Phenotypes for novel functional traits of dairy cattle

John B. Cole
Animal Genomics and Improvement Laboratory
Agricultural Research Service, USDA
Beltsville, MD 20705-2350

john.cole@ars.usda.gov
Introduction

I don’t care if my PowerPoint presentation has 320 slides. You are staying until it’s over.
What are functional traits?

- The ICAR Functional Traits Working Group currently is working on:
  - General health traits
  - Female fertility
  - Feet and legs problems
  - Udder health
  - Workability
Why are functional traits important?

- Growing emphasis on functional traits
  - Economically important because they impact other traits

- Challenges with functional traits
  - Inconsistent trait definitions
  - Many have low heritabilities
  - Unclear incentives for collection
### Functional traits are being used

<table>
<thead>
<tr>
<th>Country</th>
<th>Protein</th>
<th>Fat</th>
<th>Milk</th>
<th>Type</th>
<th>Longevity</th>
<th>Udder Health</th>
<th>Fertility</th>
<th>Other man. &amp; health traits</th>
</tr>
</thead>
<tbody>
<tr>
<td>Japan - NTP</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Israel - PD11</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>New Zealand - BW</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>France - ISU</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Italy - PFT</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Germany - RZG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Switzerland - ISEL</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Canada - LPI</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Spain - ICO</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Belgium (Walloon) - VEG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Australia - APR</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>United States - TPI</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>South Africa - BVI</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Great Britain - PLI</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Nordic Countries - TMI</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ireland - EBI</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>United States - NM</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>The Netherlands - NVI</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Source: Miglior et al., 2012
Functional traits have low heritabilities

\[ P = G + E \]

The percentage of total variation attributable to genetics is small.
- CA$: 0.07
- DPR: 0.04
- PL: 0.08
- SCS: 0.12

The percentage of total variation attributable to environmental factors is large:
- Feeding/nutrition
- Housing
- Reproductive management
What traits are commonly recorded?

<table>
<thead>
<tr>
<th>Group</th>
<th>N</th>
<th>Traits included</th>
</tr>
</thead>
<tbody>
<tr>
<td>Calving</td>
<td>4</td>
<td>Direct &amp; maternal calving ease, direct &amp; maternal stillbirth</td>
</tr>
<tr>
<td>Conformation</td>
<td>19</td>
<td>Stature, chest width, body depth, angularity, rump angle, rump width, rear leg set, rear leg rear view, foot angle, fore udder, rear udder height, udder support, udder depth, teat placement, teat length, rear teat placement, overall conformation score, overall udder score, overall feet &amp; leg score</td>
</tr>
<tr>
<td>Fertility</td>
<td>5</td>
<td>Heifer conception rate, days to first service, cow conception rate, services per conception, and days open</td>
</tr>
<tr>
<td>Longevity</td>
<td>1</td>
<td>Direct longevity</td>
</tr>
<tr>
<td>Production</td>
<td>3</td>
<td>Milk, fat, and protein yields</td>
</tr>
<tr>
<td>Udder health</td>
<td>2</td>
<td>Milk somatic cell count, clinical mastitis</td>
</tr>
<tr>
<td>Workability</td>
<td>2</td>
<td>Milking speed, temperament</td>
</tr>
</tbody>
</table>

Some traits are underutilized

- Some traits are *commonly* recorded, but *not often* genetically evaluated
  - *e.g.*, gestation length, milking speed, temperament

- Breeding objectives *differ* across countries
  - Not all traits equally valuable to all people

- New phenotypes can *supersede* old ones
## Lots of genotypes are available in the US

