Interbeef workshop: US report

Alison Van Eenennaam

University of California, Davis

Bob Weaber

Kansas State University

- Major UC beef research projects
- Current status of genomic information
- Consolidation of US genetic service providers
- How breeds are adding genomic data to national cattle evaluations

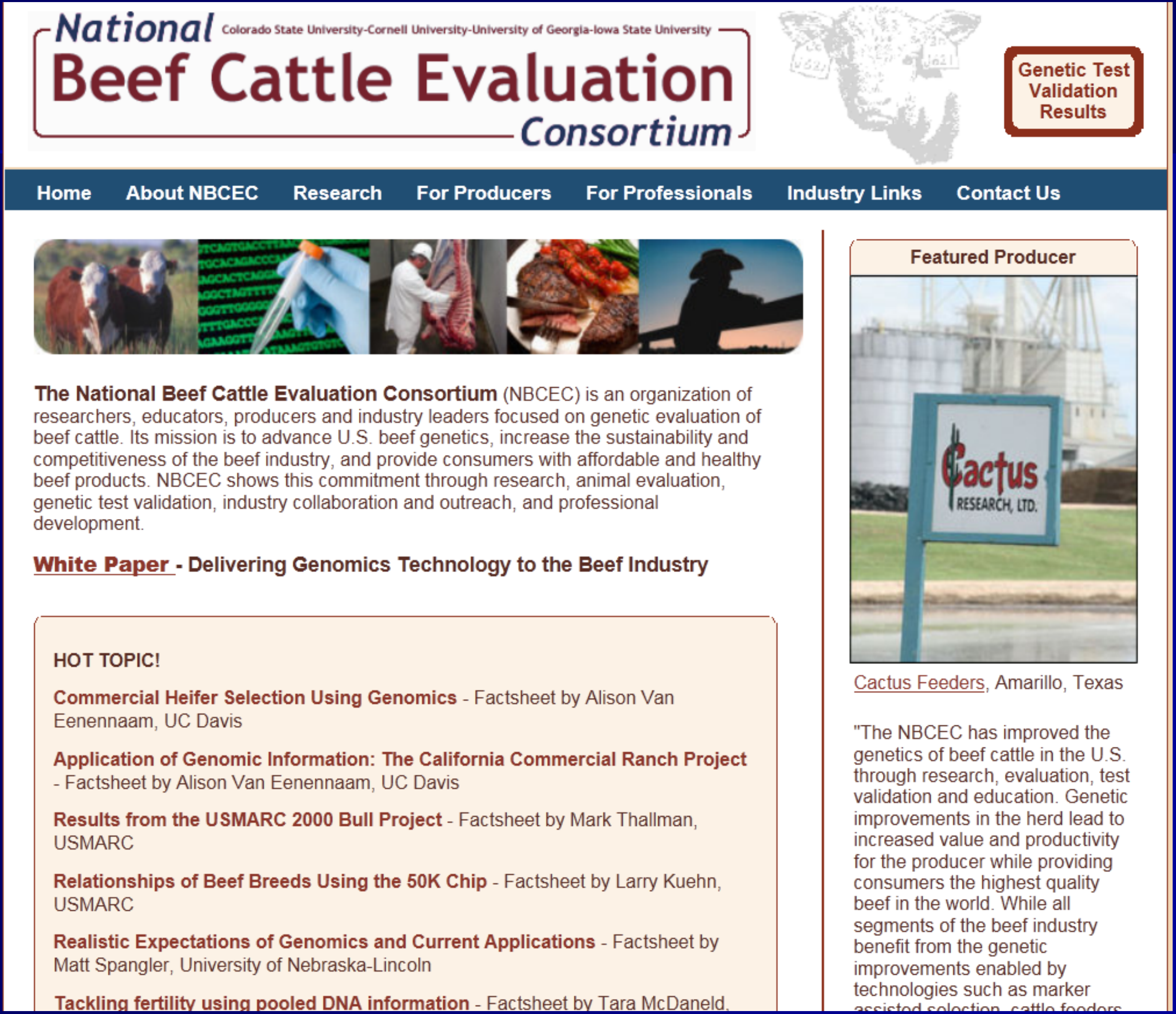
National Beef Cattle Evaluation Consortium

