Delivering genomics to the beef herd

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Outline

- How can DNA help accelerate genetic progress?
- Why genomics helps the dairy industry
- Why genomics is harder in the beef industry
- Current products on the market for beef
- Status of incorporation of DNA information into U.S. national beef cattle evaluations
- How can I use DNA-information to make money?
- Implications of genomics to industry structure
Animal breeders have used the resemblance between relatives to select parents of the next generation and make genetic change.
Rate of genetic change ($\Delta G$) is accelerated when breeders can accurately identify those individuals that have the best genetics at a young age.

$$\Delta G = \text{intensity of selection} \times \text{accuracy of selection} \times \frac{\sqrt{\text{genetic variance in population}}}{\text{generation interval}}$$
The genome age

Genes contain instructions for making proteins.

Proteins are the building blocks of life and collectively act to determine phenotype.

Van Eenennaam SBIC 1/22/2014

Animal Genomics and Biotechnology Education
What is a Genetic Marker?

A DNA sequence variation that has been associated with a given trait in one or more populations.
We want to use DNA markers (SNPs) in addition to pedigree and performance information to help select the best animals.
Information sources for EPDs – DNA just one source of data for GE-EPD

Genomic-Enhanced EPDs (GE-EPD)
High-throughput genotyping technology enabled the development of high density “SNP chips”

The sequencing of the bovine genome allowed for the development of a 50,000 SNP chip, then the 800,000 SNP chip; and now whole genome sequence (3 billion)!
We can use these SNP CHIPS for “genomic” selection?

**TRAINING POPULATION**

1,000s animals
- Phenotypes
- Genotypes

Training = estimate the value of every chromosome fragment contributing variation in a population with phenotypic observations

Prediction = the results of training can then be used to develop prediction equations to predict the merit of new animals (e.g. young bulls)
Dairy industry ideally suited to increasing rate of genetic gain ($\Delta G$) using genomic selection

- Mostly one breed
- High use of AI
- Clear selection goal ($\$ \text{ net merit}$)
- Large number of high accuracy A.I. sires for training
- Extensive, uniform collection of data on traits
- Central evaluation (AIPL) receiving genotypes
- Obvious way to decrease age of selection in sires
- AI companies funding the genotyping because they get a clear cost savings in terms of young sire program
Breeding value prediction in Dairy Sires

Young sire Parent Average

Young sire Progeny Test

Young sire Genomic Selection

Birth

5 years; $50,000 cost

Birth; << $50,000 cost

Reliability 0.20

Reliability 0.80

Reliability 0.70

Mendelian Sampling

Mendelian Sampling

Mendelian Sampling

Graphic kindly provided by Gonzalo Rincon
> 400,000 Genotypes run in US dairy cattle

Animals genotyped (no.)

- **Imputed, young**
- **Imputed, old (young cows included before March 2012)**
- **<50K, young, female**
- **<50K, young, male**
- **<50K, old, female**
- **<50K, old, male (≤ 20 bulls)**
- **≥50K, young, female**
- **≥50K, young, male**
- **≥50K, old, female**
- **≥50K, old, male**

Evaluation date

2009 2010 2011 2012 2013
The Beef Cattle Industry

- Little use of AI
- Relatively few high accuracy sires for training
- Multiple competing selection goals – cow/calf, feedlot, processor – little data sharing between sectors
- Few/no records on many economically-relevant traits
- Many breeds, some small with limited resources
- Crossbreeding is important
- No centralized “national” cattle evaluation
- Not clear who should pay for testing – breeders? Breed associations? public funds?
Translational Questions for the 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?
Technology developers had a rocky start in the beef industry.
The Power of the IGENITY® profile for Angus

The American Angus Association® through its subsidiary, Angus Genetics Inc.® (AGI), has a vision to provide Angus breeders with the most advanced solutions to their genetic selection and management needs.

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
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 SBIC database has a higher real value to cattle as Predestined. Ranking as the #1 bull for $PROFIT and $REVENUE, it is clear that their Predestined-sired cattle return the most dollars to the producer. Unlike any other 036 bull, Predestined tones down size, adds definition, and a pleasant disposition to his offspring. His conception rate is high, and he is easy to manage. His progeny look good; his bulls are thick and large. Predestined’s many talents for creating value are for real.

