What I do & my vision for the future of beef cattle genomics

Alison Van Eenennaam, Ph.D.

Cooperative Extension Specialist

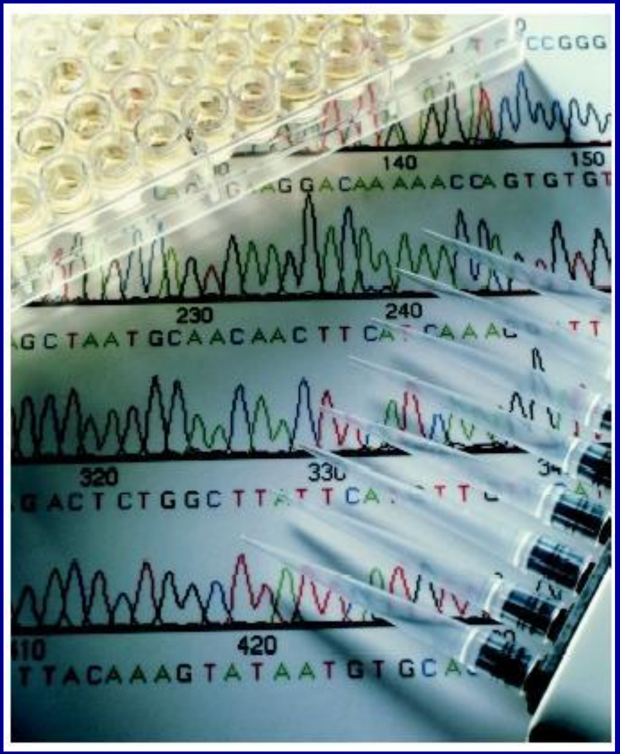
Animal Biotechnology and Genomics

Department of Animal Science

University of California, Davis

Ph: (530) 752-7942

alvaneenennaam@ucdavis.edu



"The mission of the animal genomics and biotechnology extension program is to provide broad, science-based extension programming on the uses of animal biotechnologies in livestock production systems."

http://animalscience.ucdavis.edu/animalbiotech

Dairy	Beef
High use of AI	Little use of AI
Only one breed	Many breeds, limited resources
Clear selection goal (total net merit)	Multiple competing selection goals – cow/calf, feedlot, processor – little data sharing between sectors
Large number of high accuracy A.I. sires for training	Relatively few high accuracy sires for training
Extensive, uniform collection of data on traits	Few/no records on many important traits (feed efficiency, reproduction)
Central USDA evaluation (AIPL) receiving all genotypes and recalibrating equations	No centralized "national" cattle evaluation – breed associations perform genetic evaluations
Obvious way to increase ΔG (decrease age of young progeny test sires)	Use young herd sires so less way to decrease generation interval
AI companies funding the genotyping because they get a clear cost savings in terms of young sire program	No clear beneficiary willing to pay!
	Crossbreeding is important

Many companies have come and some have gone….

GeneSTAR® SureTRAK® GeneSTAR®

SireTRACE™

Pfizer Pfizer Animal Genetics

igenity™

GENETICVISIONS®

ImmGen.

BIOGENETIC SERVICES, INC.

genmark®

GENESEEK
Molecular Solutions for Breeding and Genetics

ANGUSURE™

GENAISSANCE PHARMACEUTICALS

MMI GENOMICS, INC.
BREED TRU™
DNA VERIFIED

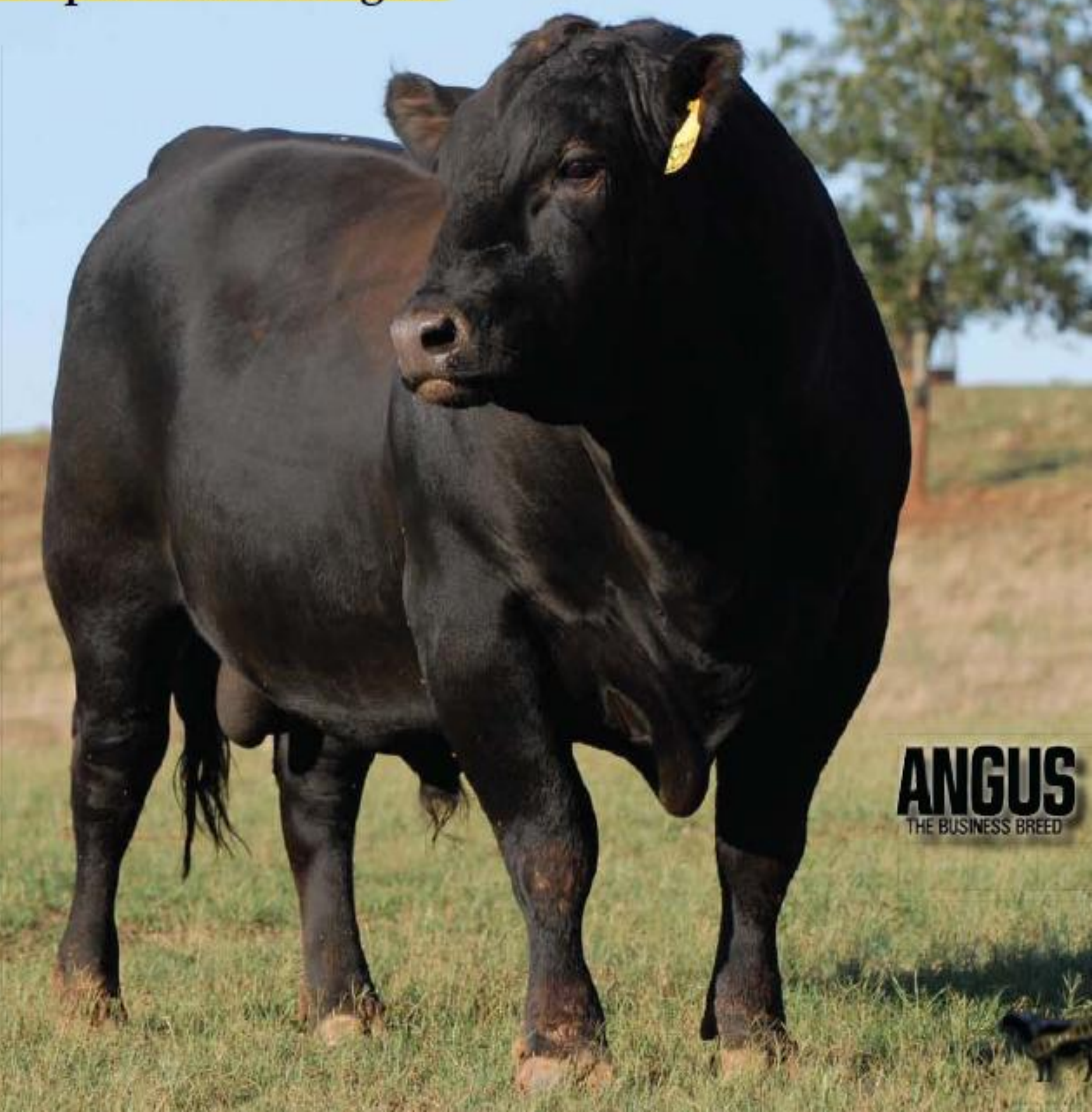
METAMORPHIX, INC.

