Genomics 101: Building for the Future

Ron Lewis
Animal Science, University of Nebraska-Lincoln
NSIP Technical Advisor

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Hyder-Burks Ag Pavilion, Tennessee Tech University
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Grateful to sponsors
United Kingdom industry example

- Terminal sire breeds
United Kingdom industry example

- Gains in industry schemes

- Gains of 2% per year
- Comparable to dairy industry

(Courtesy: Signet)
# U.S. industry example (Leading Edge)

<table>
<thead>
<tr>
<th>Category</th>
<th>Weight EPD (lb.)†</th>
<th>Post-weaning‡</th>
<th>Progeny weaning weight (lb.)§</th>
</tr>
</thead>
<tbody>
<tr>
<td>Weight</td>
<td>4.6</td>
<td>9.2</td>
<td>108.6</td>
</tr>
<tr>
<td>Muscle</td>
<td>1.9</td>
<td>4.2</td>
<td>104.1</td>
</tr>
<tr>
<td>Difference</td>
<td>2.6</td>
<td>5.0</td>
<td>4.5</td>
</tr>
</tbody>
</table>

† EPD from July 2019, weighted by the number of lambs with a wean weight from each ram.
‡ Weaning and post-weaning weights recorded at 45 to 90 and 90 to 150 days, respectively.
§ At, on average, 161 days of age.
Major genes

- A genes with a pronounced effect on performance

Causative gene
Genetic markers

A detectable gene at one location on the chromosome used to mark a causative gene at a nearby location.

Marker gene

Causative gene

Causative gene
Reference populations

To keep up-to-date, we also need to measure about 12.5% new animals each year

(Goddard, 2009; Hayes et al., 2009; van der Werf et al., 2011)
Applications

- Parentage
- Genetic conditions
- Genomic selection
- Delineating breeds
Challenges in recording pedigree information
- Particularly in multiple-sire and extensive systems

Parentage panel
- With a limited number of markers, can reliably assign parentage (Heaton et al., 2014)
## Parentage (sire)

- Typically 163 genetic markers on parentage panel
- Assignments based on **exclusion** of sires
  - Key that full suite of potential sires are included

<table>
<thead>
<tr>
<th>Animal</th>
<th>Marker 1</th>
<th>Marker 2</th>
<th>Marker 3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Lamb</td>
<td>AB</td>
<td>AA</td>
<td>BB</td>
</tr>
<tr>
<td>Sire 1</td>
<td>BB ✓</td>
<td>AA ✓</td>
<td>AB ✓</td>
</tr>
<tr>
<td>Sire 2</td>
<td>AA ✓</td>
<td>AB ✓</td>
<td>X AA ✓</td>
</tr>
</tbody>
</table>
Parentage (Leading Edge)

- **Leading Edge Project**
  - 42 Suffolk rams mob mated to 1,100 commercial white-faced ewes

- Among 1,457 lambs with a tissue (DNA) sample, 92% aligned with a sire
  - Nearly all losses were lab based
Genetic conditions

For some traits of economic interest, genes with major causative effects have been identified

Examples

- Fecundity (Demars et al., 2013; Martin et al., 2014)
- Mastitis susceptibility (Rupp et al., 2015)
- Myostatin (Clop et al., 2006)
- OPP virus resistance (Heaton et al., 2012)
- Scrapie resistance (Elsen et al., 1999; Barillet et al., 2009)
- Spider syndrome (Cockett et al., 1999; Beever et al., 2006)
Genetic conditions

- For some traits of economic interest, genes with major causative effects have been identified.
- Still, such major genes are comparatively rare.
  - Traits of interest have proven to be more complex than anticipated.
  - Most traits are influenced by thousands of genes, each gene having a small effect.

Needed a broader approach

(Meuwissen, Hayes and Goddard, 2001)
Genomic selection

- Each marker typically explains a small proportion (< 1%) of genetic variation in a trait
- **Genome-Enhanced Breeding Values (GEBV)** are predicted from the sum of the effects of all markers across the entire genome
- As an outcome, GEBV can more accurately indicate an animal’s true genetic merit

Predictions are based on associations between markers and actual performance for traits of interest
### Genomic selection (accuracy)

<table>
<thead>
<tr>
<th>Traits</th>
<th>Gain in accuracy</th>
<th>Location</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carcass, meat quality</td>
<td>5 – 10%</td>
<td>Australia</td>
<td>Daetwyler et al., 2012</td>
</tr>
<tr>
<td>Meat, fleece, litter size</td>
<td>5 – 27%</td>
<td>New Zealand</td>
<td>Auvray et al., 2014</td>
</tr>
<tr>
<td>Milk production</td>
<td>10 – 20%</td>
<td>France</td>
<td>Baloche et al., 2014</td>
</tr>
</tbody>
</table>

Gain in accuracy closely tied to the amount of genomic and performance information available.
Delineating breeds

- 64 sheep in each of 3 breeds genotyped
  - Katahdin, Rambouillet, Suffolk
- Chosen to reflect the diversity in each breed
  - Primarily rams
  - National Sheep Improvement Program (NSIP) records on themselves and on at least five progeny
Delineating breeds

Katahdin

Suffolk

Rambouillet

Emphasizes need for different reference populations within breeds
Products

- Targeted panels
- Arrays
- Whole genome sequence
Products (panels)

- Targeted panels (<2K markers)
  - Parentage; major genes
Products (low density)

- Targeted panels (<2K markers)
- Low density array (15K markers)
  - Parentage; major genes; towards genomic selection
Products (medium density)

- Targeted panels (<2K markers)
- Low density array (15K markers)
- Medium density array (50K markers)
  - Parentages, major genes; genomic selection; towards causative gene discovery
Products (high density)

- Targeted panels (<2K markers)
- Low density array (15K markers)
- Medium density array (50K markers)
- High density array (600K markers)
  - Parentages, major genes; genomic selection; causative gene discovery
Products (sequence)

- Targeted panels (<2K markers)
- Low density array (15K markers)
- Medium density array (50K markers)
- High density array (600K markers)
- Whole genome sequence
  - The “Full Monty”
# Products (used)

<table>
<thead>
<tr>
<th>Location</th>
<th>Number of markers</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>&lt;2K</td>
</tr>
<tr>
<td>AU/NZ</td>
<td>54,657</td>
</tr>
<tr>
<td>U.S.‡</td>
<td>3,185</td>
</tr>
<tr>
<td>Europe</td>
<td>131</td>
</tr>
</tbody>
</table>

‡Mostly from research groups
Ahead?

- Routine sampling
- Tackling difficult-to-measure traits
- Working together
Routine sampling

- Routinely collecting DNA samples
Routine sampling

- Routinely collecting DNA samples
Tackling difficult-to-measure traits

- Greatest opportunity with genomics is in tackling difficult-to-measure traits
Tackling difficult-to-measure traits

- Traits expressed later in an animal’s life
  - Longevity
- Traits expressed in only one sex
  - Fertility, litter size, mastitis
- Traits that are expensive and/or challenging to measure
  - Lamb survival, maternal bonding, aseasonality
  - Carcass & eating quality
  - Feed efficiency
  - Methane emissions?
Working together

- Incorporating genomics into the U.S. sheep industry can only be achieved together
- It will entail
  - Widespread performance recording
  - Extensive sample collection and genotyping
  - Integrating that information into a genetic evaluation system to everyone’s advantage
- It is a long term commitment

...yet all signs are it is worth it!
Thank you for listening

Questions?

Every second of life is a miracle