Where are we with beef cattle genomics and what is the opportunity?

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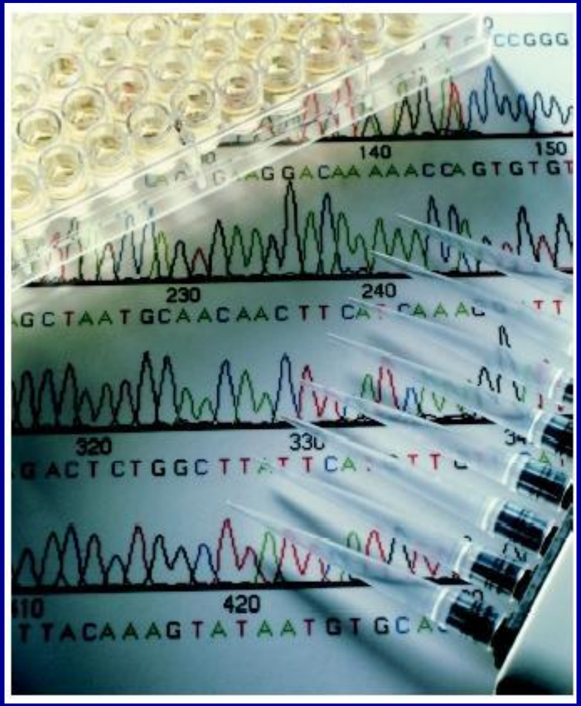


animalscience.ucdavis.edu/animalbiotech

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 national beef cattle evaluations
- Development of tests for hard-to-measure traits and value to beef cattle sectors
- Opportunity for Simplot

Animal breeders have used the resemblance between relatives to select parents of the next generation and make genetic change

Rate of change is accelerated when breeders can accurately identify those individuals that have the best genetics at a young age