Colorado State University-Cornell University-University of Georgia-Iowa State University

NBCEC projects http://www.nbcec.org

- Genomic selection in beef cattle (Garrick - IA)
- Single-step approach to incorporating genomic information into EPDs (Misztal - GA)
- Reducing data loss and improving accuracy in National Cattle Evaluation (Bertrand - GA)
- Industry effort to enhance beef cattle selection aka Weight Trait Project (Pollak/Spangler - NE)
- Developing selection tools for longevity and reproduction (Pollak – US MARC)
- Genetics of feedlot cattle health (Enns, CO – funded by Pfizer)
- Healthfulness of beef project (Reecy, IA – funded by Pfizer)

http://www.nbcec.org



National Beef Cattle Evaluation Consortium

Colorado State University-Cornell University-University of Georgia-Iowa State University

The National Beef Cattle Evaluation Consortium (NBCEC) is an organization of researchers, educators, producers and industry leaders focused on genetic evaluation of beef cattle. Its mission is to advance U.S. beef genetics, increase the sustainability and competitiveness of the beef industry, and provide consumers with affordable and healthy beef products. NBCEC shows this commitment through research, animal evaluation, genetic test validation, industry collaboration and outreach, and professional development.

White Paper - Delivering Genomics Technology to the Beef Industry

HOT TOPIC!

Commercial Heifer Selection Using Genomics - Factsheet by Alison Van Eenennaam, UC Davis

Application of Genomic Information: The California Commercial Ranch Project - Factsheet by Alison Van Eenennaam, UC Davis

Results from the USMARC 2000 Bull Project - Factsheet by Mark Thallman, USMARC

Relationships of Beef Breeds Using the 50K Chip - Factsheet by Larry Kuehn, USMARC

Realistic Expectations of Genomics and Current Applications - Factsheet by Matt Spangler, University of Nebraska-Lincoln

Tackling fertility using pooled DNA information - Factsheet by Tara McDaneld,

Featured Producer

Cactus Feeders, Amarillo, Texas

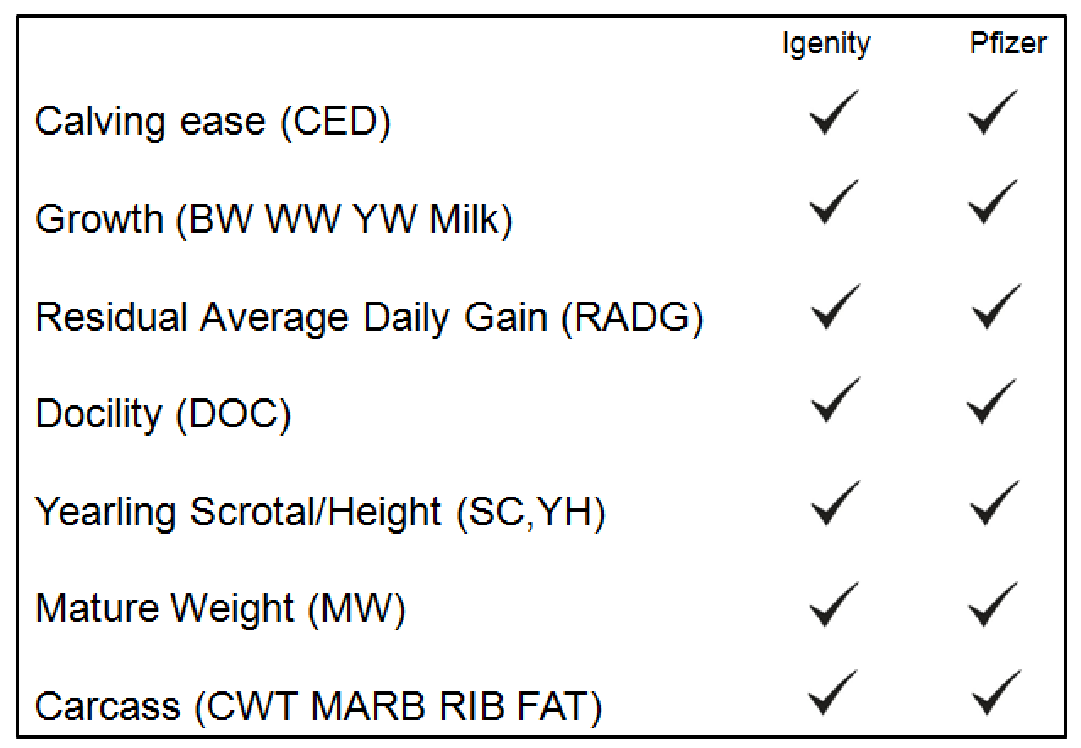
"The NBCEC has improved the genetics of beef cattle in the U.S. through research, evaluation, test validation and education. Genetic improvements in the herd lead to increased value and productivity for the producer while providing consumers the highest quality beef in the world. While all segments of the beef industry benefit from the genetic improvements enabled by technologies such as marker assisted selection, cattle feeders