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



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

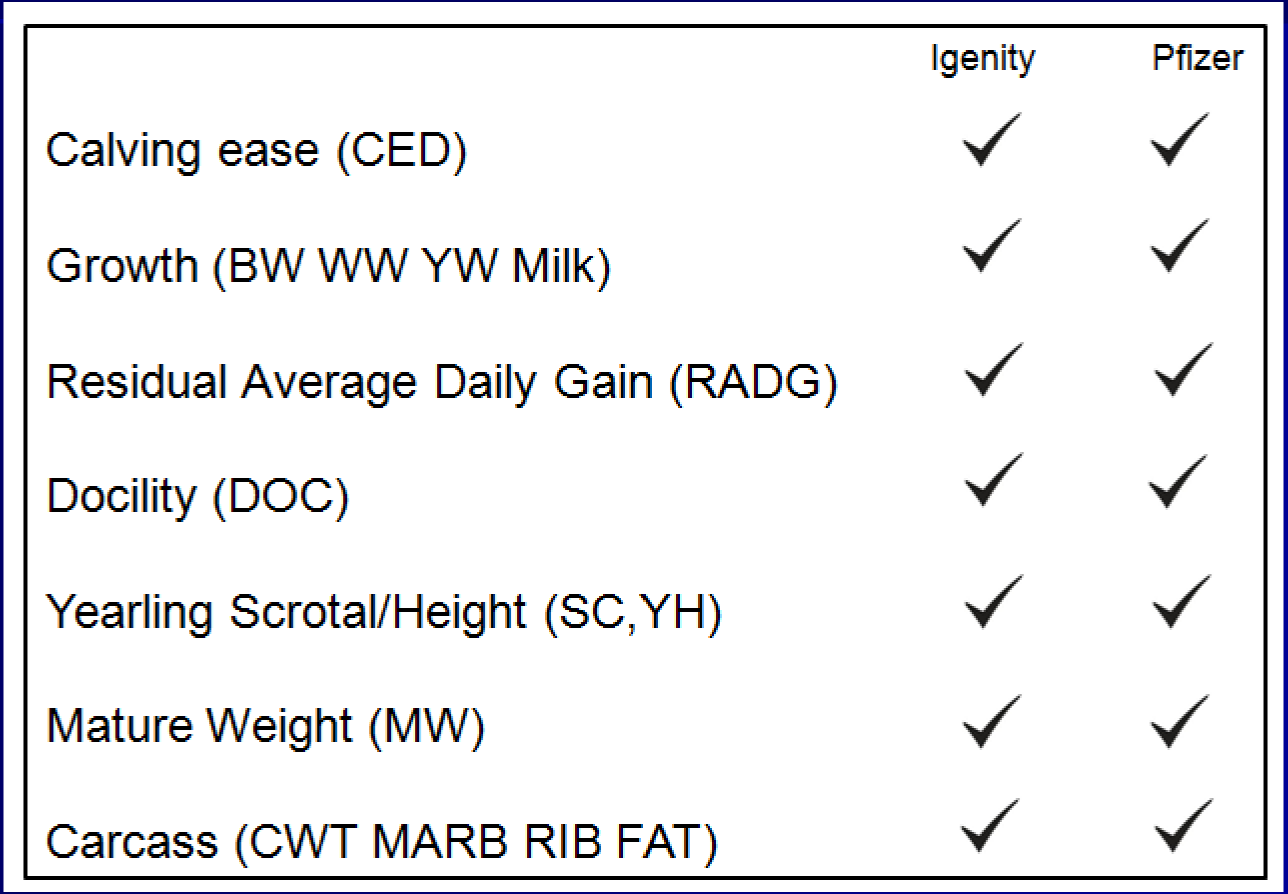
Lead Today with 50K

Pfizer

Pfizer Animal Health
Animal Genetics

50K SNP chip assays
50,000 SNPs spread
throughout genome

American Angus Association performs weekly evaluations with genomic data – recently updated to include new traits



