryce, Yvette de Haas, Ben Hayes, Mike Coffey and Roel Veerkamp
Outline

Gross efficiency versus metabolic efficiency

Genomic prediction of measures related to intake

- Australia and New Zealand
- Australia, Netherlands and UK
- Australia, Canada, Denmark, Ireland, Germany, Netherlands, New Zealand, UK, USA

Feed efficiency traits in the breeding objective
Importance of feed efficiency

Feed a growing population

Feed is a major variable cost in animal production

Environmental impact – greenhouse gases
Feed utilisation complex (simplified)

- Feed intake
- Body energy
- Energy available
  - Milk
  - Maintenance
  - Growth
  - Reproduction
  - Health
Gross efficiency

Feed intake → Energy available → Milk intake

Energy available →
- Milk
- Maintenance
- Growth
- Reproduction
- Health

Body energy
Gross efficiency

Feed intake → Energy available

Energy available →
- Milk
- Maintenance
- Growth
- Reproduction
- Health

Output intake
Countries that select for gross efficiency

Australian Profit Ranking (APR)
New Zealand (Breeding Worth; BW)
Others?....

\[
\frac{\text{income} - \text{costs}}{\text{kg DM}}
\]

Approximated using maintenance and production requirements
Genetic gain in milksolids and liveweight in the 10 years prior to and after introduction of BW in NZ

<table>
<thead>
<tr>
<th></th>
<th>Milksolids</th>
<th>Liveweight</th>
</tr>
</thead>
<tbody>
<tr>
<td>1986-1996</td>
<td>+19.7 kg</td>
<td>+15.5 kg</td>
</tr>
<tr>
<td>1996-2006</td>
<td>+25.1 kg</td>
<td>+3.1 kg</td>
</tr>
</tbody>
</table>

(Harris et al., 2007; AAABG)
Metabolic efficiency

Feed intake → Energy available → Efficiency → Milk, Maintenance, Growth, Reproduction, Health

Body energy → Efficiency
Metabolic efficiency

Metabolic efficiency is the efficiency of converting feed into growth, milk, maintenance etc.

Residual feed intake (RFI) is the difference between actual feed intake and predicted feed intake.
Data required to calculate residual feed intake in lactation

Requirement – accurate measurements of:

- Dry matter intake (expensive)
- Liveweight (not often measured – predicted using type)
- Liveweight change/growth (difficult)
- Milk, fat and protein (easy!)
- Body condition score (difficult)
- Energy for reproduction, health (usually not included)
Data required to calculate residual feed intake in growing heifers

Requirement – accurate measurements of:

- Dry matter intake (expensive)
- Liveweight (OK)
- Liveweight change/growth (OK)
Residual feed intake (RFI) heifer trial

• Beef industry has demonstrated selection for RFI is possible
• Collect RFI data and DNA from 2000 calves (Aus & NZ)
• Develop genetic and physiological tests that can be used to predict RFI of animals
• Create a herd of high and low efficiency animals for further research
Experimental design

Phase 1

Batch 1 heifers n=300

Batch 2 heifers n=300

Batch 3 heifers n=300

Phase 2

Nov 2010

Extreme high RFI n=30 lactation trial

Extreme low RFI n=30 lactation trial

Nov 2011

Methane measurement n=8

Methane measurement n=8

Nov 2012

Second trial as lactating cows (2\textsuperscript{nd} lactation)

Nov 2011

Methane measurement n=8

Methane measurement n=8

April 2013

Trial of cows selected on basis of DNA markers for RFI in lactation trial
• Modified existing research feedlot
• 56 to 70 day trial period plus additional adaptation period
• DMI every meal, liveweight 2x per week
• Electronics designed specifically for the project
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• 56 to 70 day trial period plus additional adaptation period
• DMI every meal, liveweight 2x per week
• Electronics designed specifically for the project

Feed intake unit
EID reader
Feed bin
Load cells
Genetic improvement is feasible

<table>
<thead>
<tr>
<th>Trait</th>
<th>Heritability (average ±SE)</th>
<th>Phenotypic SD</th>
</tr>
</thead>
<tbody>
<tr>
<td>RFI (kg/d)</td>
<td>0.27 (± 0.12)</td>
<td>0.44</td>
</tr>
<tr>
<td>Liveweight (kg)</td>
<td>0.32 (± 0.12)</td>
<td>21.9</td>
</tr>
<tr>
<td>DM intake (kg)</td>
<td>0.17 (± 0.10)</td>
<td>0.85</td>
</tr>
<tr>
<td>Growth rate (kg/d)</td>
<td>0.22 (± 0.10)</td>
<td>0.13</td>
</tr>
</tbody>
</table>
Genomic predictions

NZ heifers (1000) + Aus trial 1 + 2 (600) Genotypes + Phenotypes

Prediction Equation

\[ RFI = x_1 + x_2 + x_3 + x_4 \ldots + x_{625,000} \]

Aus trial 3 (300) \( r(\text{Predicted RFI, actual RFI}) \)
Genomic predictions

Prediction Equation: \( RFI = x_1 + x_2 + x_3 + x_4 \ldots + x_{625,000} \)

