“Beef Cattle Industry Structure: Implications for whole genome selection”

Alison Van Eenennaam, Ph.D.
Cooperative Extension Specialist
Animal Biotechnology and Genomics
Department of Animal Science
University of California, Davis
(530) 752-7942
alvaneenennaam@ucdavis.edu

http://animalscience.ucdavis.edu/animalbiotech/
Overview

- Dairy Model
- What is different about beef?
- What do the data show?
- Implications?
Application of WGS in Dairy Cattle Has Been Successful

Training 1: Old Progeny Tested Bulls

Training 2: Old & New Progeny Tested Bulls

Validation: New Progeny Tested Bulls

Application: New Sire Candidates

Slide courtesy of Marc Thallman, US MARC
Dairy industry suited to WGS

- High use of AI
- Only one breed
- Clear selection goal (total 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 increase rate of genetic gain
- AI companies funding the genotyping because they get a clear cost savings in terms of young sire program
Genomic selection can double rate of genetic gain

Rate of genetic gain $\Delta G$

$\Delta G = \frac{i_m r_m + i_f r_f}{L_m + L_f}$ genetic standard deviation/year

= $(2 \times 0.8 + 0)/(6 + 2)$ = 0.2 s.d./year (progeny test)

= $(2 \times 0.6 + 0.8 \times 0.6)/(2 + 2)$ = 0.42 (genomic selection)

$i$ = intensity of selection
$r$ = accuracy of selection
$L$ = generation interval

Modified from Goddard. (2009) BIF Meeting
Velogenetics

(Georges and Massey (1991) Theriogenology 35:151-159)

- Harvest oocytes from in-utero calves
- In-vitro
  - maturation
  - fertilization
- Selection based on genetic markers
- Implant in recipient cows
- L = 6 months (0.5 instead of 6 years)
Velogenetics could increase rate of genetic gain 8X

Rate of genetic gain $\Delta G$

$$\Delta G = \frac{i_m r_m + i_f r_f}{L_m + L_f} \text{ genetic standard deviation/year}$$

$$= \frac{2 \times 0.8 + 0}{(6+2)} = 0.2 \text{ (progeny test)}$$

$$= \frac{2 \times 0.6 + 0.8 \times 0.6}{(2+2)} = 0.42 \text{ (genomic selection)}$$

$$= \frac{2 \times 0.6 + 0.8 \times 0.6}{(0.5+0.5)} = 1.68 \text{ (velogenetics) i.e. 8X}$$
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
Beef training populations

- 2000 Angus AI bulls put together by Jerry Taylor at University of Missouri and Merial
  - Smaller collections of other breeds (e.g., Limousin)
- US MARC collection of some 2,000 recent AI bulls including 16 breeds (2000 bull project)

- Angus 402
- Hereford 317
- Simmental 253
- Red Angus 173
- Gelbvieh 136
- Limousin 131
- Charolais 125
- Shorthorn 86
- Brangus 68
- Beefmaster 64
- Maine-Anjou 59
- Brahman 53
- Chiangus 47
- Santa Gertrudis 43
- Salers 42
- Braunvieh 27
Correlations between genomic merit predictions derived from the Angus bull population and realized performance range from 0.5 to 0.7

Similar to the performance of genomic predictions in dairy cattle

They will account for 25% to 50% of the genetic variation

Compared to a trait with heritability of 25%, the genomic predictions would be equivalent to observing 6 to 15 offspring in a progeny test

Modified from Taylor/Garrick. (2009). BIF
Validation: Purpose is to estimate the correlation between the prediction and the true genetic merit.

Degree of genetic relationship between populations (ideally similar)
### Commercial genetic test validations

**Summary of NBCEC validations for commercially-available DNA-tests for complex (quantitative or multigenic) traits in beef cattle** (note: validations do not include tests for "simple" traits such as coat color, horned/pollled, AM status etc.)