ΔG = ***intensity of selection X***

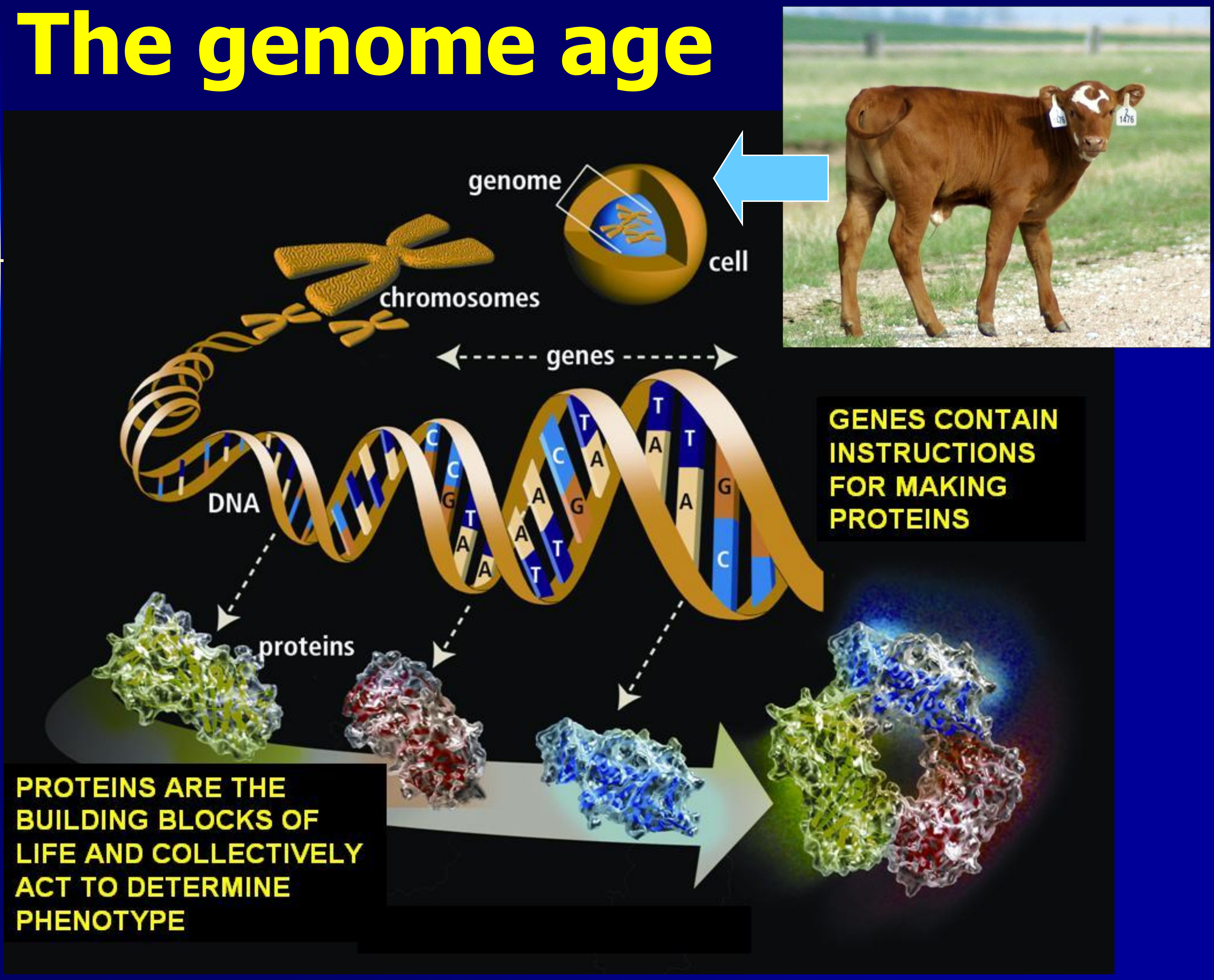
accuracy of selection X

____

(√genetic variance in population /

generation interval)

The genome age

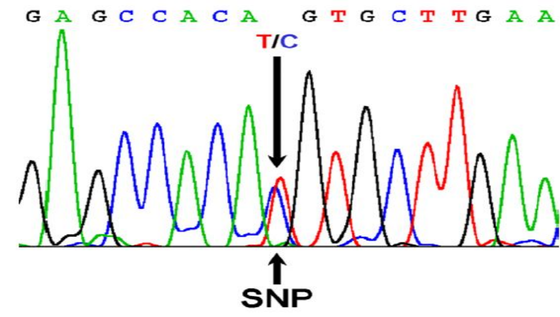


GENES CONTAIN INSTRUCTIONS FOR MAKING PROTEINS

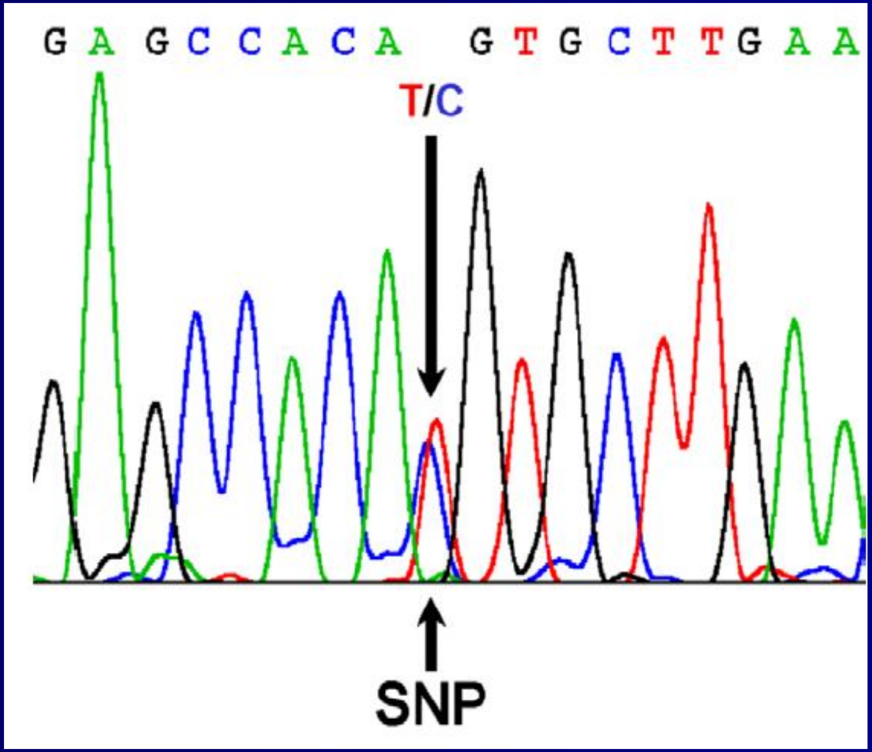
PROTEINS ARE THE BUILDING BLOCKS OF LIFE AND COLLECTIVELY ACT TO DETERMINE PHENOTYPE

