Genetic dissection of dairy cow feed efficiency

What is the importance of feed efficiency?

- **Feed** represents more than 50% of the total production costs.

- Benefits of improving feed efficiency:
  - Increase farm profitability
  - Reduce the environmental impact of dairy farming
    (less land needed, reduced greenhouse gas emissions)
What is the importance of genetic selection?
What is the importance of genetic selection?

Genetics 57%

Management 43%
What is the importance of having genetic tools?
## Genetic variation of feed efficiency

**Table 2.** Estimated variance components and heritability for feed efficiency and its component traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>Genetic variance</th>
<th>Residual variance</th>
<th>Heritability</th>
</tr>
</thead>
<tbody>
<tr>
<td>MILKE</td>
<td>2.69 ± 0.25</td>
<td>9.50 ± 0.24</td>
<td>0.22 ± 0.02</td>
</tr>
<tr>
<td>MBW</td>
<td>26.42 ± 1.64</td>
<td>31.98 ± 1.03</td>
<td>0.45 ± 0.02</td>
</tr>
<tr>
<td>DMI</td>
<td>1.08 ± 0.10</td>
<td>3.52 ± 0.09</td>
<td>0.23 ± 0.02</td>
</tr>
<tr>
<td>RFI</td>
<td>0.40 ± 0.05</td>
<td>2.09 ± 0.05</td>
<td>0.16 ± 0.02</td>
</tr>
<tr>
<td>DMI</td>
<td>MILKE,MBW</td>
<td>0.38 ± 0.05</td>
<td>2.09 ± 0.05</td>
</tr>
</tbody>
</table>

*MILKE = milk energy (Mcal); MBW = metabolic BW (kg^{0.75}); DMI = dry matter intake (kg); RFI = residual feed intake (kg); DMI|MILKE,MBW = DMI conditional on milk energy and metabolic BW (kg/Mcal, kg^{0.75}).