- NZ heifers (1000)
- Aus trial 1 + 3 (600) Genotypes + Phenotypes
- Aus trial 2 (300) \( r(\text{Predicted RFI, actual RFI}) \)
Results: Accuracy of genomic predictions

<table>
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<tr>
<th>Validation</th>
<th>GBLUP</th>
<th>BayesMulti</th>
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<tbody>
<tr>
<td>AU trial 1</td>
<td>0.28</td>
<td>0.41</td>
</tr>
<tr>
<td>AU trial 2</td>
<td>0.31</td>
<td>0.39</td>
</tr>
<tr>
<td>AU trial 3</td>
<td>0.29</td>
<td>0.42</td>
</tr>
<tr>
<td>Average</td>
<td>0.29</td>
<td>0.41</td>
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Accuracy of genomic predictions of residual feed intake and 250-day body weight in growing heifers using 625,000 single nucleotide polymorphism markers
Genomic predictions

NZ heifers (1000)  Genotypes + Phenotypes

Prediction Equation  RFI = x1 + x2 + x3 + x4 ... + x625,000

Aus heifers  r(Predicted RFI, actual RFI)
## Results: Accuracy of genomic predictions

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<th>Validation</th>
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<tr>
<td>Australia</td>
<td>0.14</td>
<td>0.21</td>
</tr>
<tr>
<td>New Zealand</td>
<td>0.01</td>
<td>0.03</td>
</tr>
</tbody>
</table>

Accuracy of genomic predictions of residual feed intake and 250-day body weight in growing heifers using 625,000 single nucleotide polymorphism markers
Results

Australian Heifers

New Zealand Heifers
Does RFI\_calf predict RFI\_lact?
Experimental design

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April 2013

Trial of cows selected on basis of DNA markers for RFI in lactation trial
Does RFI_calf predict RFI_lact?

- **Our experiment**
  - 108 heifers measured (in two batches) for
    - Dry matter intake (DMI)
    - Liveweight, liveweight change (BW)
    - Body condition score, change (BCS)
    - Milk volume, lactose, protein, milk
  - Over 32 days, with 14 day adjustment

- \[ \text{DMI} = \text{BW} + \text{BW}_\Delta + \text{BCS} + \text{BCS}_\Delta + \text{milk} + \text{protein} + \text{fat} + \text{lactose} + \text{RFI}_{lact} \]
Does RFI calf predict RFI_lact?

Both cohort#1 and cohort#3 data

Significant at P<0.01

Difference between efficient/inefficient cows ~ 0.6kg day
Can we get higher accuracies by sharing data?
Shared data

Australia (DPI)
  • 843 calves with genotypes (624,930 SNPs)

RobustMilk (SAC & WLR)
  • 599 Dutch cows with genotypes (37,069 SNPs)
  • 359 Scottish cows with genotypes (37,069 SNPs)

Common
  • 40 bulls genotyped in both datasets
### Accuracy of genomic selection for dry matter intake (shared data)

#### Multi-trait model

<table>
<thead>
<tr>
<th></th>
<th>Within</th>
<th>Shared</th>
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<tbody>
<tr>
<td><strong>Australia</strong></td>
<td>0.38 (0.03)</td>
<td>0.39 (0.04)</td>
</tr>
<tr>
<td><strong>UK</strong></td>
<td>0.30 (0.04)</td>
<td>0.33 (0.03)</td>
</tr>
<tr>
<td><strong>Netherlands</strong></td>
<td>0.33 (0.10)</td>
<td>0.34 (0.09)</td>
</tr>
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</table>

*de Haas et al, in press (JDS)*
Global dry matter initiative (gDMI)

Led by Roel Veerkamp
Combine DMI phenotypes
Common pedigree
Combine genotypes

Key research questions:
• Genomic similarity between population?
• How to combine, homogenise and standardise phenotypes?
• Can we predict DGV for DMI for different partners?
Phenotypes

#cows: 5000
#lactations: 11700
#calves: 1800
Pedigree

Sires in each dataset and in common between datasets
Genotypes

50k AU, DK, DEU IRL, NLD, NZ, UK

HD AU, DK, DEU IRL, NLD, NZ, UK

Combined HD dataset
imputed genotypes

50k CAN, UK, USA

HD CAN, UK, USA

Ref (HD) N=3151

Ref (HD) N=1840
Breeding goal

Residual feed intake or dry matter intake?

Selection for RFI could lead to an improvement in metabolic efficiency
  Risky if not confident that mobilisation of body tissue is correctly adjusted
  RFI could just be indicator of body reserve mobilisation!
Do genetic correlations between RFI and other traits exist?
  RFI independent of milk, liveweight, growth phenotypically
  Not necessarily the case genetically

Selecting for reduced DMI (as part of a multi-trait index) probably more sensible
  Still require a measure of body reserves (e.g. BCS) in breeding objective, so that you do not reduce DMI at the expense of BCS
Conclusions

• Feed efficiency is important in dairy production
• Selection is possible using genomic selection
• A challenge is to increase the accuracies of prediction
  • combine data internationally and use multi-trait genomic prediction models
Acknowledgements

• American Society of Animal Science
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• gDMI colleagues