<table>
<thead>
<tr>
<th>Chip</th>
<th>Traditional evaluation?</th>
<th>Animal sex</th>
<th>Holstein</th>
<th>Jersey</th>
<th>Brown Swiss</th>
<th>Ayrshire</th>
</tr>
</thead>
<tbody>
<tr>
<td>≥50K</td>
<td>Yes</td>
<td>Bulls</td>
<td>25,276</td>
<td>4,262</td>
<td>5,862</td>
<td>678</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cows</td>
<td>22,094</td>
<td>1,203</td>
<td>136</td>
<td>27</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>Bulls</td>
<td>51,122</td>
<td>4,428</td>
<td>806</td>
<td>427</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cows</td>
<td>38,182</td>
<td>1,462</td>
<td>201</td>
<td>196</td>
</tr>
<tr>
<td>&lt;50K</td>
<td>Yes</td>
<td>Bulls</td>
<td>24</td>
<td>13</td>
<td>28</td>
<td>14</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cows</td>
<td>48,552</td>
<td>17,246</td>
<td>757</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>Bulls</td>
<td>35,639</td>
<td>3,935</td>
<td>243</td>
<td>43</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Cows</td>
<td>294,875</td>
<td>34,018</td>
<td>1,149</td>
<td>677</td>
</tr>
<tr>
<td>Imputed</td>
<td>Yes</td>
<td>Cows</td>
<td>2,983</td>
<td>265</td>
<td>96</td>
<td>15</td>
</tr>
<tr>
<td></td>
<td>No</td>
<td>Cows</td>
<td>1,394</td>
<td>50</td>
<td>99</td>
<td>16</td>
</tr>
<tr>
<td>All</td>
<td></td>
<td></td>
<td>520,141</td>
<td>66,882</td>
<td>9,377</td>
<td>2,097</td>
</tr>
</tbody>
</table>

International Committee for Animal Recording, Berlin, Germany, May 22, 2014 (9)
Other countries are doing genomics, too!

<table>
<thead>
<tr>
<th>Country</th>
<th>Animals (no.)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Australia</td>
<td>5,314</td>
</tr>
<tr>
<td>Denmark/Finland/Sweden</td>
<td>23,961</td>
</tr>
<tr>
<td>France</td>
<td>24,313</td>
</tr>
<tr>
<td>Germany</td>
<td>25,624</td>
</tr>
<tr>
<td>Italy</td>
<td>21,041</td>
</tr>
<tr>
<td>Netherlands</td>
<td>23,047</td>
</tr>
<tr>
<td>Poland</td>
<td>3,174</td>
</tr>
<tr>
<td>Switzerland (Red Holstein)</td>
<td>4,194</td>
</tr>
</tbody>
</table>
## Phenotypes may come from genotypes

<table>
<thead>
<tr>
<th>Name</th>
<th>Chrome</th>
<th>Location (Mbp)</th>
<th>Carrier Freq</th>
<th>Earliest Known Ancestor</th>
</tr>
</thead>
<tbody>
<tr>
<td>HH1</td>
<td>5</td>
<td>62-68</td>
<td>4.5</td>
<td>Pawnee Farm Arlinda Chief</td>
</tr>
<tr>
<td>HH2</td>
<td>1</td>
<td>93-98</td>
<td>4.6</td>
<td>Willowholme Mark Anthony</td>
</tr>
<tr>
<td>HH3</td>
<td>8</td>
<td>92-97</td>
<td>4.7</td>
<td>Glendell Arlinda Chief, Gray View Skyliner</td>
</tr>
<tr>
<td>HH4</td>
<td>1</td>
<td>1.2-1.3</td>
<td>0.37</td>
<td>Besne Buck</td>
</tr>
<tr>
<td>HH5</td>
<td>9</td>
<td>92-94</td>
<td>2.22</td>
<td>Thornlea Texal Supreme</td>
</tr>
<tr>
<td>JH1</td>
<td>15</td>
<td>11-16</td>
<td>23.4</td>
<td>Observer Chocolate Soldier</td>
</tr>
<tr>
<td>BH1</td>
<td>7</td>
<td>42-47</td>
<td>14.0</td>
<td>West Lawn Stretch Improver</td>
</tr>
<tr>
<td>BH2</td>
<td>19</td>
<td>10-12</td>
<td>7.78</td>
<td>Rancho Rustic My Design</td>
</tr>
<tr>
<td>AH1</td>
<td>17</td>
<td>65.9-66.2</td>
<td>26.1</td>
<td>Selwood Betty’s Commander</td>
</tr>
</tbody>
</table>

For a complete list, see: http://aipl.arsusda.gov/reference/recessive_haplotypes_ARR-G3.html.
Why do we need new phenotypes?