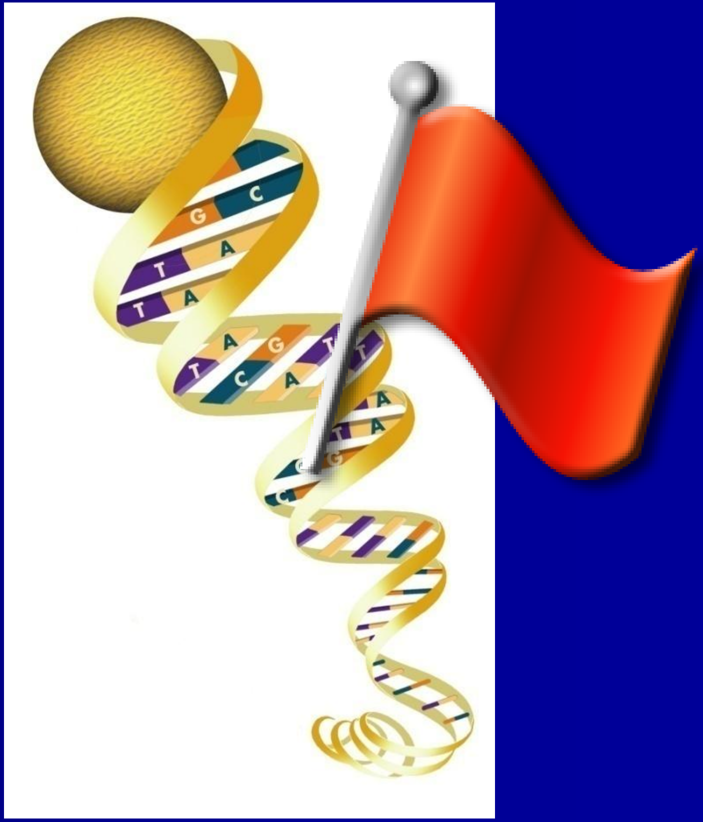
What is a Genetic Marker ?

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





High-throughput genotyping technology enabled a new approach

- The sequencing of the bovine genome allowed for the development of a 50,000 marker chip!
- Can simultaneously test 50,000 markers

With high density (50K) SNP chips it is possible to:

- Divide genome into 50,000 chromosome segments based on marker intervals
- Marker density must be sufficiently high to ensure that all of the genes affecting a traits are “linked” (close to) a marker
- Idea is to capture all genetic variance with evenly spread markers and assign an “EPD” value to each segment

What is needed for "genomic" selection?