USDA funded projects – competitive call for proposals

- BIGS – Bioinformatics to implement genomic selection – finishes 4/14 (Garrick/Snelling/Golden) See website http://bigs.ansci.iastate.edu/
- Identification of molecular markers to improve fertility of beef cattle (Thomas, CO) – finished 12/2011
  - >10,000 DNA samples and phenotypes on heifers
- Integrating DNA information into beef cattle production systems (Van Eenennaam, CA) – finishes 12/2013
  - 7,000 DNA samples & weaning weight records, 4500 carcass records
- National program for genetic improvement of feed efficiency in beef cattle (Taylor, MO) – finishes 4/2016
  - Genotype ~ 2,400 head on HD chips
  - $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
  - Collection and HD genotypes on 6,000 BRD case-control animals
  - $10 million, 5 year project; April 2011 – April 2016

Current status of US breed incorporation of genomic information

- Angus is incorporating MBVs from Igenity (purchased by Neogen) and Pfizer weekly into genomically-enhanced EPDs for the following traits



	Igenity	Pfizer
Calving ease (CED)	✓	✓
Growth (BW WW YW Milk)	✓	✓
Residual Average Daily Gain (RADG)	✓	✓
Docility (DOC)	✓	✓
Yearling Scrotal/Height (SC,YH)	✓	✓
Mature Weight (MW)	✓	✓
Carcass (CWT MARB RIB FAT)	✓	✓

http://www.angus.org/AGI/GenomicChoice11102011.pdf (updated 11/18/2011)

