Genetic Improvement of Beef Cattle: Current Practice and Future Prospects

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Animal breeders have used selection on phenotypes to great effect!
Plant and animal breeders have perhaps the most compelling sustainability story of all time.

https://grist.files.wordpress.com/2015/12/corn-hybrid-yields.jpeg
US Cattle Inventory 1961 – 2015
Stocks Down (‘000 Head; blue, left) vs. Production Up (‘000 Tonnes; red, right)
2016 Global Beef Production Numbers

Cattle numbers (‘000 Head; blue, left) vs. Beef production (‘000 Tonnes; red, right)
SCIENCE
Time line for beef breeding

Bull purchase/selection

Progeny born

Progeny slaughtered

Female progeny used for breeding

Image adapted from “More Beef from Breeding” Workshop (2007). Meat and Livestock (MLA), Australia

Van Eenennaam 2/2019
Practical Guide to Bull Buying

- Determine marketing strategy
  - Will heifers be retained?
- Determine management level
  - Labor
  - Nutrition
- Assure bulls are reproductively sound
  - BSE
- Check for structural soundness
Practical Guide to Bull Buying

- Set performance levels based on resource availability
- Select for performance using EPDs/Indexes
- Determine other selectable factors
  - Visual Appraisal
  - Disposition
  - Color
  - Horned/Polled
Performance

- Actual Measurement
- Ratios
- Expected Progeny Differences (EPD)
- Genomics
EPDs

- Best tool for selecting for performance traits
- Uses all information: actual measurement, relatives, environment, genomics
- Risk management tool
Information sources for EPDs

**Accuracy (r)** – correlation between test result and actual genetic merit
Expect the average difference in offspring to be 15 pounds.
Expect the average difference in offspring of the sires daughters to be 10 pounds.
Calving Ease

Bull – Calving Ease Direct
Heifers/Cows
Time spent with calving females

Heifers – Calving Ease Maternal
If replacements are kept

Does not replace buying CED bull
Be careful not to put too much emphasis on selection for calving ease.
Birth Weight Trends

![Graph showing birth weight trends for different breeds from 1972 to 2014. The breeds include Hereford, Angus, Red Angus, Simmenthal, Gelbvieh, Limousin, and Charolais. The graph illustrates the changes in birth weight over time for each breed.](https://example.com/graph.png)
Growth

• Use EPD closest to marketing endpoint
  – Weaning Wt EPD
  – Yearling Wt EPD
  – Carcass Wt EPD

• Be aware of correlated traits
  – Milk
  – Mature Size
  – Calving Ease


1986. "Coblepond New Yorker" weighed 2529 lbs and measured 65 inches tall at 35 mos. (Frame 10) when he was Denver Champion.

Weaning Weight Trends
Yearling Weight Trends

- Hereford
- Angus
- Red Angus
- Simmental
- Gelbvieh
- Limousin
- Charolais
Maternal

- Milk
- Reproduction
  - Heifer Pregnancy
  - 30-Month Pregnancy
  - Stayability
  - Sustained Cow Fertility
Milk Trends

The graph shows milk trends from 1990 to 2014 for different beef breeds, including Hereford, Angus, Red Angus, Simmental, Gelbvieh, Limousin, and Charolais. Each breed's milk production trend line is indicated by a different color and symbol, allowing for easy comparison over time.
When making selection decisions to improve fertility – which group of cattle should selection focus upon?

1. Bulls
2. Cows
3. Heifers
Genetic composition of the herd: 87% of genetic composition of calf crop is determined by the sires used over the last 3 generations.

- Maternal great-grand sires (12.5%)
- Maternal grand sires (25%)
- Sires (50%)

Carcass

- Carcass Wt EPD
- Quality Factors
  - Marbling EPD
  - % IMF EPD
- Yield Factors
  - Fat EPD
  - Ribeye Area EPD
Other

- Disposition
  - Docility EPD
  - Visual

- Scrotal Circumference
  - SC EPD
  - Actual Measurement

- Color/Horned-Polled
  - Homozygous vs Double bred
  - Carrier
## 2018 Purebred Simmental Percentile Table

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</table>
Historically not all cattle breeding objectives have been economic.
**Selection Index**

- Allows comparison on single value
- Weights traits according to economic importance
- Selection index
  
  \[ = a_1 \text{EPD}_1 + a_2 \text{EPD}_2 + \ldots + a_k \text{EPD}_k \]
Selection Index

- Easy to use, selection based on one value
- Should be aware of EPD in index that is not of value to your beef operation
- If missing relevant EPDs, use SI in tandem with those EPDs
Many beef breeds have indexes which combine EPDs according to economics

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<td>$B, $F, $G (Angus)</td>
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<td>$M (Beefmaster)</td>
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<td>$Profit (Topline-Leachman Bulls)</td>
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<td>$T (Beefmaster)</td>
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Genomics
The bovine genome is similar in size to the genomes of humans, with an estimated size of 3 billion base pairs.