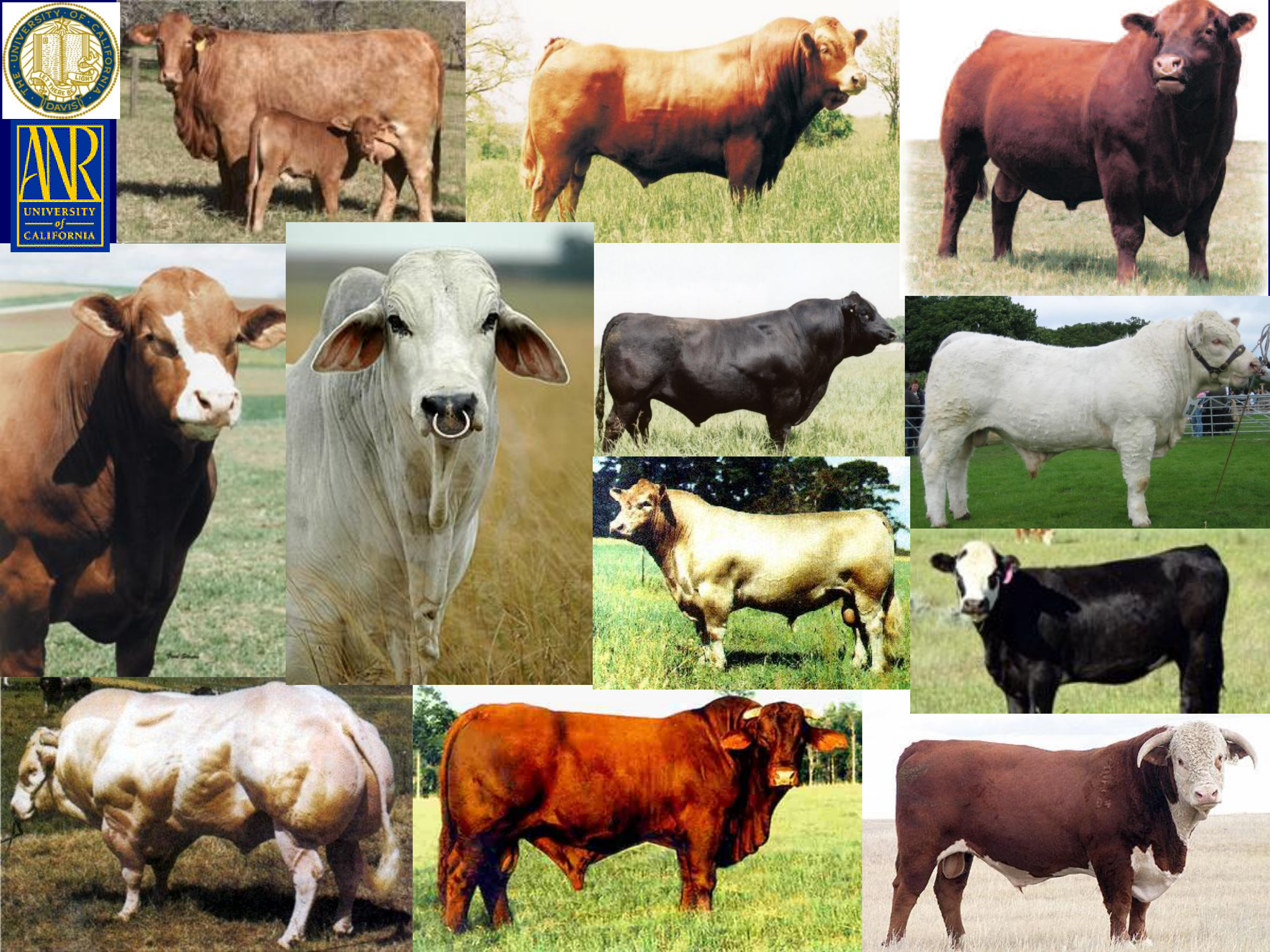
	Igenity	Pfizer
Calving ease (CED)	✓	✓
Growth (BW WW YW Milk)	✓	✓
Residual Average Daily Gain (RADG)	✓	✓
Docility (DOC)	✓	✓
Yearling Scrotal/Height (SC,YH)	✓	✓
Mature Weight (MW)	✓	✓
Carcass (CWT MARB RIB FAT)	✓	✓

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

ANGUS

		384 SNP		50K SNP	
Genetic Correlation (r)/(r^2%)/PE	**h^2**	**Igenity/ Neogen**		**Pfizer**	
Calving Ease Direct	0.20	.47 (22%)	5	.33 (11%)	2
Birth Weight	0.42	.57 (32%)	4	.51 (26%)	3
Weaning Weight	0.20	.45 (20%)	5	.52 (27%)	7
Yearling Weight	0.20	.34 (12%)	2	.64 (41%)	13
Dry Matter Intake	0.31	.45 (20%)	3	.65 (42%)	9
Yearling Height	0.45	.38 (14%)	2	.63 (40%)	5
Yearling Scrotal	0.43	.35 (12%)	1	.65 (42%)	6
Docility	0.37	.29 (8%)	1	.60 (36%)	5
Milk	0.14	.24 (6%)	1	.32 (10%)	3
Mature Weight	0.55	.53 (28%)	2	.58 (34%)	3
Mature Height	0.82	.56 (31%)	1	.56 (31%)	1
Carcass Weight	0.31	.54 (29%)	5	.48 (23%)	3
Carcass Marbling	0.26	.65 (42%)	10	.57 (32%)	7
Carcass Ribeye Area	0.32	.58 (34%)	6	.60 (36%)	6
Carcass Backfat Thick	0.26	.50 (25%)	4	.56 (31%)	7

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



Translational Questions for the Beef Industry

? How many phenotypic records are required in the initial experiment estimating the effect of chromosome segments?

? How many markers are needed– 384, 9K, 50K, 800K, whole genome?

? How does the relationship between the training population and the selection candidate affect accuracy?

? How often do chromosome segment effects need to be re-estimated? Every generation?

? Do predictions work across breeds?

? What is the value generated by the increased accuracy?

? Does this technology change breeding program design?

Van Eenennaam, A. L. 2011. Beef translational genomics: Lessons from the literature. Association for the Advancement of Animal Breeding and Genetics. 19: 271-278.

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

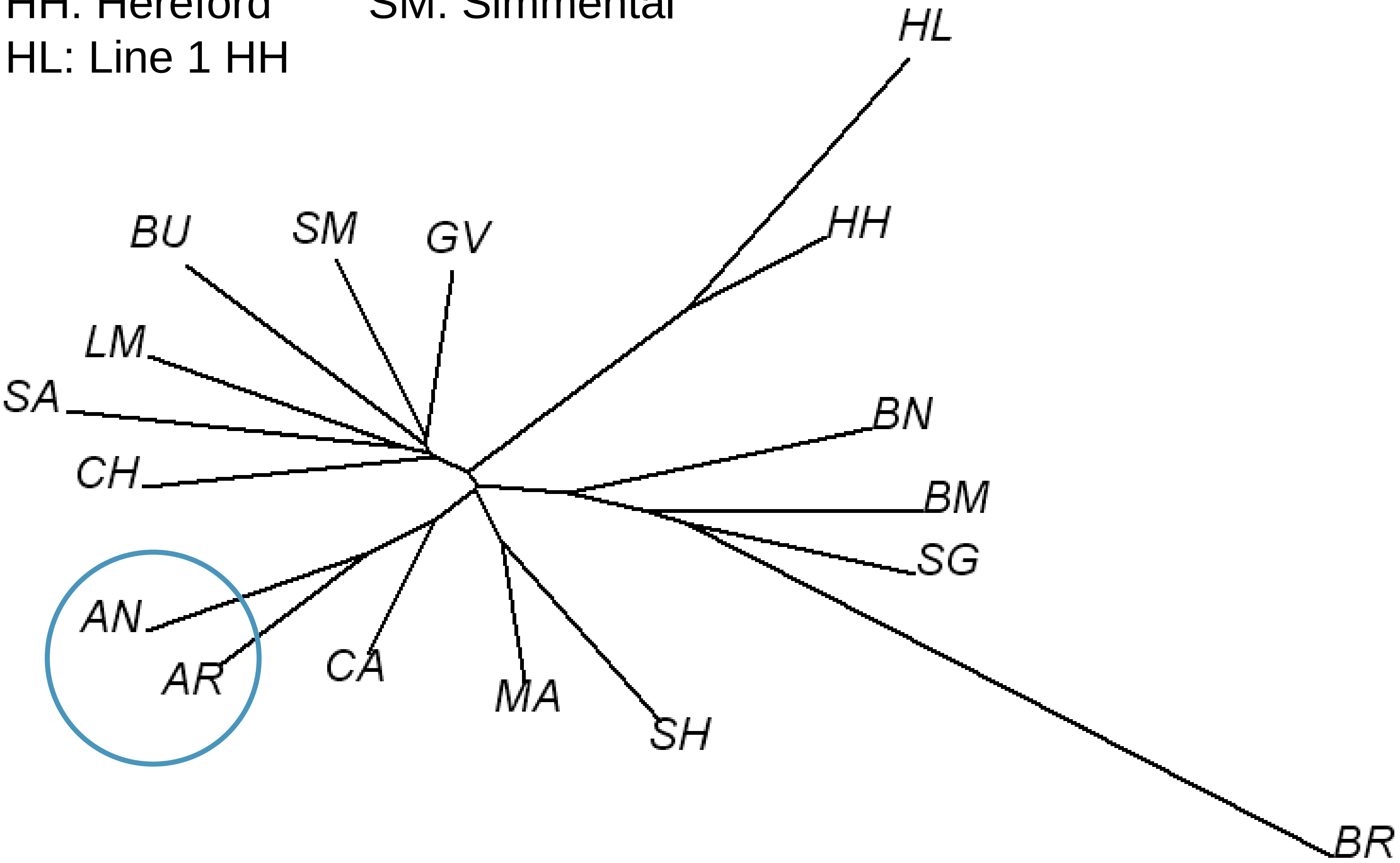
Angus = ASREML 5-fold validation Red Angus = correlation
Training on de-regressed EPDs Saatchi et al (GSE)