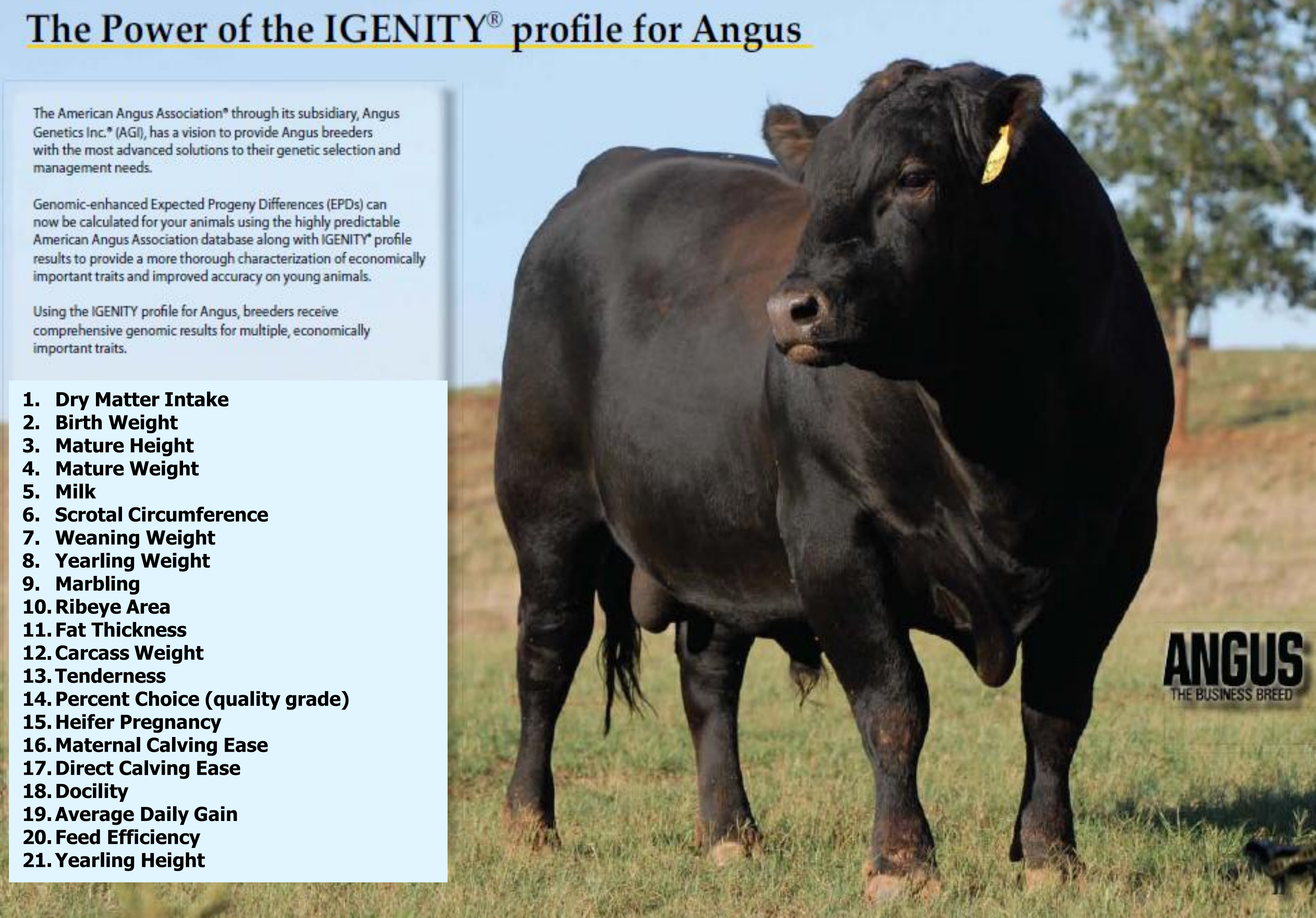
Lead Today with 50K

1. Birth weight
2. Weaning weight
3. Weaning maternal (milk)
4. Calving ease direct
5. Calving ease maternal
6. Marbling
7. Backfat thickness
8. Ribeye area
9. Carcass weight
10. Tenderness
11. Postweaning average daily gain
12. Daily feed intake
13. Feed efficiency (net feed intake)

Pfizer Animal Health
Animal Genetics

50K SNP chip assay;
~ US $139

384 SNP product; ~US$65



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.

Genomic-enhanced Expected Progeny Differences (EPDs) can now be calculated for your animals using the highly predictable American Angus Association database along with IGENITY® profile results to provide a more thorough characterization of economically important traits and improved accuracy on young animals.

Using the IGENITY profile for Angus, breeders receive comprehensive genomic results for multiple, economically important traits.

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**

	384 SNP	50K SNP
Genetic Correlation (r)/(r^2%)	**Igenity**	**Pfizer**
Calving Ease Direct	.47 (22%)	.33 (11%)
Birth Weight	.57 (32%)	.51 (26%)
Weaning Weight	.45 (20%)	.52 (27%)
Yearling Weight	.34 (12%)	.64 (41%)
Dry Matter Intake (component of RADG)	.45 (20%)	.65 (42%)
Yearling Height	.38 (14%)	.63 (40%)
Yearling Scrotal	.35 (12%)	.65 (42%)
Docility	.29 (.08%)	.60 (36%)
Milk	.24 (06%)	.32 (10%)
Mature Weight	.53 (28%)	.58 (34%)
Mature Height	.56 (31%)	.56 (31%)
Carcass Weight	.54 (29%)	.48 (23%)
Carcass Marbling	.65 (42%)	.57 (32%)
Carcass Rib	.58 (34%)	.60 (36%)
Carcass Fat	.50 (25%)	.56 (31%)

http://www.angus.org/AGI/GenomicChoice11102011.pdf (updated 11/18/2011)

Current status of US breed incorporation of genomic information

- The following breed associations are working with Dorian Garrick to develop their own 50K-based prediction equations