### Production 

<table>
<thead>
<tr>
<th>Trait</th>
<th>CED</th>
<th>BW</th>
<th>WW</th>
<th>YW</th>
<th>SC</th>
<th>YW</th>
<th>SC</th>
<th>Milk</th>
<th>MEd</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACC</td>
<td>7.84</td>
<td>9.73</td>
<td>9.69</td>
<td>9.65</td>
<td>9.69</td>
<td>9.69</td>
<td>9.65</td>
<td>9.73</td>
<td>7.84</td>
</tr>
<tr>
<td>DP (50)</td>
<td>245</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
</tr>
</tbody>
</table>

### Carcass Usuals

<table>
<thead>
<tr>
<th>Trait</th>
<th>CED</th>
<th>BW</th>
<th>WW</th>
<th>YW</th>
<th>SC</th>
<th>YW</th>
<th>SC</th>
<th>Milk</th>
<th>MEd</th>
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<tbody>
<tr>
<td>Acc</td>
<td>+26</td>
<td>+1.07</td>
<td>+39</td>
<td>+39</td>
<td>+39</td>
<td>+39</td>
<td>+39</td>
<td>+39</td>
<td>+39</td>
</tr>
<tr>
<td>DP (50)</td>
<td>245</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
<td>1135</td>
</tr>
</tbody>
</table>

### Ribeye Area

- Carcass Weight
  - Percent Choice
  - Marbling

<table>
<thead>
<tr>
<th>Ribeye Area</th>
<th>Carcass Weight</th>
<th>Percent Choice</th>
<th>Marbling</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td>2</td>
<td>8</td>
<td>9</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>G A R Predestined</th>
<th>13395344</th>
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</thead>
<tbody>
<tr>
<td>EPD</td>
<td>7</td>
</tr>
<tr>
<td>ACC</td>
<td>0.84</td>
</tr>
<tr>
<td>EPD % Rank</td>
<td>30</td>
</tr>
<tr>
<td>MVP</td>
<td>13</td>
</tr>
<tr>
<td>MVP % Rank</td>
<td>3</td>
</tr>
</tbody>
</table>

Van Eenenam SBIC 1/22/2014
“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

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)&lt;sup&gt;b&lt;/sup&gt;</th>
<th>Angus (3,500)</th>
<th>Hereford (2,980)</th>
<th>Simmenttal (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>

<sup>a</sup>Data taken from References 29, 30, 131; D. Garrick, unpublished data (personal communication).
<sup>b</sup>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 \hspace{1cm} (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>Contractual 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|
Compare 20th century response to dwarfism to 21st century response

An early '50's advertisement that superimposed a measuring stick in the picture of this bull who was nick-named "Short Snorter."

Based upon his height and age, he was less than a frame score 1.

Image from https://www.msu.edu/~ritchieh/historical/shortsnorter.jpg
From September 8 – November 3, 2008 identified genetic problem, developed test, and released carrier status of 736 bulls!

- In the 11 months following the release of the test, the AAA posted the results of tests for AM on about 96,247 cattle.

This amounts to $2.4 million in testing costs

- Of these, 20% (19,529) were carriers of AM. That leaves 23,638 bulls and more than 53,000 heifers which tested as free of AM.

At $4K/bull and $2K/heifer ~$200 million

Potential Value of DNA information to the commercial sector

Estimate the value of using DNA test information to increase the accuracy of bull and replacement selection in a commercial herd

The expected returns from using DNA testing to improve the accuracy of selection for
– commercial sires sourced from a seedstock herd
– replacement commercial females.

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>$/\text{bull}$</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?

The diagram above shows the Feedlot Index for Self-Replacing animals, categorized by the accuracy of DNA test used. The categories are:

- No DNA test
- Intermediate
- High

The graph illustrates the following parameters:

- **Calving ease**
- **Sale weight**
- **Fertility**

The economic value ($\text{\$ per commercial sire}$) is presented for each category:

- **No DNA test:** $\text{\$340}$ (Producer: $\text{\$211}$; Processor: $\text{\$129}$)
- **Intermediate:** $\text{\$674}$ (Producer: $\text{\$453}$; Processor: $\text{\$221}$)
- **High:** $\text{\$574}$ (Producer: $\text{\$407}$; Processor: $\text{\$167}$)

The diagram highlights the potential financial gains from increasing the accuracy of DNA tests in genetic selection for different traits.
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.
- These values are unique to the hypothetical DNA tests modeled in this study, and are not intended to represent commercial products.
- 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.
The Future

NEXT EXIT
Hype cycle: the over-enthusiasm or "hype" and subsequent disappointment that typically happens with the introduction of new technologies.
Potential uses of genomic information for beef sectors