- Changes in production economics
  - Rising feed costs drive demand for increased efficiency

- Technology enables collection of new phenotypes
  - Milking speed in AMS
  - Pedometry for changes in behavior

- Better understanding of biology
Sources of novel phenotypes

**Barn**: flooring type, bedding materials, density, weather data

**Cow**: body temperature, activity, rumination time, intake

**Parlor**: yield, composition, milking speed, conductivity, progesterone, temperature

**Herdsmen/consultants**: health events, foot/claw health, veterinary treatments

**Pasture**: soil type/composition, nutrient composition

**Silo/bunker**: ration composition, nutrient profiles

http://commons.wikimedia.org/wiki/File:Amish_dairy_farm_3.jpg

International Committee for Animal Recording, Berlin, Germany, May 22, 2014 (13) Cole
Novel phenotypes studied recently

- Claw health (Van der Linde et al., 2010)
- Dairy cattle health (Parker Gaddis et al., 2013)
- Embryonic development (Cochran et al., 2013)
- Immune response (Thompson-Crispi et al., 2013)
- Methane production (de Haas et al., 2011)
- Milk fatty acid composition (Soyeurt et al., 2011)
- Persistency of lactation (Cole et al., 2009)
- Rectal temperature (Dikmen et al., 2013)
- Residual feed intake (Connor et al., 2013)
What do current phenotypes look like?

- Low-dimensionality
  - Usually **few** observations per lactation
  - Close **correspondence** of phenotypes with values measured
  - Easy transmission and storage
What do new phenotypes look like?

- **High dimensionality**
- **Ex.:** MIR produces **1,060** points/obs.
- **Disconnect** between phenotype and measurement
- **More resources** needed for transmission, storage, and analysis
Who pays for new phenotypes?

**Costs**
- Labor and materials for recording
- Data transmission, storage, and processing

**Benefits**
- **Farmers** provide data and consume services
- **Centers** consume data and provide services
Data collected on farms

Dairy Records Processing Centers

National database

Milk processing plants

Data trapped in on-farm systems

Data on non-milk recording farms

Analytical laboratories

Genetic evaluation center
New phenotypes should add information

- Novel phenotypes include some new information
- Novel phenotypes include much new information
- Novel phenotypes contain little new information
- Novel phenotypes contain some new information
What can farmers do with novel traits?

- Put them into a selection index
  - Correlated traits are helpful
- Apply selection for a long time
  - There are no shortcuts
- Collect phenotypes on many daughters
  - Repeated records of limited value
  - Genomics can increase accuracy
What can DRPCs do with novel traits?

- **Short-term** - Benchmarking tools for herd management
- **Medium-term** - Custom indices for herd management
  - Additional types of data will be helpful
- **Long-term** - Genetic evaluations
  - Lots of data needed, which will take time
What do US dairy farmers want?

- National workshop in Tempe, AZ in February
- Producers, industry, academia, and government
- Farmers want new tools
- Additional traits (novel phenotypes)
- Better management tools
- Foot health and feed efficiency were of greatest interest

Advancing Dairy Cattle Genetics: Genomics and Beyond
February 17-19, 2014

Advancing Dairy Cattle Genetics: Genomics and Beyond was the focus of a three-day workshop on the future of dairy cattle genetics. It marked the first time in over a decade that the entire dairy cattle community gathered to discuss the long-term future. Commercial dairy producers and
International challenges

- National datasets are siloed
- Recording standards differ between countries
  - ICAR standards help here
- Farmers are concerned about the security of their data
- Many populations are small
  - Low accuracies
  - Small markets
Conclusions

• New technology is enabling the collection of novel phenotypes
• New phenotypes support increased focus on economically important aspects of dairy production
• Infrastructure for moving new phenotypes from the farm to the data center is needed
Acknowledgments

- ICAR Functional Traits Working Group
- Paul VanRaden, AGIL
- AFRI grant 1245-31000-101-05, “Improving Fertility of Dairy Cattle Using Translational Genomics”
Questions?

\[ \sqrt{16 \cdot x} = 2 \sqrt{x} \]
\[ I = \frac{4 \times 10^3}{50} \]
\[ E = mc^2 \]
\[ \int \sqrt{a^2 - x^2} \, dx = \frac{x}{2} \sqrt{a^2 - x^2} + \frac{a^2}{2} \sin^{-1} \frac{x}{a} + C \]
\[ 46 < x \]
\[ a \cdot x + b \cdot x + c = 0 \]
\[ a = b^2 - 4ac \]
\[ a \neq 0 \]
\[ f(x) = a \left( x^2 + \frac{b}{a} x + \frac{c}{a} \right) \]