Approximate genetic distance between breeds using data from the 2,000 Bull Project.

Larry Keuhn, USDA MARC

http://www.nbcec.org/topics/BeefBreeds.pdf

AN: Angus
BM: Beefmaster
BN: Brangus
BR: Brahman
BU: Braunvieh
CA: Chiangus
CH: Charolais
HH: Hereford
HL: Line 1 HH
GV: Gelbvieh
LM: Limousin
MA: Maine Anjou
RA: Red Angus
SA: Salers
SG: Santa Gertrudis
SH: Shorthorn
SM: Simmental



So what about other breeds?

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

Breed	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

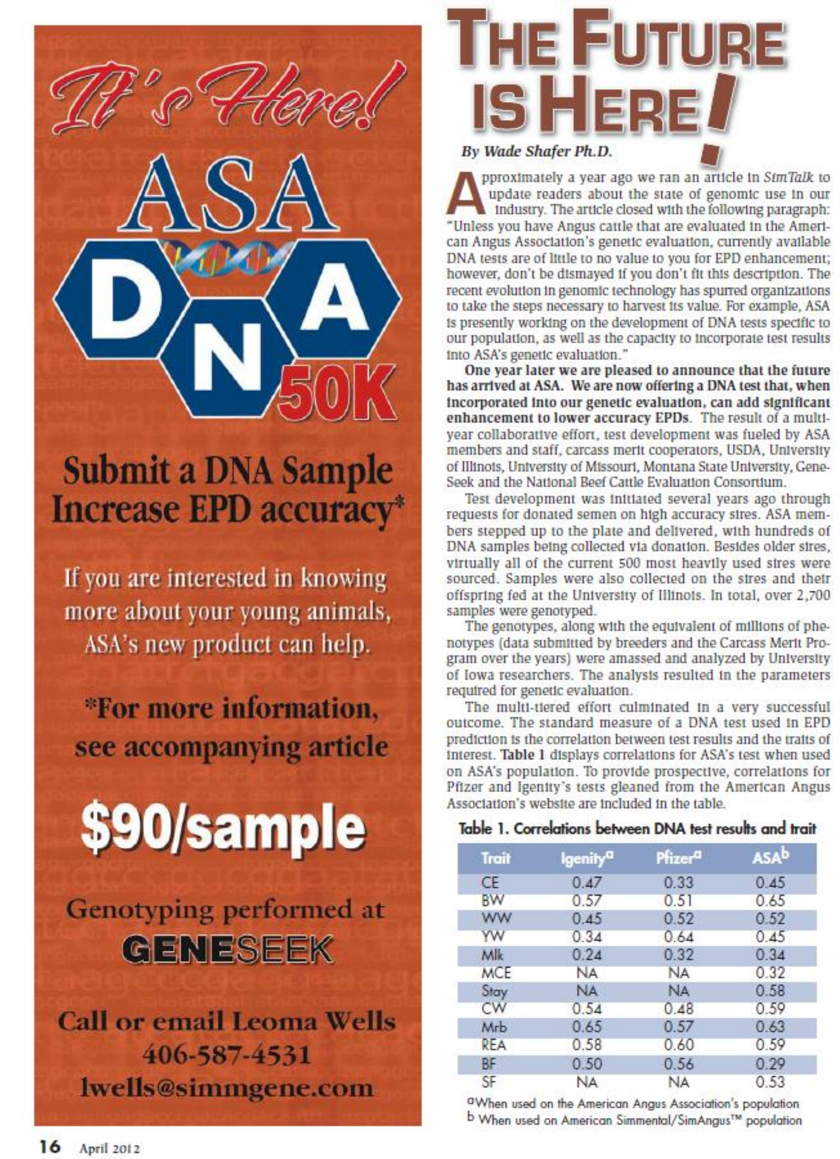
(Data provided by Dorian Garrick)

# 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

Simmental

2,800 records in training

		ASA	
Trait	**r**	**(r^2%)**	**PE**
Calving Ease Direct	0.45	(20%)	5
Birth Weight	0.65	(42%)	6
Weaning Weight	0.52	(27%)	4
Yearling Weight	0.45	(21%)	3
Milk	0.34	(12%)	3
Maternal Calving Ease	0.32	(10%)	3
Stayability	0.58	(34%)	9
Carcass Weight	0.59	(35%)	4
Carcass Marbling	0.63	(40%)	4
Carcass Rib Eye Area	0.59	(35%)	4
Carcass Backfat Thick.	0.29	(8%)	1
Shear Force (Tenderness)	0.53	(28%)	6



If you are interested in knowing more about your young animals, ASA's new product can help.

*For more information, see accompanying article

$90/sample

Genotyping performed at GENESEEK

Call or email Leoma Wells
406-587-4531
lwells@simmgene.com

THE FUTURE IS HERE!