<table>
<thead>
<tr>
<th>Use</th>
<th>Seedstock</th>
<th>Commercial</th>
<th>Feedlot</th>
<th>Processor</th>
</tr>
</thead>
<tbody>
<tr>
<td>DNA-assisted selection</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Parentage</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Recessive allele testing</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Control of Inbreeding</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Mate selection</td>
<td>X</td>
<td>X</td>
<td></td>
<td></td>
</tr>
<tr>
<td>DNA-assisted management</td>
<td>X</td>
<td>X</td>
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<td>X</td>
</tr>
<tr>
<td>DNA-based purchasing</td>
<td></td>
<td></td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Product differentiation</td>
<td></td>
<td></td>
<td></td>
<td>X</td>
</tr>
<tr>
<td>Traceability</td>
<td></td>
<td></td>
<td></td>
<td>X</td>
</tr>
</tbody>
</table>

Only these sectors produce new animals.
Ideally cattle would be genotyped ONCE early in life and genotypes shared with downstream production sectors to derive the maximum value from the fixed DNA collection and extraction costs.

<table>
<thead>
<tr>
<th>Cattle industry Sector</th>
<th>Type of DNA product // DNA information access required</th>
<th>Cost?? ($US)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Nucleus seedstock/AI bulls</td>
<td>Full genome sequence</td>
<td>$250</td>
</tr>
<tr>
<td>Seedstock/bull multiplier</td>
<td>HD 770 K genotype</td>
<td>$50</td>
</tr>
<tr>
<td>Registered females and stock bulls for commercial sector</td>
<td>50K genotype + parentage + single gene traits/recessives</td>
<td>$25</td>
</tr>
<tr>
<td>Commercial cattle – Marker-assisted management (MAM), replacement heifer selection</td>
<td>Imputation LD chip + parentage + single gene traits/recessives</td>
<td>$10</td>
</tr>
<tr>
<td>Feedlot cattle purchasing, sorting and marker-assisted management (MAM)</td>
<td>Access genotypes from supplier (subset of LD imputation chip).</td>
<td>&lt;$1</td>
</tr>
<tr>
<td>Traceability for voluntary labelling e.g. Angus beef</td>
<td>Access genotypes from supplier (subset of LD imputation chip).</td>
<td>&lt;$1</td>
</tr>
<tr>
<td>Traceability for disease outbreak/contaminated meat</td>
<td>Access genotypes from supplier (subset of LD imputation chip).</td>
<td>&lt;$1</td>
</tr>
</tbody>
</table>
Seedstock Sector  

Nucleus and multipliers herds

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
<table>
<thead>
<tr>
<th>2003</th>
<th>2008</th>
<th>2013</th>
<th>2020</th>
</tr>
</thead>
<tbody>
<tr>
<td>- single marker/single trait</td>
<td>- multimarker tests for a few traits reported in a variety of formats</td>
<td>- panels with thousands of markers for many traits</td>
<td>- universal causative SNP marker panel used by worldwide beef cattle community</td>
</tr>
<tr>
<td>- reported genotypes</td>
<td>- no tie between DNA test results and national genetic evaluation or breed associations</td>
<td>- results reported in units of the trait</td>
<td>- seamless submission of genotype data to national genetic evaluation/breed associations</td>
</tr>
<tr>
<td>- single marker accounted for small amount of genetic variation</td>
<td>- tests accounted for &lt; 10% additive genetic variation</td>
<td>- incorporation of DNA information into national genetic evaluation</td>
<td>- testing cost is low</td>
</tr>
<tr>
<td>- limited adoption</td>
<td>- limited validation</td>
<td>- DNA-based evaluations improve accuracy of EPDs</td>
<td>- DNA information used for traceability, parentage, genetic defects, selection, marker-assisted management, product differentiation</td>
</tr>
<tr>
<td>- technology oversold</td>
<td>- technology not in a form producers could use</td>
<td>- large numbers of genotyped populations being developed for hard to measure traits</td>
<td></td>
</tr>
</tbody>
</table>
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.

Thanks for inviting me!

National Research Initiative competitive grant no. 2009-55205-05057 (“Integrating DNA information into beef cattle production systems”) from the USDA National Institute of Food and Agriculture Animal Genome Program.
Questions?
USDA funded projects – competitive call for proposals: Part 2 (new NIFA AFRI proposals)

- **National program for genetic improvement of feed efficiency in beef cattle**
  (Taylor, MO) – finishes 4/2016 ([http://www.beefefficiency.org](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](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