Human & cattle genomes are 83% identical.
1000 Bull Genomes Run 6

2703 Sequenced Animals, 11x
~55 Breeds: Dairy, Beef, Dual Purpose, Crosses, Composites

2703 x 11 x 3 billion = 90,000,000,000,000

Slide courtesy Ben Hayes, QAAFI

Van Eenennaam 2/2019
1000 Bull Genomes Run 6

86.5 million single-nucleotide polymorphisms (SNPs) and 2.5 million small insertion deletions

Run 6 – Taurus only
44.7 million filtered variants
43 million SNP, 1.7 million Indel

Run 6 – Taurus Indicus
86.5 million filtered variants
84 million SNP, 2.5 million Indel

High-throughput genotyping technology enabled the development of high density “SNP chips”

The 2009 sequencing of the bovine genome allowed for the development of a 50,000 SNP chip, also known as the “50K”
We can use these SNPs 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).
Angus: Current implementation size

- 7.7M birth weights
- 8.4M weaning weights
- 4.1M post-weaning gain records
- 1.5M heifer calving ease scores
- 112K carcass records
- 1.8M ultrasound records
- 19K individual intake records
- 237K docility scores
- 57K heifer pregnancy observations
- 199K mature cow weights

Slide courtesy of Steve Miller 5/9/2017
Genetic Correlation between genomic prediction results and phenotypic AAA data

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<th>$r$</th>
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<td>Yearling Weight</td>
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Steve Miller (AGI), 2016 NBCEC Brown Bagger
Information sources for EPDs – DNA just one source of data for GE-EPD

Accuracy (r) – correlation between test result and actual genetic merit

Genomic-Enhanced EPDs (GE-EPD)
Genomics in National Cattle Evaluation (NCE)

- Currently several breeds are using genomic information in their national cattle evaluation programs
  - Angus - Hereford
  - Red Angus - Gelbvieh
  - Limousin - Charolais
  - Simmental - Santa Gertrudis
  - Beefmaster - Brangus

- Other breeds are trying to incorporate genomic information

- Virtually only National Cattle Evaluation traits – only traits with enough data
How much do genetic tests cost?

- ~ $13-20 for parentage testing
- ~$20-$30 per animal for a single mutation test for a disease or trait
- $75-90 for the high-density SNP chips for genomic-enhanced EPDs.
- $45-50 for the low-density imputation chips.

Breed associations work to include that genomic information to provide genomic-enhanced EPDs (GE-EPD) that have improved accuracy due to the inclusion of the genomic information in the EPD calculations.

If multiple tests can be performed on a single DNA sample or a large volume of samples is tested then the cost per test is reduced.

Additional costs can include the cost of DNA cards, sample collection, sample storage and shipping and sample processing, again depending on sample type, test and application.

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There are several tests that are being marketed for use on commercial cattle that are not directly part of a breed association genetic evaluation program.

- **GeneMax Advantage** ($39) and **GeneMax Focus** ($17). Distributed by Angus Genetics Inc. (AGI) and marketed by Zoetis® for cattle that are at least 75% Angus.

- **PredicGEN** ($19.50) is a test marketed by Zoetis® as “a heifer selection tool for straight-bred or crossbred British/Continental animals.”

- **The Igenity Beef Profile** ($29) marketed by Neogen® as “DNA profiles for crossbred and purebred cattle.” Predictions for weaning weight, yearling weight and hot carcass weight for a total of 16 traits scored on a 1–10 scale, plus two new selection indexes. “The Igenity profile was designed and validated for crossbred or straightbred cattle with backgrounds of Angus, Red Angus, Simmental, Hereford, Limousin and Gelbvieh.

