Selection for feed intake in dairy cattle using genomic selection.

Roel Veerkamp, Mario Calus and Yvette de Haas

RobustMilk & gDMI
Introduction

- Importance of feed efficiency
  - Global food, forest or fuel discussions
  - Environmental issues (manure & greenhouse gas)
  - Feed important variable cost at farm level

→ Selection impossible in progeny testing scheme.

“Can we beat this dilemma in the era of genomics”

(work in progress)
Outline

- Predict EBV feed efficiency from correlated traits
- Genomics
  - Individual genes
  - Genome wide selection
- Future perspective
  - Progeny tested bull
  - Genomically tested bull
Predict EBV from correlated traits
Predictor traits

- Data Dutch research herds
  - nearly 2000 lactations with feed intake, ration, chemical composition, liveweight ...

- Can LW$^{0.75}$ and FPCM predict EBV for feed efficiency?
Predicting EBV for feed efficiency (35-70 DIM)

\[ EB = NE_{intake} - (NE_{maintenance} + NE_{milk}) \]
\[ EFF = NE_{milk}/NE_{intake} \]
\[ EFM = NE_{milk}/(NE_{intake} - NE_{maintenance}) \]
Predicting EBV for feed intake

<table>
<thead>
<tr>
<th></th>
<th>Energy Intake (35-70 DIM+ 120 – 155 DIM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk 305</td>
<td>0.61</td>
</tr>
<tr>
<td>Fat 305</td>
<td>0.54</td>
</tr>
<tr>
<td>Protein 305</td>
<td>0.67</td>
</tr>
<tr>
<td>Stature</td>
<td>0.76</td>
</tr>
<tr>
<td>Body depth</td>
<td>0.21</td>
</tr>
<tr>
<td>Chest with</td>
<td>0.60</td>
</tr>
<tr>
<td>Rump with</td>
<td>0.10</td>
</tr>
<tr>
<td>BCS</td>
<td>0.06</td>
</tr>
</tbody>
</table>

Probably too high? 

$r_g$ between liveweight and intake was: 0.52
EBV DMI based on yield and type

Predicted accuracy = 0.82 with 100 daughters milk, fat and protein yield & 75 with stature and chest width
Genomics: Individual genes
Individual genes

- 500 unique genes in vicinity of SNP; 27 both BCS & DMI
- Biology: 32 genes smell, taste & pheromone
- Three SNP for DMI in genes:
  - Tryptophan
  - Insulin genes
  - Epidermal growth factors

Veerkamp et al, in press
Genomics: Genome wide selection
Genome wide selection

- Data in own country was initially 600 cows with feed efficiency.

- Accuracy of GWS in the order of 0.36 for feed efficiency (e.g. Verbyla et al.)

- Phenotype is king → collaboration
Genome wide selection: 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
### Genetic parameters (with Genomic RM)

<table>
<thead>
<tr>
<th></th>
<th>AU</th>
<th>UK</th>
<th>NL</th>
</tr>
</thead>
<tbody>
<tr>
<td>AU</td>
<td>0.41 (0.09)</td>
<td></td>
<td></td>
</tr>
<tr>
<td>UK</td>
<td>0.74 (0.34)</td>
<td>0.38 (0.12)</td>
<td></td>
</tr>
<tr>
<td>NL</td>
<td>0.36 (0.22)</td>
<td>0.50 (0.28)</td>
<td>0.59 (0.10)</td>
</tr>
</tbody>
</table>

- Need a multitrait GBLUP model

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De Haas et al, submitted
# Accuracy of genomic selection

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

- Need a multitrait GBLUP model; otherwise might lose accuracy
- Variable results in NL depending on validation set

De Haas et al, submitted
Global dry matter initiative: gDMI

- 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?
DMI phenotypes

#cows: 7000
#lactations: 11700
#calves: 1800
(Donagh Berry)
Genotypes

#genotyped: 6347

Impute all 50k genotypes to HD with 777K

Jennie Pryce (DPI Melbourne) & Jarmila Johnston & Filippo (CDN)
Future perspective: combination
Prospective for a progeny tested bull

Accuracy GEBV for DMI

- Predictors
- +DGV NL
- +DGV NL UK
- +DGV gDMI

Animal Breeding & Genomics Centre
Prospective for genomically tested bull

$h^2 = 0.50$

![Graph showing the relationship between the number of cows in the reference population and accuracy of selection, with different lines representing different scenarios such as 20,000 bulls (with cows), 20,000 bulls (no cows), and 0 bulls (with cows).](image)

Calus et al, in press
Conclusions

- Selection for feed efficiency impossible a few years ago, with genomics a realistic prospect for future
  - Yield and type to make the first step
  - Genomics should identify ‘net efficient cows’

- Breeding goals is more complicated
  - Energy balance; liveweight; economics fat:protein

- Phenotyping is still king; collaboration is leading
Acknowledgements

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Global Dry Matter Initiative (gDMI)
Feed utilisation complex

- Intake
  - Body energy
    - Available energy
      - Production
      - Maintenance
      - Reproduction
      - Health
      - Growth
  - Net efficiencies