Breed	**ICAR breed code**	**# Training Records**
Hereford	HER	1,725
Red Angus	RAN	296
Simmental	SIM	2,853
Brangus	BRG	896
Limousin	LIM	2,319
Gelbvieh	GVH	847
Maine Anjou	RDP	115

Predictions in Some Beef Breeds

(Data provided by Dorian Garrick)

# Records in training	Angus (3,500)	Hereford (800)	Simmental (2,800)	Gelbvieh (847)	Gelbvieh including Angus (1,181)
BirthWt	0.64	0.43	0.65	0.38	0.41
WeanWt	0.67	0.32	0.52	0.31	0.34
YearlingWt	0.75	0.30	0.45	0.21	NC
Milk	0.51	0.22	0.34	0.36	0.34
Fat	0.70	0.40	0.29	NA	NA
REA	0.75	0.36	0.59	0.38	0.48
Marbling	0.80	0.27	0.63	0.54	0.56
CED	0.69	0.43	0.45	NC	0.48
CEM	0.73	0.18	0.32	NC	NC
SC	0.71	0.28	NA	0.50	0.50

International Hereford Comparisons - Combined Pan American International Evaluation (Data provided by Dorian Garrick)

Genetic Correlations	ASREML 4-fold x validation	Raw Corr 99 URG bulls	Raw Corr 75 CDN bulls	Raw Corr 59 ARG bulls (unrelated)	Raw Corr 41 ARG bulls (US-like)
Birth weight	0.43	0.22	0.40	0.15	0.24
Weaning weight	0.32	0.13	0.07	-0.35	0.23
Yearling weight	0.30	0.03	0.12	-0.27	0.32
Milk	0.22	0.23	0.09	0.15	-0.03
Calving Ease (D)	0.43		0.25		
Calving Ease (M)	0.18		0.44		
Backfat thickness	0.40	0.22	0.39	0.02	0.10
Marbling	0.27	0.25	0.29	0.17	0.35
Ribeye Area	0.36	0.01	-0.01	-0.11	0.18
Scrotal Circumfr.	0.28	0.36	0.19	-0.03	0.10

Angus predictions are not very accurate in Red Angus (Data provided by Dorian Garrick)

Trait	Validating in American Angus	Validating in Red Angus
BirthWt	0.64	0.27
WeanWt	0.67	0.28
YearlingWt	0.75	0.23
Fat	0.70	0.21
REA	0.75	0.29
Marbling	0.80	0.21
CalvEase (D)	0.69	0.14
CalvEase (M)	0.73	0.18

Angus = ASREML 5-fold validation Red Angus = correlation
Training on de-regressed EPDs Saatchi et al (GSE)
Red Angus is more closely related to Angus than is Hereford

US Genetic Evaluation Service Providers

- Angus Genetics Inc. (AGI)
  - Angus*, Limousin, Charolais, Gelbvieh
  - Growth traits and some auxiliary traits
  - Multi-breed models using U. of Georgia software
- American Simmental Association
  - Simmental*, Simbrah, Red Angus, Maine Anjou, Chianina, composites
  - Multi-breed growth, carcass and calving ease
  - Genomically enhanced Spring 2012
- *Genomically enhanced

US Genetic Evaluation Service Providers

- Colorado State
  - Calving Ease, Carcass, Fertility Traits: US and CAN Limousin, Gelbvieh; All traits for Shorthorn, Braunvieh, Romanola; Carcass & Fert Red Angus
- University of Georgia
  - Growth/carcass traits: Brahman, Beefmaster, Brangus
- Cornell University – exited service
- Iowa State – exited service

US Genetic Evaluation Service Providers

- National Center for Beef Excellence
  - Emerging resource for multi-breed
  - Utilize U. of Georgia software
  - NBCEC multi-breed database
  - Missouri and USDA grant funding support to build infrastructure
  - Virtual center
  - University and industry collaborators

Incorporation of Genomic Data into National Cattle Evaluation

- Modeled as correlated trait
  - Multiple panels of markers
  - Angus model
- Fit as external genetic predictor
  - Scaled and weighted by accuracy
  - Simmental/Red Angus/Chi/Maine-Anjou
- Index of EPD and MBV
  - Post evaluation
  - Hereford