- **There aren’t yet any independent, peer-reviewed papers documenting the field performance of these tests for commercial cattle.**
Crossbreed

- Should always be a consideration for commercial cattle producers
- Greatest benefit to reproduction and longevity
- Rule of thumb – no females with >75% one breed!
eBEEF was developed as part of USDA NIFA grants
#2011-68004-30367
#2011-68004-30214
DNA testing can be used to identify parentage, genetic defects, and to improve the accuracy of breed EPDs.

Tests have not been shown to work well in predicting genetic merit of crossbreds.

Economics of testing commercial cattle needs to be carefully considered – will depend on a number of factors – return greater on males than females.
There are several tests that are being marketed for use on commercial cattle that are not directly part of a breed association genetic evaluation program.

**Germline:** Efficient beef production (e.g. Angus)

- Genomic selection of superior bulls and cows
- In vitro fertilization (IVF)
- 100s of embryos
- Establish ESCs
- Genomic selection of superior male ESCs
- Option to gene edit ESCs (e.g. SRY, POLLED, SLICK)

**Surrogate line:** Environmentally adapted (e.g. Brahman)

- Selection of bulls and cows
- In vitro fertilization (IVF)
- 100s of embryos
- Gene edit embryos to be germ cell deficient
- PCR selection of male embryos
- (Gene edited) superior male ESCs
- Germ cell deficient, male embryos

**Surrogate Sire Production Model**

- Germline complementation
- Embryo transfer to recipient cow
- Gestation & maturation
- Environmentally adapted (e.g. Brahman) bull with superior beef production (e.g. Angus) sperm
Will gene editing allow an additional inflection point in rate of livestock genetic gain?


Animal Biotechnology and Genomics Education
Gene Edited Polled Calves

Naturally-occurring bovine allele at polled locus

Precision Breeding Offers New Alternative to Dehorning Cattle
https://www.youtube.com/watch?v=-Qks_LMmodw
Editing is the Cherry on Top of Breeding Sundae
It will be able to introduce useful alleles, and potentially bring in useful novel genetic variation to improve livestock rapidly, without “linkage” drag

Genome Editing
- Somatic cell nuclear transfer cloning
- Genomic Selection
- Embryo Transfer
- Artificial insemination
- Progeny testing
- Performance recording
- Development of breeding goals
- Association of like minded breeders
Cracking the genetic code for complex traits in cattle

20 February 2018

A massive global study involving 58,000 cattle has pinpointed the genes that influence the complex genetic trait of height in cattle, opening the door for researchers to use the same approach to map high-value traits including those important for beef and milk production.

The University of Queensland’s Professor Ben Hayes, who heads the global 1000 Bull Genomes Consortium of 57 researchers from 30 institutes, said it had previously been a major challenge to identify variants in the genome affecting complex traits, due to variations within multiple genes, and behavioural and environmental factors.

“To overcome this issue, the consortium pooled large genomic datasets and phenotypes collected from 58,000 cattle around the world to gain the clearest picture so far of their genetics,” Professor Hayes said.

“We needed access to vast resources of data in order to demonstrate that the genes affecting a complex trait like height can be accurately identified.

“By applying the same collaborative big data approach, it may now be possible to identify genes associated with high-value complex traits that are really important to the industry, such as beef and milk production, feed efficiency and reduced methane emissions.”

The 1000 Bull Genomes Consortium’s findings on height were confirmed by analysing the genetic material of miniature cattle and the DNA sequenced from a 6500-year-old wild auroch bone.

“Aurochs are an extinct species of large wild ox – which were domesticated by ancient humans about 10,000 years ago and bred to be shorter – and are the ancestor to all cattle breeds,” Professor Hayes said.

“From analysing the DNA of this animal, we could predict its height, and then verify our prediction with the fossil records of auroch skeletons.”


Van Eenennaam 2/2019
Strategy to combine big data and genomic selection as a unifying approach to deliver innovative “step changes” in the rate of genetic gain at scale.

Hickey et al., 2017; *Genomic prediction unifies animal and plant breeding programs to form platforms for biological discovery*. Nat Genet. 49:1297-1303.
Thanks for inviting me!

My laboratory receives public funding support from the National Institute of Food and Agriculture and the Biotechnology Risk Assessment Grant (BRAG) program, U.S. Department of Agriculture, under award numbers 2011-68004-30367, 2013-68004-20364, 2015-67015-23316 and 2015-33522-24106.