<table>
<thead>
<tr>
<th>Company</th>
<th>Test Name</th>
<th>Trait</th>
<th>Date of validation</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Igenity</strong></td>
<td>Profile®</td>
<td>Fat Thickness</td>
<td>12/2008</td>
</tr>
<tr>
<td><a href="http://www.igenity.com">www.igenity.com</a></td>
<td>Profile®</td>
<td>Marbling Score</td>
<td>12/2008</td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Quality Grade (% z Choice)</td>
<td>12/2008</td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Rib Eye Area</td>
<td>12/2008</td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Yield Grade</td>
<td>12/2008</td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Average Daily Gain</td>
<td>12/2008</td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Tenderness</td>
<td>12/2007</td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Residual Feed Intake (RFI) (for Bos indicus influenced cattle)</td>
<td>12/2007</td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Residual Feed Intake (RFI) (for Bos taurus cattle)</td>
<td>6/2008</td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Dry matter intake (DMI) (for Bos indicus influenced cattle)</td>
<td>12/2007</td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Heifer Pregnancy Rate</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Stayability (longevity)</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Maternal Calving Ease</td>
<td></td>
</tr>
<tr>
<td></td>
<td>Profile®</td>
<td>Docility</td>
<td></td>
</tr>
<tr>
<td><strong>Pfizer Animal Genetics</strong></td>
<td>GeneSTAR® Tenderness MVP</td>
<td>Tenderness</td>
<td>2/2009</td>
</tr>
<tr>
<td>(Bovigen)</td>
<td>GeneSTAR® Marbling MVP</td>
<td>% IMF (Feedlot cattle)</td>
<td>2/2009</td>
</tr>
<tr>
<td><a href="http://www.bovigen.com">www.bovigen.com</a></td>
<td>GeneSTAR® Feed Efficiency MVP</td>
<td>Net Feed Intake (NFI)</td>
<td>2/2009</td>
</tr>
<tr>
<td><strong>MMI genomics</strong></td>
<td>Tru-Marbling™</td>
<td>Marbling Score and Quality Grade</td>
<td></td>
</tr>
<tr>
<td><a href="http://www.metamorphixinc.com">www.metamorphixinc.com</a></td>
<td>Tru-Tenderness™</td>
<td>Tenderness</td>
<td></td>
</tr>
</tbody>
</table>
Australian beef DNA results

As part of its role in delivering DNA markers to the Australian beef industry, Beef CRC has agreed to independently test new panels of DNA markers as they are commercialised by companies such as Pfizer Animal Genetics, Integrity Aerial and Metamorphix Inc.

Results of all independent testing of commercially-available DNA markers undertaken by Beef CRC will be presented on this site, outlining the size and direction of effect and the amount of genetic variation that is accounted for by each panel of markers for the different traits (e.g. marbling, feed efficiency, tenderness etc).

Additional information is provided to help beef businesses interpret the results for themselves to determine the value to their own businesses from an investment in the particular panel of DNA markers.

Those decisions very much depend on the individual business’ attitude to risk and can only be made effectively by the individual business.

It is possible that the panel of markers has also been independently evaluated in North American herds by the US National Beef Cattle Evaluation Consortium, so for further information on the size and direction of effect of the markers in those populations, please visit http://www.anisci.cornell.edu/nbecc/

Pfizer Genestar results
Pfizer interpretation
Maybe Fisher was right.

For most economic traits we need to track very many genes in order to explain a large part of the genetic variance.
2000 Bull Project

Training:
USMARC Cycle VII
USMARC Ongoing GPE
DNA Testing Companies
Seedstock Field Data
(where applicable)

Validation:
2,000 Bull Project
International Collaboration

Application:
Seedstock Breeders

AI Sires: AN, HH, AR, SM, CH, LM, GV
Base Cows: AN, HH, MARC III

r₀

r₁

Slide courtesy of Marc Thallman, US MARC
Simulation comparing correlation between MBV and true breeding value given different #s QTLs when trained and validated on different populations

<table>
<thead>
<tr>
<th></th>
<th>Train in Multibreed</th>
<th>Train in Purebreed</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Validate in Purebreed</td>
<td>Validate in Multibreed</td>
</tr>
<tr>
<td>50k</td>
<td></td>
<td></td>
</tr>
<tr>
<td>50 QTL</td>
<td>0.39</td>
<td>0.42</td>
</tr>
<tr>
<td>100 QTL</td>
<td>0.29</td>
<td>0.31</td>
</tr>
<tr>
<td>250 QTL</td>
<td>0.25</td>
<td>0.28</td>
</tr>
<tr>
<td>500 QTL</td>
<td>0.20</td>
<td>0.30</td>
</tr>
</tbody>
</table>