---

Lu et al. (2018) JDS 101(4): 3140-3154

Grant 2011-68004-30340
Heritability ($h^2$) estimates

<table>
<thead>
<tr>
<th>PTA trait</th>
<th>Milk</th>
<th>Fat</th>
<th>Protein</th>
<th>PL</th>
<th>SCS</th>
<th>BWC</th>
<th>Udder</th>
<th>Feet/legs</th>
<th>DPR</th>
<th>CA$</th>
<th>HCR</th>
<th>CCR</th>
<th>LTV</th>
<th>HTH$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Milk</td>
<td>0.20</td>
<td>0.43</td>
<td>0.83</td>
<td>0.10</td>
<td>0.02</td>
<td>-0.12</td>
<td>-0.10</td>
<td>-0.02</td>
<td>-0.23</td>
<td>0.19</td>
<td>-0.03</td>
<td>-0.16</td>
<td>0.03</td>
<td>0.03</td>
</tr>
<tr>
<td>Fat</td>
<td>0.69</td>
<td>0.20</td>
<td>0.59</td>
<td>0.15</td>
<td>-0.09</td>
<td>-0.05</td>
<td>-0.07</td>
<td>0.01</td>
<td>-0.15</td>
<td>0.13</td>
<td>0.03</td>
<td>-0.10</td>
<td>0.06</td>
<td>0.08</td>
</tr>
<tr>
<td>Protein</td>
<td>0.90</td>
<td>0.75</td>
<td>0.20</td>
<td>0.13</td>
<td>0.04</td>
<td>-0.09</td>
<td>-0.14</td>
<td>-0.01</td>
<td>-0.18</td>
<td>0.22</td>
<td>-0.07</td>
<td>-0.15</td>
<td>0.05</td>
<td>0.04</td>
</tr>
<tr>
<td>PL</td>
<td>0.15</td>
<td>0.17</td>
<td>0.16</td>
<td>0.08</td>
<td>-0.45</td>
<td>-0.10</td>
<td>0.18</td>
<td>0.14</td>
<td>0.64</td>
<td>0.40</td>
<td>0.32</td>
<td>0.62</td>
<td>0.70</td>
<td>0.56</td>
</tr>
<tr>
<td>SCS</td>
<td>-0.10</td>
<td>-0.10</td>
<td>-0.10</td>
<td>-0.40</td>
<td>0.12</td>
<td>-0.10</td>
<td>-0.23</td>
<td>-0.15</td>
<td>-0.27</td>
<td>-0.14</td>
<td>-0.12</td>
<td>-0.25</td>
<td>-0.25</td>
<td>-0.44</td>
</tr>
<tr>
<td>BWC</td>
<td>0.06</td>
<td>0.05</td>
<td>0.05</td>
<td>-0.20</td>
<td>-0.11</td>
<td>0.40</td>
<td>0.27</td>
<td>0.38</td>
<td>-0.052</td>
<td>-0.07</td>
<td>-0.01</td>
<td>-0.14</td>
<td>-0.14</td>
<td>-0.26</td>
</tr>
<tr>
<td>Udder</td>
<td>-0.02</td>
<td>-0.05</td>
<td>-0.06</td>
<td>0.15</td>
<td>-0.30</td>
<td>0.45</td>
<td>0.27</td>
<td>0.45</td>
<td>0.09</td>
<td>0.10</td>
<td>0.03</td>
<td>0.04</td>
<td>0.08</td>
<td>-0.01</td>
</tr>
<tr>
<td>Feet/legs</td>
<td>-0.14</td>
<td>-0.11</td>
<td>-0.18</td>
<td>0.08</td>
<td>-0.02</td>
<td>0.35</td>
<td>0.40</td>
<td>0.15</td>
<td>0.03</td>
<td>-0.01</td>
<td>-0.04</td>
<td>0.06</td>
<td>0.02</td>
<td>0.02</td>
</tr>
<tr>
<td>DPR</td>
<td>-0.10</td>
<td>-0.10</td>
<td>-0.10</td>
<td>0.20</td>
<td>-0.05</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.04</td>
<td>0.41</td>
<td>0.87</td>
<td>0.35</td>
<td>0.43</td>
<td>0.42</td>
</tr>
<tr>
<td>CA$</td>
<td>0.02</td>
<td>0.02</td>
<td>0.02</td>
<td>0.20</td>
<td>-0.03</td>
<td>-0.01</td>
<td>0.00</td>
<td>-0.02</td>
<td>0.09</td>
<td>0.07</td>
<td>0.16</td>
<td>0.34</td>
<td>0.36</td>
<td>0.33</td>
</tr>
<tr>
<td>HCR</td>
<td>-0.05</td>
<td>-0.05</td>
<td>-0.05</td>
<td>0.10</td>
<td>-0.04</td>
<td>-0.02</td>
<td>-0.05</td>
<td>-0.05</td>
<td>0.10</td>
<td>0.16</td>
<td>0.01</td>
<td>0.54</td>
<td>0.22</td>
<td>0.18</td>
</tr>
<tr>
<td>CCR</td>
<td>-0.10</td>
<td>-0.10</td>
<td>-0.10</td>
<td>0.40</td>
<td>-0.20</td>
<td>-0.10</td>
<td>0.03</td>
<td>-0.04</td>
<td>0.70</td>
<td>0.20</td>
<td>0.45</td>
<td>0.02</td>
<td>0.43</td>
<td>0.36</td>
</tr>
<tr>
<td>LIV</td>
<td>0.11</td>
<td>0.13</td>
<td>0.12</td>
<td>0.70</td>
<td>-0.40</td>
<td>-0.20</td>
<td>0.10</td>
<td>0.05</td>
<td>0.40</td>
<td>0.35</td>
<td>0.20</td>
<td>0.15</td>
<td>0.01</td>
<td>0.55</td>
</tr>
<tr>
<td>HTH$</td>
<td>0.02</td>
<td>0.04</td>
<td>0.02</td>
<td>0.28</td>
<td>-0.22</td>
<td>-0.13</td>
<td>0.00</td>
<td>0.01</td>
<td>0.21</td>
<td>0.17</td>
<td>0.09</td>
<td>0.18</td>
<td>0.28</td>
<td>0.01</td>
</tr>
</tbody>
</table>

1Holstein heritabilities in orange on diagonal; heritabilities for other breeds are the same except for BWC (0.35), udder (0.20), and Jersey and Brown Swiss yield traits (0.23).
Genetic dissection of dairy cow feed efficiency

Why some cows are more efficient than others?

(some cows need less feed than others of similar body weight and milk production)

- they digest feed better
- they spend less energy on unproductive activities
- they have a more efficient metabolism
Feed efficiency: deciphering the genetic basis

open the black box:
identify genetic variants, candidate genes and biological pathways

Why we want to decipher the genetic basis?