By Wade Shafer Ph.D.

Approximately a year ago we ran an article in *SimTalk* to update readers about the state of genomic use in our industry. The article closed with the following paragraph: "Unless you have Angus cattle that are evaluated in the American Angus Association's genetic evaluation, currently available DNA tests are of little to no value to you for EPD enhancement; however, don't be dismayed if you don't fit this description. The recent evolution in genomic technology has spurred organizations to take the steps necessary to harvest its value. For example, ASA is presently working on the development of DNA tests specific to our population, as well as the capacity to incorporate test results into ASA's genetic evaluation."

One year later we are pleased to announce that the future has arrived at ASA. We are now offering a DNA test that, when incorporated into our genetic evaluation, can add significant enhancement to lower accuracy EPDs. The result of a multi-year collaborative effort, test development was fueled by ASA members and staff, carcass merit cooperators, USDA, University of Illinois, University of Missouri, Montana State University, GeneSeek and the National Beef Cattle Evaluation Consortium.

Test development was initiated several years ago through requests for donated semen on high accuracy sires. ASA members stepped up to the plate and delivered, with hundreds of DNA samples being collected via donation. Besides older sires, virtually all of the current 500 most heavily used sires were sourced. Samples were also collected on the sires and their offspring fed at the University of Illinois. In total, over 2,700 samples were genotyped.

The genotypes, along with the equivalent of millions of phenotypes (data submitted by breeders and the Carcass Merit Program over the years) were amassed and analyzed by University of Iowa researchers. The analysis resulted in the parameters required for genetic evaluation.

The multi-tiered effort culminated in a very successful outcome. The standard measure of a DNA test used in EPD prediction is the correlation between test results and the traits of interest. **Table 1** displays correlations for ASA's test when used on ASA's population. To provide prospective, correlations for Pfizer and Igenity's tests gleaned from the American Angus Association's website are included in the table.

Table 1. Correlations between DNA test results and trait

Trait	Igenity[a]	Pfizer[a]	ASA[b]
CE	0.47	0.33	0.45
BW	0.57	0.51	0.65
WW	0.45	0.52	0.52
YW	0.34	0.64	0.45
Mlk	0.24	0.32	0.34
MCE	NA	NA	0.32
Stay	NA	NA	0.58
CW	0.54	0.48	0.59
Mrb	0.65	0.57	0.63
REA	0.58	0.60	0.59
BF	0.50	0.56	0.29
SF	NA	NA	0.53

[a] When used on the American Angus Association's population
[b] When used on American Simmental/SimAngus™ population

16 April 2012

http://www.simmental.org/site/pdf/register/April%2012%20Register%20The%20Future%20is%20Here.pdf

Hereford announces genomic-enhanced EPDs (8/20/12)

1,200 records in training

[Home](#) > [News](#) > [Latest](#) > Hereford introduces genomic-enhanced EPDs

Hereford introduces genomic-enhanced EPDs

American Hereford Association | Updated: August 20, 2012

The American Hereford Association (AHA) is the first beef breed to develop and market its own genomic predictions.

The AHA approach is the first of its kind to work with the scientific community and the National Beef Cattle Evaluation Consortium (NBCEC) to build its own training and validation population. This approach is important because AHA now has access to all of the genotypes, phenotypes and pedigrees, which will allow the Association and its members to continue to train and build the Hereford-specific panel.

Today more than 1,200 Herefords have been 50k genotyped and eight sires whole-genome sequenced. This population has been used to train and validate the Hereford-specific panel. Dorian Garrick, Iowa State University Lush Chair in animal breeding and genetics and NBCEC executive director, has led the research and development.

According to Garrick AHA took a pro-active approach testing and validating the tools available to make sure when releasing a Hereford genomic product it was reliable and useful to AHA members. During this process the Association aligned itself with researchers and worked collaboratively with the NBCEC, U.S. Department of Agriculture (USDA) Meat Animal Research Center and other global Hereford associations.

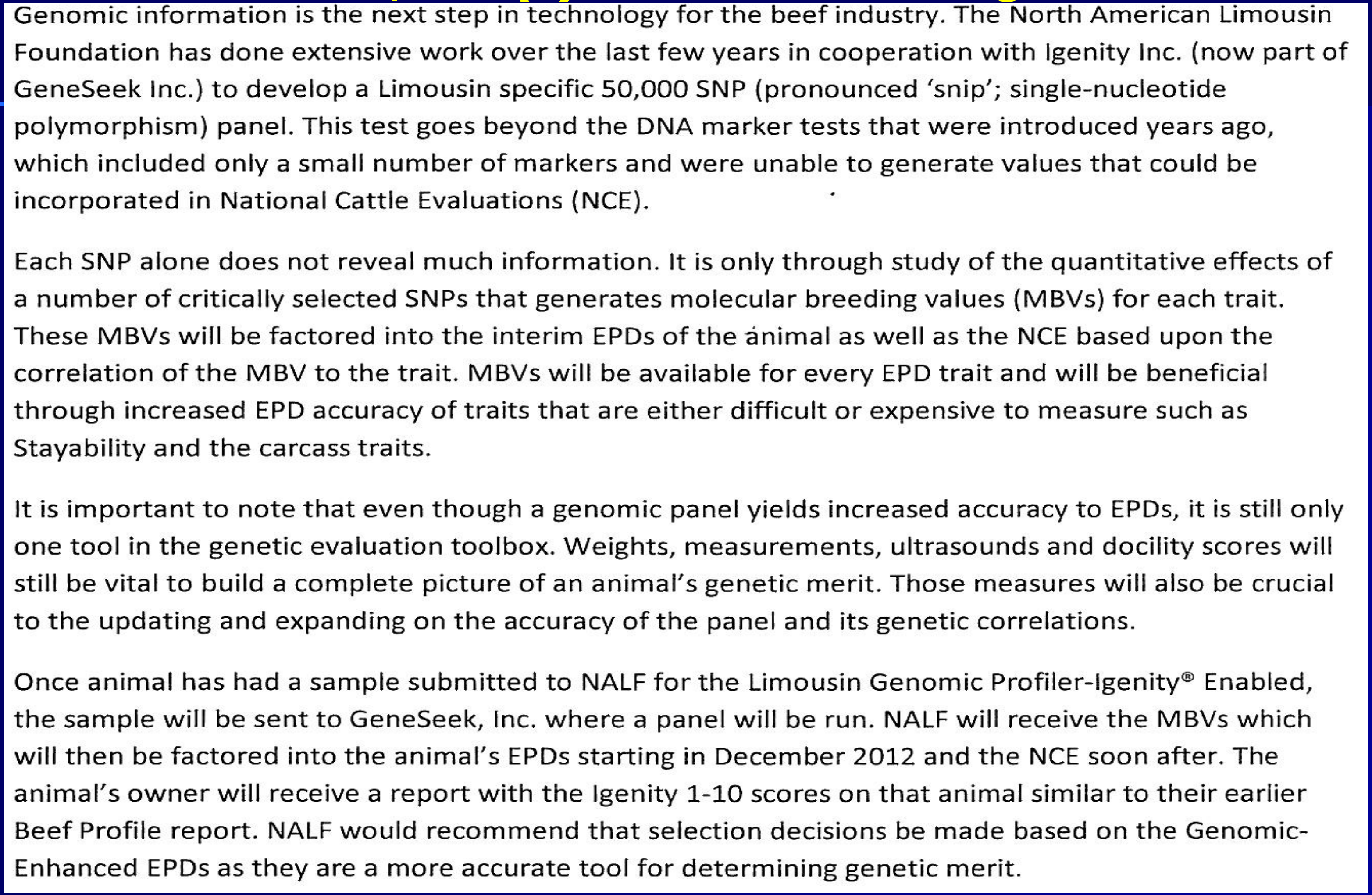
In late June AHA transitioned its DNA testing to GeneSeek Inc. located in Lincoln, Neb. With this move, Hereford breeders have the option to utilize a 50k panel to obtain genomic information to enhance the accuracy of Hereford expected progeny differences (EPDs). The genomic information obtained is blended with conventional EPDs to produce genomic-enhanced EPDs (GE-EPDs). GE-EPDs are available on all traits reported by the AHA.