- These correlations account for < 20% variation if 50 genes and <10% variation if 500 genes

50k across-breed predictions

- Current prospects for across-breed predictions are not promising
- Better results will be achievable with a higher density SNP panel (e.g. 500k rather than 50k chip)
- More animals in the training analyses may also improve results
- Use multiple breeds in training population if prediction equation is to be used in multiple breeds

Modified from Garrick. (2009). BIF
The good news is…. there is lots of room for the development of new EPDs


“In marked contrast to swine, poultry, sheep, and dairy cattle industries, where economic indexes are a critical component of selection strategies, the U.S. beef industry has done little to promote the value proposition associated with improvement….some goal trait groups are totally absent.”

- Feed Efficiency
- Animal Health
- Beef Healthfulness

- Adaptability
- Cow Fertility
- Cow Productivity
The bad news is that many of these goal traits are lowly heritable ........

<table>
<thead>
<tr>
<th>Trait</th>
<th>Heritability</th>
</tr>
</thead>
<tbody>
<tr>
<td>Carcass/end product</td>
<td>High</td>
</tr>
<tr>
<td>Skeletal measurements</td>
<td>High</td>
</tr>
<tr>
<td>Mature weight</td>
<td>High</td>
</tr>
<tr>
<td>Growth rate</td>
<td>Medium</td>
</tr>
<tr>
<td>Birth weight</td>
<td>Medium</td>
</tr>
<tr>
<td>Weaning weight</td>
<td>Medium</td>
</tr>
<tr>
<td>Yearling weight</td>
<td>Medium</td>
</tr>
<tr>
<td>Milk Production</td>
<td>Medium</td>
</tr>
<tr>
<td>Maternal ability</td>
<td>Low</td>
</tr>
<tr>
<td>Reproduction</td>
<td>Low</td>
</tr>
<tr>
<td>Health</td>
<td>Low</td>
</tr>
<tr>
<td>Cow longevity</td>
<td>Low</td>
</tr>
<tr>
<td>Overall cow productivity</td>
<td>Low</td>
</tr>
</tbody>
</table>
Accuracy of the prediction equation depends on:

\[
\frac{Th^2}{NeL}
\]

T: total number of animals in the training population
\(h^2\): heritability of the trait
\(N_e\): effective population size
L: length of chromosomes (in Morgans)

**BOTTOM LINE**

Traits with low heritability need more animals in training population; OR increase \(h^2\) by using proven AI bulls

*Modified from Goddard. (2009). BIF*
Effect of number of animals on accuracy of prediction equation


Goddard. (2009). BIF
How can the beef industry benefit from genomic selection?
An animal is born and tagged...
a single SNP panel run on each animal one time....

DNA from uniquely IDed calf will be run through a multiple SNP panel of

- unique permanent genetic fingerprint,
- genetic tests for SNP markers linked to economically relevant traits, and to
- confirm parentage.
- Genotype data then stored for future traceback of products derived from that animal, and incorporated into herd and breed EPD calculations.
...and animal is then managed according to genetic potential.

Results are used to make decisions regarding:

- Markets
- Feeding strategies
- Health product requirements
- Breeding decisions — guide selection and replacement choices. Which bulls are producing good calves, no calves? Which bull should be used with each heifer calf to maximize her offspring’s performance.
How can cattle producers benefit from genomic selection?

Rate of genetic gain \( \Delta G \)

\[
\Delta G = \frac{(i_m r_m + i_f r_f)}{(L_m + L_f)} \text{ genetic standard deviation/year}
\]

- **Nucleus sector**: similar rationale to dairy scenario
- **Bull multiplier sector**: may improve accuracy of female selection, may have genetic estimates for new traits not currently included in NCE, and will offer bulls with more accurate EPDs to commercial producers
- **Commercial sector**: risk reduction as young herd bulls EPDs will have higher accuracies; potentially new traits; may open up ranch-bull development opportunities
May see development of herd bulls from commercial sector

