Genomics in the beef industry: US situation

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Translational Questions for the US Beef Industry

- How many phenotypic records and animals are required in the training population?
- How does the relationship between the training population and the selection candidate affect accuracy of prediction?
- Do predictions work across breeds? Or only within breed?
- How many markers are needed—1, 384, 50K, 800K, genome?
- How often do prediction have to be recalibrated—especially hard to measure traits as measurement is hard/expensive?
- What is the value generated by these tests—do they pay?
- Does this technology change optimal breeding program design?
Seedstock Sector

Nucleus and multipliers herds

Change of ownership

Commercial Cow-Calf Producers (as of 1/1/2012)
- 30 million head beef cows
- 734,000 operations (Avg. 40 cows)
- > 80% run less than 50 cows

Stockers/backgrounders (as of 1/1/2012)
- 11.69 million head

Feedlots (2011)
- Those 1920 operations (3%) with 1,000+ head capacity market over 88% of fed cattle in US

Processors (2010)
- 28.4 million head killed
- 7 operations killing more than 6 million head
- Top three processed 75% of 2010 kill

Technology developers had a rocky start in the beef industry.

Van Eenennaam Armidale 2/7/2014
Animal Genomics and Biotechnology Education
The Power of the IGENITY® profile for Angus

1. Dry Matter Intake
2. Birth Weight
3. Mature Height
4. Mature Weight
5. Milk
6. Scrotal Circumference
7. Weaning Weight
8. Yearling Weight
9. Marbling
10. Ribeye Area
11. Fat Thickness
12. Carcass Weight
13. Tenderness
14. Percent Choice (quality grade)
15. Heifer Pregnancy
16. Maternal Calving Ease
17. Direct Calving Ease
18. Docility
19. Average Daily Gain
20. Feed Efficiency
21. Yearling Height

- Arthrogryposis Multiplex (AM)
- Neuropathic Hydrocephalus (NH)
- Bovine Viral Diarrhea – Persistently Infected (BVD PI)
- Coat Color

384 SNP chip assay
Lead Today with 50K

1. Calving ease direct
2. Birth weight
3. Weaning weight
4. Yearling weight
5. Yearling height
6. Mature weight
7. Mature height
8. Dry matter intake
9. Residual feed intake
10. Scrotal circumference
11. Docility
12. Calving ease maternal
13. Milking ability
14. Carcass weight
15. Fat thickness
16. Ribeye area
17. Marbling score
18. Tenderness

50K SNP chip assays
50,000 SNPs spread throughout genome
**G A R Predestined**

From start to finish—conception to carcass—no other bull in the Black Angus breed has the real value to cattle as Predestined. Ranking as the #1 bull for $158 as of 3/22/10, we know that their Predestined-sired cattle return the most dollars to their owners. Unlike any other 036 son, Predestined tones down size, adds dollars, and a pleasant disposition to his offspring. His conception rate is excellent in timed-AI programs. His progeny look good—his bulls are thick and muscular and always display additional shape and capacity. He ended 2006 as our #2 bull. Predestined’s many talents for creating value are for real.
“Information from DNA tests only has value in selection when incorporated with all other available forms of performance information for economically important traits in National Cattle Evaluation (NCE), and when communicated in the form of an EPD with a corresponding BIF accuracy.

For some economically important traits (e.g. feed efficiency), information other than DNA tests may not be available. Selection tools based on these tests should still be expressed as EPD within the normal parameters of NCE” (Tess, 2008).
Information sources for EPDs – DNA just one source of data for GE-EPD

- **Performance**
- **Progeny**
- **Pedigree**
- **Genomic Test Result**

**Accuracy (r)** – correlation between test result and actual genetic merit
Realized accuracies ($r$) resulting from genomic selection prediction equations trained in US beef cattle breeds

<table>
<thead>
<tr>
<th>Trait</th>
<th>Red Angus (6,412)$^b$</th>
<th>Angus (3,500)</th>
<th>Hereford (2,980)</th>
<th>Simmental (2,800)</th>
<th>Limousin (2,400)</th>
<th>Gelbvieh (1,181)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Birth weight</td>
<td>0.75</td>
<td>0.64</td>
<td>0.68</td>
<td>0.65</td>
<td>0.58</td>
<td>0.41</td>
</tr>
<tr>
<td>Wean weight</td>
<td>0.67</td>
<td>0.67</td>
<td>0.52</td>
<td>0.52</td>
<td>0.58</td>
<td>0.34</td>
</tr>
<tr>
<td>Yearling weight</td>
<td>0.69</td>
<td>0.75</td>
<td>0.60</td>
<td>0.45</td>
<td>0.76</td>
<td>—</td>
</tr>
<tr>
<td>Milk</td>
<td>0.51</td>
<td>0.51</td>
<td>0.37</td>
<td>0.34</td>
<td>0.46</td>
<td>0.34</td>
</tr>
<tr>
<td>Fat thickness</td>
<td>0.90</td>
<td>0.70</td>
<td>0.48</td>
<td>0.29</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Rib eye area</td>
<td>0.75</td>
<td>0.75</td>
<td>0.49</td>
<td>0.59</td>
<td>0.63</td>
<td>0.48</td>
</tr>
<tr>
<td>Marbling</td>
<td>0.85</td>
<td>0.80</td>
<td>0.43</td>
<td>0.63</td>
<td>0.65</td>
<td>0.56</td>
</tr>
<tr>
<td>Calving ease direct</td>
<td>0.60</td>
<td>0.69</td>
<td>0.68</td>
<td>0.45</td>
<td>0.52</td>
<td>0.48</td>
</tr>
<tr>
<td>Calving ease (maternal)</td>
<td>0.32</td>
<td>0.73</td>
<td>0.51</td>
<td>0.32</td>
<td>0.51</td>
<td>—</td>
</tr>
<tr>
<td>Scrotal circumference</td>
<td>—</td>
<td>0.71</td>
<td>0.43</td>
<td>—</td>
<td>0.45</td>
<td>0.50</td>
</tr>
</tbody>
</table>