- Arkansas agritourism pushes on d
- Commentary: Family farmer: Who
- Low Mississippi River
- NBAF: The reviews are done and i
- Grain TV: Crop tour results to mov Sunday night
- Feeder cattle review: Cost-of-gain markets
- USDA feeder cattle market: Yearli steady

http://www.cattlenetwork.com/e-newsletters/drovers-daily/166794826.html

Limousin plans to start using DNA in EPDs in December 2012

2,400 (?) records in training



Genomic information is the next step in technology for the beef industry. The North American Limousin Foundation has done extensive work over the last few years in cooperation with Igenity Inc. (now part of GeneSeek Inc.) to develop a Limousin specific 50,000 SNP (pronounced 'snip'; single-nucleotide polymorphism) panel. This test goes beyond the DNA marker tests that were introduced years ago, which included only a small number of markers and were unable to generate values that could be incorporated in National Cattle Evaluations (NCE).

Each SNP alone does not reveal much information. It is only through study of the quantitative effects of a number of critically selected SNPs that generates molecular breeding values (MBVs) for each trait. These MBVs will be factored into the interim EPDs of the animal as well as the NCE based upon the correlation of the MBV to the trait. MBVs will be available for every EPD trait and will be beneficial through increased EPD accuracy of traits that are either difficult or expensive to measure such as Stayability and the carcass traits.

It is important to note that even though a genomic panel yields increased accuracy to EPDs, it is still only one tool in the genetic evaluation toolbox. Weights, measurements, ultrasounds and docility scores will still be vital to build a complete picture of an animal's genetic merit. Those measures will also be crucial to the updating and expanding on the accuracy of the panel and its genetic correlations.

Once animal has had a sample submitted to NALF for the Limousin Genomic Profiler-Igenity® Enabled, the sample will be sent to GeneSeek, Inc. where a panel will be run. NALF will receive the MBVs which will then be factored into the animal's EPDs starting in December 2012 and the NCE soon after. The animal's owner will receive a report with the Igenity 1-10 scores on that animal similar to their earlier Beef Profile report. NALF would recommend that selection decisions be made based on the Genomic-Enhanced EPDs as they are a more accurate tool for determining genetic merit.

http://www.nalf.org/pdf/2012/dna-genomics/Limousin_Genomic_Profiler_and_Genomic-Enhanced_EPDs_7.27.12.pdf


The Future
NEXT EXIT

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)

USDA funded projects – competitive call for proposals: Part 1 (old CREES proposals)

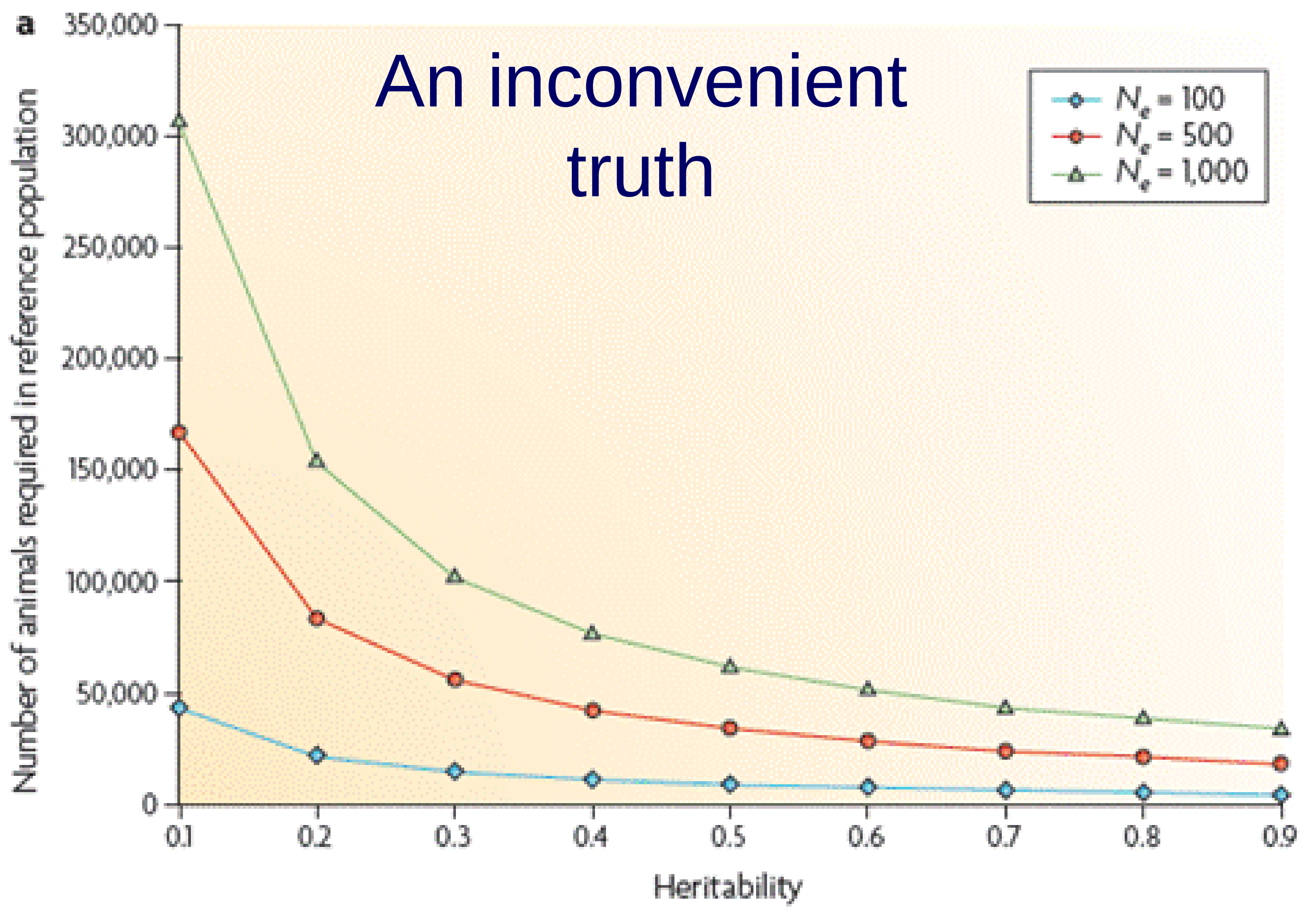
- **Identification of molecular markers to improve fertility of beef cattle** (Thomas, CO) – finished 12/2011
  - >10,000 DNA samples and phenotypes on heifers
- **BIGS – Bioinformatics to implement genomic selection** (Garrick/Snelling/Golden)/ **Enhanced Bioinformatics to implement genomic selection (BIGS)** (Garrick, Dekkers, Fernando, Reecy, Rothschild) finishes 4/30/2014 See website http://bigs.ansci.iastate.edu/
- **Integrating DNA information into beef cattle production systems** (Van Eenennaam, CA) – finishes 12/2013
  - 7,000 DNA samples & weaning weight records, 4500 carcass records