Modified from Garrick. (2008). BIF
Modified from Garrick. (2008). BIF
THERE ARE MORE ELITE ANIMALS IN COMMERCIAL THAN SEEDSTOCK

Modified from Garrick. (2008). BIF
Structure of breeding industry may be changed

- May see development of herd bulls from commercial sector
- May encourage more vertical integration to collect phenotypes to enable predictions for ERTs for all sectors
- May see genetic evaluations developed for novel traits – if large enough populations can be amassed and data shared
- Only want to genotype once and use that data in all sectors: Will beef follow the pig/poultry model of vertically-integrated breeding companies owning all sectors?
“DNA technology will be increasingly used on an industry wide basis.... In the future it will be the data processing, analysis, and electronic storage and transfer of results that will be as much the challenge for increasing industry adoption rather than the DNA marker measurement technology.”
Current beef cattle evaluation system industry structure

<table>
<thead>
<tr>
<th>Stakeholders in NCE</th>
<th>Current Business Model</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breed Associations</td>
<td>Cash</td>
</tr>
<tr>
<td>Bull Breeders</td>
<td>Bull breeders collect data at own expense</td>
</tr>
<tr>
<td>Bull Buyers</td>
<td>Bull breeders pay Breed Associations</td>
</tr>
<tr>
<td>AI Companies</td>
<td>Breed Associations pay Service entity</td>
</tr>
<tr>
<td>EPD Servicing Entities</td>
<td></td>
</tr>
<tr>
<td>Researchers interested in NCE</td>
<td>Non cash</td>
</tr>
<tr>
<td>Others (BIF, NBCEC, Cooperative Extension)</td>
<td>pedigree/performance data for the collective benefit</td>
</tr>
</tbody>
</table>

Modified from Garrick. (2008). BIF
How will this technology be commercialized? Who does each of these tasks will determine how implementation occurs.

Genotype selection candidates
(CC, GT, AC...)

Apply prediction equation

MBVs + existing EPDs

New EPDs (GEPDs)

Training and Validation
Population
Phenotypes and genotypes
Dairy industry evaluations performed by national NCE

“Keeping the characteristics of the fundamental evaluation system outside the realm of marketing will help the process remain unbiased and gain wider acceptance within the whole industry”

New stakeholders and new questions raised by evaluation system using WGS

<table>
<thead>
<tr>
<th>Stakeholders in WGS</th>
<th>Future Business Model ??</th>
</tr>
</thead>
<tbody>
<tr>
<td>Genotyping Companies</td>
<td>Development of training data</td>
</tr>
<tr>
<td>Genomics Companies</td>
<td>Genotyping/analysis costs</td>
</tr>
<tr>
<td>Owners/Controllers of Training datasets</td>
<td>Servicing (EPDs, MGVs, merged combination)</td>
</tr>
<tr>
<td>Breed Associations</td>
<td>How are bull breeders rewarded for better EPDs</td>
</tr>
<tr>
<td>EPD Servicing Entities</td>
<td>Does data get shared for collective benefit</td>
</tr>
<tr>
<td>AI Companies</td>
<td>Researchers participate/improve analyses motivated by $$</td>
</tr>
<tr>
<td>Bull Breeders</td>
<td></td>
</tr>
<tr>
<td>Bull Buyers</td>
<td></td>
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Modified from Garrick. (2008). BIF
Current Beef Model is companies develop MBV

- Genomics company provides “MBVs” based on their proprietary training equation
  - Precludes running NCE based on genotypic data
  - MBVs vary with company, panel, and over time

- Not yet clear how will they be incorporated into NCE
  - Need to develop covariances among all MBVs for NCE
  - Will prediction equations need to be breed-specific?
  - Likely there will be both large and small panel tests
  - Large tests most likely applied to AI sires and candidates
  - Small panels may be more widely used
Summary

- Most WGS work in beef cattle to date in Angus
- Mostly done on growth & carcass traits
- Low heritability traits not currently in NCE will require thousands of genotyped/phenotyped individuals in training populations
- Across-breed predictions need more breed diversity in training populations and denser SNP panels
- Using DNA to profile for management purposes may increase vertical-alliances in beef cattle industry.
- WGS is NOT a scale neutral technology!
Anderson. 2009. BIF – representing the Beef Breeds Council