- to better understand the biology of this complex phenotype
- to generate information that can lead to the development of new nutritional therapies
- to develop novel genomic strategies for improving feed efficiency via selective breeding
Genetic dissection of dairy cow feed efficiency

How do we decipher the genetic basis?

phenotypic variation

+ genome-wide SNP information

identify regions/SNPs associated with the trait under study

-genome-wide association study whole-genome scan
Residual Feed Intake: genomic scan (1)

- 5k Holstein cows (US + Canada + UK + the Netherlands) / 57k SNPs

Hardie et al. (2017) JDS 100(11): 9061-9075
Genetic dissection of dairy cow feed efficiency

Milk production: genomic scan

% Genetic Variance

Chromosome

DGAT1
GHR
Genetic dissection of dairy cow feed efficiency

Residual Feed Intake: genomic scan (11)

- 4k Holstein cows (9 US research herds) / 278k SNPs

5 SNP-windows

Li et al. (2019) JDS in press
Residual Feed Intake: genomic scan (III)

- 4k Holstein cows (9 US research herds) / 58k SNPs

Single marker regression

Genetic dissection of dairy cow feed efficiency
Residual Feed Intake: genomic scan (III)

- 4k Holstein cows (9 US research herds) / 58k SNPs
Whole Genome Association Analysis

- **genome-wide association studies** are **valuable tools**
- they focus on **genetic markers** with the **strongest evidence of association**
- these significant markers explain a **small component** of the **genetic variance**

Pathway Analysis

- test the **association** of a **set of functionally related genes**
- **multiple contributing factors** are considered simultaneously
- opportunity to identify mechanisms and pathways underlying complex phenotypes
Residual Feed Intake: pathway analysis

Relevant pathways:
- Biosynthesis of amino acids
- Metabolism of proteins
- Digestion of carbohydrates
- Skeletal muscle development
- Immunity
- Rumen bacteria activity
- Mitochondrial electron transport

Li et al. (2019) JDS in press
Mitochondrial function

Genetic dissection of dairy cow feed efficiency

Beef cattle: low RFI vs high RFI
- greater mitochondrial density
- greater mitochondrial function
- greater antioxidant capacity
- lower oxidative stress

[Diagram showing liver and mitochondria with electron transport process]
Genomic selection: the latest revolution

the use of genetic markers across the genome to predict breeding values

allows to select animals at an early age

JOIN THE REVOLUTION
Genetic dissection of dairy cow feed efficiency

Genomics and feed efficiency

feed intake, body weight, milk energy output

+ genome-wide SNP information

Genomic prediction

predict genomic PTAs for the entire population, including young selection candidates
### Genomic prediction

**Table 4. Estimated prediction accuracies for residual feed intake (RFI), DMI, net energy in milk (MilkE), and metabolic body weight (MBW)**

<table>
<thead>
<tr>
<th>Trait</th>
<th>NLD Across</th>
<th>NLD Interaction</th>
<th>SAC Across</th>
<th>SAC Interaction</th>
<th>NAM Across</th>
<th>NAM Interaction</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>With SAC</td>
<td>With NAM</td>
<td>With SAC</td>
<td>With NAM</td>
<td>With SAC</td>
<td>With NAM</td>
</tr>
<tr>
<td>RFI (kg/d)</td>
<td>0.27</td>
<td>0.24</td>
<td>0.29</td>
<td>0.26</td>
<td>0.17</td>
<td>0.12</td>
</tr>
<tr>
<td>DMI (kg/d)</td>
<td>0.35</td>
<td>0.31</td>
<td>0.32</td>
<td>0.31</td>
<td>0.52</td>
<td>0.52</td>
</tr>
<tr>
<td>MilkE (Mcal/d)</td>
<td>0.20</td>
<td>0.22</td>
<td>0.18</td>
<td>0.17</td>
<td>0.61</td>
<td>0.63</td>
</tr>
<tr>
<td>MBW (kg(^{0.75}))</td>
<td>0.31</td>
<td>0.33</td>
<td>0.29</td>
<td>0.30</td>
<td>0.41</td>
<td>0.43</td>
</tr>
</tbody>
</table>

\(^{1}\)Accuracies were measured as the correlation between genomic predicted breeding values and adjusted phenotypes. Environments included North America (NAM), the Netherlands (NLD), and Scotland (SAC). Models were across-environment, within-environment, and interaction model. The average SD of correlations across 10 training-testing partitions were about 0.06, 0.08, and 0.03 for NLD, SAC, and NAM, respectively.
Distribution of GEBV for RFI

**GEBVs** calculated for 16k bulls using a **reference population** of 3.5k cows
Take home messages

- Feed efficiency is an economically relevant trait.
- Residual feed intake is a heritable trait ($h^2 \approx 15\%$).
- Genetic selection can effectively improve dairy feed efficiency.
- Residual feed intake is highly polygenic, many genes with small effects.
- Some relevant biological mechanisms:
  - Metabolism of proteins and sugars, rumen bacteria activity, mitochondrial function.
- Genomic predictive correlations around 20%.
- Future: more feed intake records, more reliable genomic predictions.
Genetic dissection of dairy cow feed efficiency

Thanks for your attention!

Contact Information:
Phone: +1 (352) 294-6988
E-mail: fpenagaricano@ufl.edu
Website: fpenagaricano-lab.org