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)
  - 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 200 cattle from up to 10 different beef breeds
  - $3 million, 5 year project; Jan 2013 – December 2017

Effect of population size and heritability on the number of animals required in the training population (for an accuracy of 0.7)

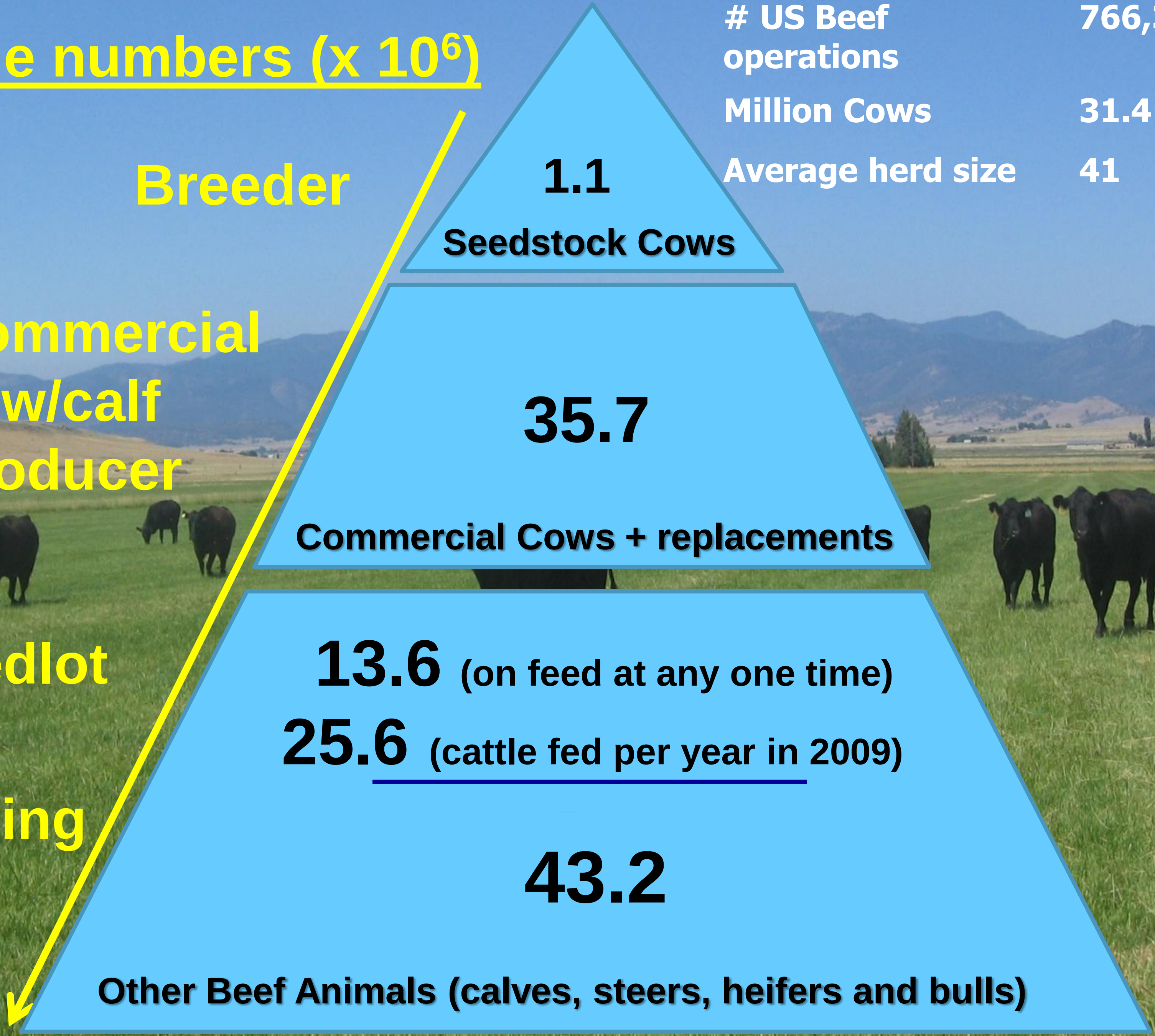


An inconvenient truth

Goddard, M. E., and B. J. Hayes. 2009. Mapping genes for complex traits in domestic animals and their use in breeding programmes. Nature Reviews Genetics 10: 381-391.