$^a$Data taken from References 29, 30, 131; D. Garrick, unpublished data (personal communication).

$^b$Numbers indicate training population. The Red Angus training data set includes some Black Angus cattle that have expected progeny difference in the Red Angus Association.
Angus predictions \( (r) \) are not very accurate in Red Angus \( \text{(Data provided by Dorian Garrick)} \)

<table>
<thead>
<tr>
<th>Trait</th>
<th>Trained in Black Angus/Validated in Black Angus</th>
<th>Trained in Black Angus/Validated in Red Angus</th>
</tr>
</thead>
<tbody>
<tr>
<td>BirthWt</td>
<td>0.64</td>
<td>0.27</td>
</tr>
<tr>
<td>WeanWt</td>
<td>0.67</td>
<td>0.28</td>
</tr>
<tr>
<td>YearlingWt</td>
<td>0.75</td>
<td>0.23</td>
</tr>
<tr>
<td>Fat</td>
<td>0.70</td>
<td>0.21</td>
</tr>
<tr>
<td>Rib Eye Area</td>
<td>0.75</td>
<td>0.29</td>
</tr>
<tr>
<td>Marbling</td>
<td>0.80</td>
<td>0.21</td>
</tr>
<tr>
<td>CalvEase (D)</td>
<td>0.69</td>
<td>0.14</td>
</tr>
<tr>
<td>CalvEase (M)</td>
<td>0.73</td>
<td>0.18</td>
</tr>
</tbody>
</table>

Angus = ASREML 5-fold validation Red Angus = correlation Training on de-regressed EPDs Saatchi et al (GSE)
Approximate genetic distance between breeds using data from the 2,000 Bull Project.
Larry Keuhn, USDA MARC
http://www.nbcec.org/topics/BeefBreeds.pdf
American Angus Association performs weekly evaluations with genomic data – recently updated to include heifer pregnancy

- Association’s genetic evaluations, the DNA test results are incorporated into the EPDs using a correlated trait approach.

- The correlations (r) between the HD 50K prediction and the phenotypic data at the Association are updated with each recalibration effort and effectively range from .60 to .70, except for milk (.38) and heifer pregnancy (.49).

- The December 6, 2013, EPD update includes HD 50K predictions from over 51,000 registered Angus animals with genotypes retained at the Association. Results are incorporated into at least 15 EPDs which are then components of the Angus $Value selection index suite.

Other breeds?
The following U.S. breed associations have/are working with Dorian Garrick (IA State) to develop their own 50K-based prediction equations

<table>
<thead>
<tr>
<th>Breed</th>
<th>Breed code</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hereford</td>
<td>HER</td>
</tr>
<tr>
<td>Red Angus</td>
<td>RAN</td>
</tr>
<tr>
<td>Simmental</td>
<td>SIM</td>
</tr>
<tr>
<td>Brangus</td>
<td>BRG</td>
</tr>
<tr>
<td>Limousin</td>
<td>LIM</td>
</tr>
<tr>
<td>Gelbvieh</td>
<td>GVH</td>
</tr>
<tr>
<td>Maine Anjou</td>
<td>RDP</td>
</tr>
</tbody>
</table>
Can I use genomics/DNA-information to make money?

<table>
<thead>
<tr>
<th>AGI DNA Tests</th>
<th>Price</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parentage</td>
<td>$18.00</td>
</tr>
<tr>
<td>Coat Color Test</td>
<td>$18.00</td>
</tr>
<tr>
<td>Arthrogryposis Multiplex (AM) Test</td>
<td>$22.00</td>
</tr>
<tr>
<td>Neuropathic Hydrocephalus (NH) Test</td>
<td>$22.00</td>
</tr>
<tr>
<td>Contractural Arachnodactyly (CA) Test</td>
<td>$22.00</td>
</tr>
<tr>
<td>Developmental Duplication (DD) Test</td>
<td>$22.00</td>
</tr>
<tr>
<td>Myostatin (M1) Test</td>
<td>$22.00</td>
</tr>
<tr>
<td>Dwarfism (D2) Test</td>
<td>$22.00</td>
</tr>
</tbody>
</table>

Additional Sample handling fee of 2.00 will be charged per sample for samples submitted in blood tubes or hair not on proper hair cards.