US cattle numbers (x 10^6)

# US Beef operations	766,350
Million Cows	31.4
Average herd size	41



Breeder

Commercial cow/calf producer

Feedlot

Processing

Retailer

1.1

Seedstock Cows

35.7

Commercial Cows + replacements

13.6 (on feed at any one time)

25.6 (cattle fed per year in 2009)

43.2

Other Beef Animals (calves, steers, heifers and bulls)

Extracting DNA multiple times in different labs for different applications makes about as much sense as simultaneously paying to have access to all of the following communication devices

TECHNOLOGICAL CHALLENGE: How do we collect phenotypes and DNA on all animals and make genotype information available to all sectors?

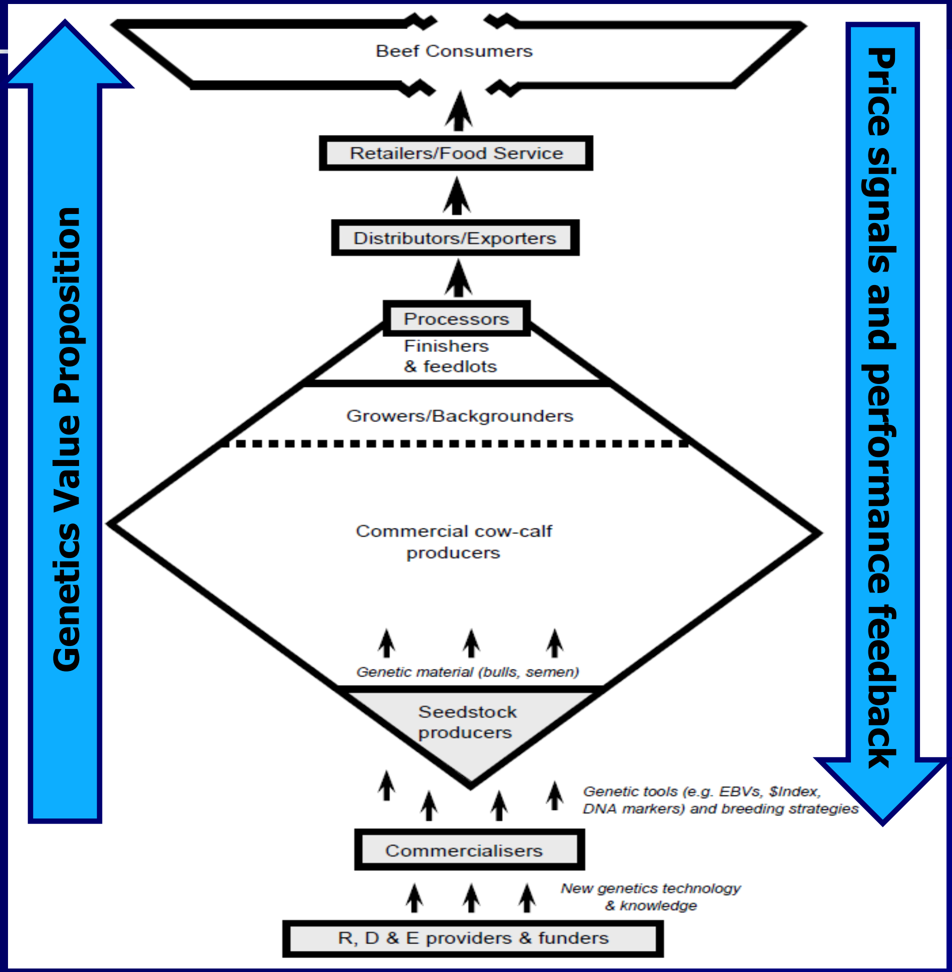
ONLY THESE SECTORS PRODUCE NEW ANIMALS

Use	Seedstock	Commercial	Feedlot	Processor
DNA-assisted selection	XXXX	X	XXXX	XXXX
Parentage	XX	X		
Recessive allele testing	XX	X		
Control of Inbreeding	XX	X		
Mate selection	XX	X		
DNA-assisted management/purchasing		X	XX	XX
Product differentiation				XXXX
Traceability				XX

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

Cattle industry Sector	Type of DNA product // DNA information access required	Cost?? ($US)	Mobile Device// Data Access Plan
Nucleus seedstock/AI bulls	Full genome sequence	$250	ipad
Seedstock/bull multiplier	HD 770 K genotype	$50	iphone
Registered females and stock bulls for commercial sector	50K genotype + parentage + single gene traits/recessives	$25	Talk and text smart phone
Commercial cattle – Marker-assisted management (MAM), replacement heifer selection	Imputation LD chip + parentage + single gene traits/recessives	$10	Prepaid cellular phone
Feedlot cattle purchasing, sorting and marker-assisted management (MAM)	Access genotypes from supplier (subset of LD imputation chip).	<$1	Pay as you go contract
Traceability for voluntary labelling e.g. Angus beef	Access genotypes from supplier (subset of LD imputation chip).	<$1	Friends and family plan
Traceability for disease outbreak/contaminated meat	Access genotypes from supplier (subset of LD imputation chip).	<$1	Emergency only phone (911 calls)

Industry structure may evolve to enable the exchange of information and value between the different sectors.



Genetics Value Proposition

Price signals and performance feedback

Beef Consumers

Retailers/Food Service

Distributors/Exporters

Processors

Finishers
& feedlots

Growers/Backgrounders

Commercial cow-calf
producers

Genetic material (bulls, semen)

Seedstock
producers

*Genetic tools (e.g. EBVs, $Index,
DNA markers) and breeding strategies*

Commercialisers

*New genetics technology
& knowledge*

R, D & E providers & funders

For widespread technology adoption, breeders need to be adequately rewarded for making DNA investments and selection decisions for traits that benefit the different sectors of the beef industry.

Parnell, P.F. 2007. Effective value chain partnerships are essential for rapid adoption of beef genetics technology. Association for the Advancement of Animal Breeding and Genetics. 18. 167-174 .

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

Ramifications of genomics to beef industry

- The benefits of genomics are best captured in well-structured industries that are already making significant genetic progress
- May encourage more vertical integration to collect phenotypes to enable predictions for economically relevant traits for all sectors
- May see genetic evaluations developed for novel traits – if large enough phenotyped populations can be amassed
- Feedlots stand to gain the most from collecting phenotypes and sharing data back with suppliers
- Will beef follow the pig/poultry model of developing a single breeding objective optimized for industry good?

Concluding thought….

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.

Van Eenennaam, A. L., and D. J. Drake. 2012. Where in the beef cattle supply chain might DNA tests generate value? Animal Production Science. 52(3) 185-196.

Questions?