<table>
<thead>
<tr>
<th>Genomic Tests</th>
<th>Price</th>
</tr>
</thead>
<tbody>
<tr>
<td>Zoetis® HD50K (includes Parentage)</td>
<td>$75.00</td>
</tr>
<tr>
<td>Add Coat Color</td>
<td>$5.00</td>
</tr>
<tr>
<td>Add AM Test</td>
<td>$8.00</td>
</tr>
<tr>
<td>Add NH Test</td>
<td>$8.00</td>
</tr>
<tr>
<td>Add CA Test</td>
<td>$8.00</td>
</tr>
<tr>
<td>Add DD Test</td>
<td>$10.00</td>
</tr>
</tbody>
</table>

| GeneSeek® GGP-HD (includes Parentage)| $75.00|
| Add Coat Color                       | $5.00 |
| Add AM Test                          | $8.00 |
| Add NH Test                          | $8.00 |
| Add CA Test                          | $8.00 |
| Add DD Test                          | $10.00|
| Add M1 Test                          | $18.00|
| Add Dwarfism (D2) Test               | $20.00|
Value of improved selection response for commercial bulls due to DNA-test increase in index accuracy

<table>
<thead>
<tr>
<th>Variable</th>
<th>Unit</th>
<th>Accuracy of DNA test used</th>
<th>$ Feedlot Index Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Increased value derived from $\Delta G$ in commercial sires</td>
<td>$/bull$</td>
<td>Intermediate</td>
<td>340</td>
</tr>
<tr>
<td></td>
<td></td>
<td>High</td>
<td>574</td>
</tr>
</tbody>
</table>

Where are returns from genetic gain ($\Delta G$) realized?

![Bar chart showing the impact of DNA test accuracy on Feedlot Index.](chart.png)

- **Calving ease**
- **Sale weight**
- **Fertility**
- **Marbling**
- **Rib Eye Area**
- **Yield grade**

Accuracy of DNA test used:
- No DNA test
- Intermediate
- High

Costs associated with different accuracy levels:
- $340
- $574

Van Eenennaam Perth 7/22/2011
What is the value of genetic improvement in commercial females?

- The breakeven cost of testing replacement heifers was $3.63 and $6.53 per test for the intermediate and high accuracy DNA tests, respectively.
- The value of increasing the accuracy of commercial replacement heifer genetic evaluations is less (ten-fold in this case) than that for commercial bulls because bulls produce more descendants from which to derive returns for accelerated genetic improvement.
- This assumes the test includes accurate predictions for traits of importance for commercial heifer replacement decisions.
> 400,000 Genotypes run in US dairy cattle
Dams of Cows – Net Merit

Year of Birth

Net Merit

-500 -400 -300 -200 -100 0 100 200 300


Slide provided by Van Tassell

Unpublished data
The Future

NEXT EXIT
Hype cycle: the over-enthusiasm or "hype" and subsequent disappointment that typically happens with the introduction of new technologies
USDA funded projects – competitive call for proposals: NIFA AFRI-funded projects

- **National program for genetic improvement of feed efficiency in beef cattle**
  (Taylor, MO) – finishes 4/2016 (http://www.beefefficiency.org)
  - Genotype ~ 2,400 head on HD chips; 7000 records FE records
  - $5 million, 5 year project; April 2011 – April 2016

- **Integrated program for reducing bovine respiratory disease (BRD) in beef and dairy cattle** (Womack, TX) – finishes 4/2016 (http://www.brdcomplex.org)
  - Collection and HD genotypes on 6,000 BRD case-control animals
  - $10 million, 5 year project; April 2011 – April 2016

- **Identification and management of alleles impairing heifer fertility while optimizing genetic gain in Angus cattle**
  (Patterson, Taylor, et al. MO; Van Eenennaam, CA) – finishes 12/17
  - Sequence up to 250 cattle from up to 10 different beef breeds
  - $3 million, 5 year project; Jan 2013 – December 2017

Van Eenennaam Armidale 2/7/2014
CONCLUSION: Ramifications of DNA-enabled selection

- The benefits of genomic selection are best captured in well-structured industries (e.g. dairy/poultry/swine) that are already making significant genetic progress
- May encourage more vertical integration to collect phenotypes to enable predictions for EPDs for all sectors
- May see genetic evaluations developed for novel traits – e.g. feed efficiency, disease resistance if large enough populations can be amassed and data shared
- May see breeds/countries start to share data – especially with whole genome sequencing and causative SNP
- This technology might accelerate vertically-integrated breeding companies owning all sectors of industry
Breeds/groups that can organize themselves and **technologically** and **structurally** to seamlessly obtain and marry entire supply chain phenotypes and genotypes and take advantage of the rapidly-declining cost of genotyping to capture the cumulative value derived from using genomic information for multiple purposes (selection, parentage, genetic defects, marker-assisted management, product differentiation, traceability) will be ideally positioned to fully realize the nascent potential of genomic information.

Questions?