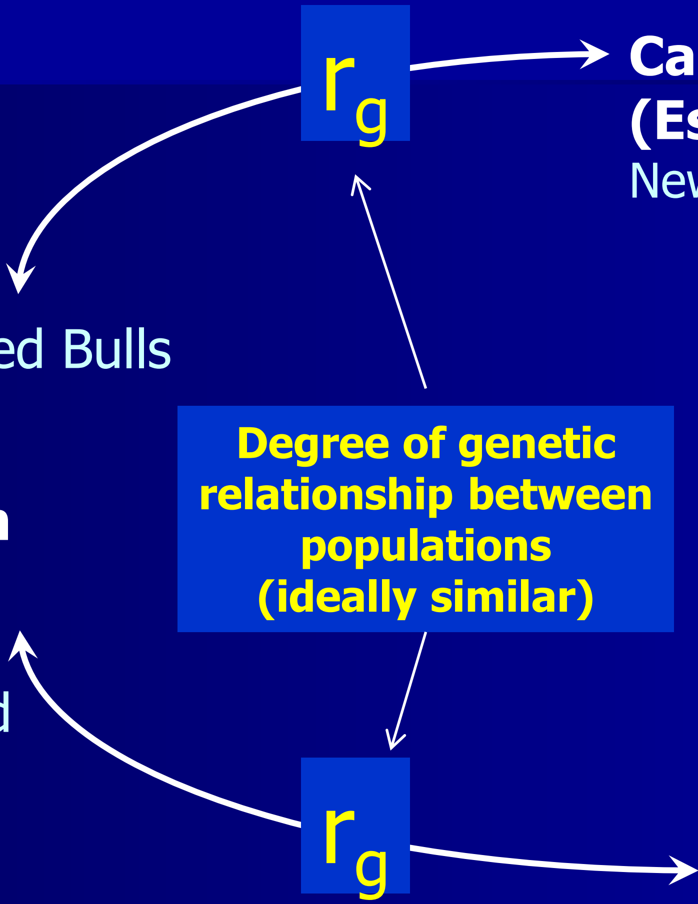
THEORY

- Population
- 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 predict the merit of new animals, not contained in the training data set

Implementation of Genomic Selection



Calibration (Validation) (Estimation of r_g):
New Progeny of Tested Bulls

Training 1:
Old Progeny Tested Bulls

Degree of genetic relationship between populations (ideally similar)

Retraining each generation:
Old Bulls & New Progeny of Tested Bulls

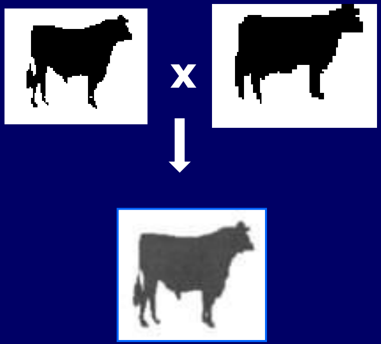
Application:
New Sire Candidates

Slide modified from Marc Thallman, US MARC

Breeding value prediction in Dairy Sires

Graphic kindly provided by Gonzalo Rincon

**Young sire
Parent Average**



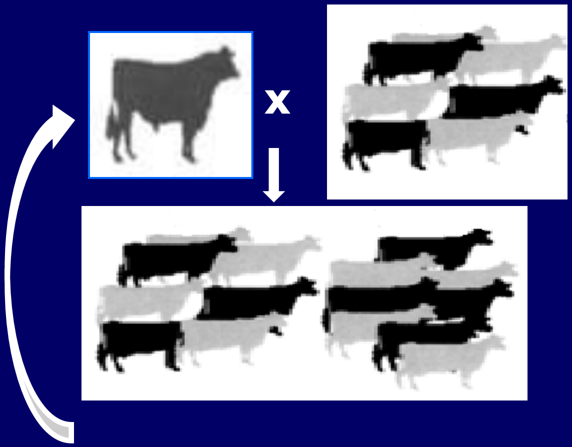
Birth

A_S A_D

Mendelian Sampling ?

Reliability **0.20**

**Young sire
Progeny Test**



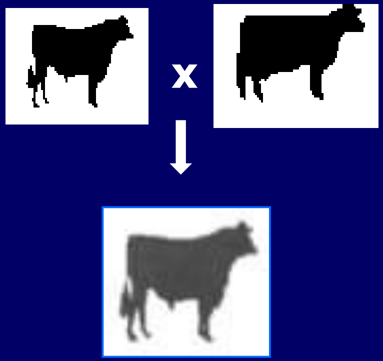
5 years; $50,000 cost

A_S A_D

Mendelian Sampling

Reliability **0.80**

**Young sire
Genomic
Selection**



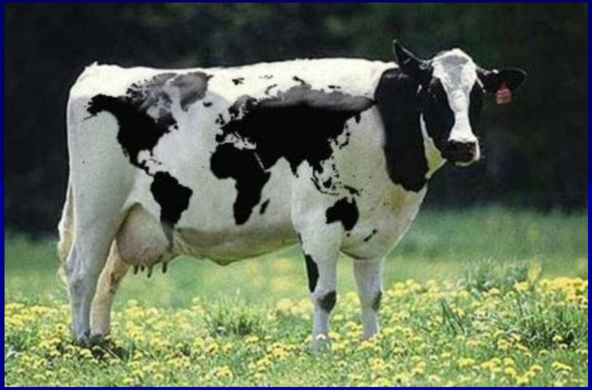
Birth; << $50,000 cost

A_S A_D

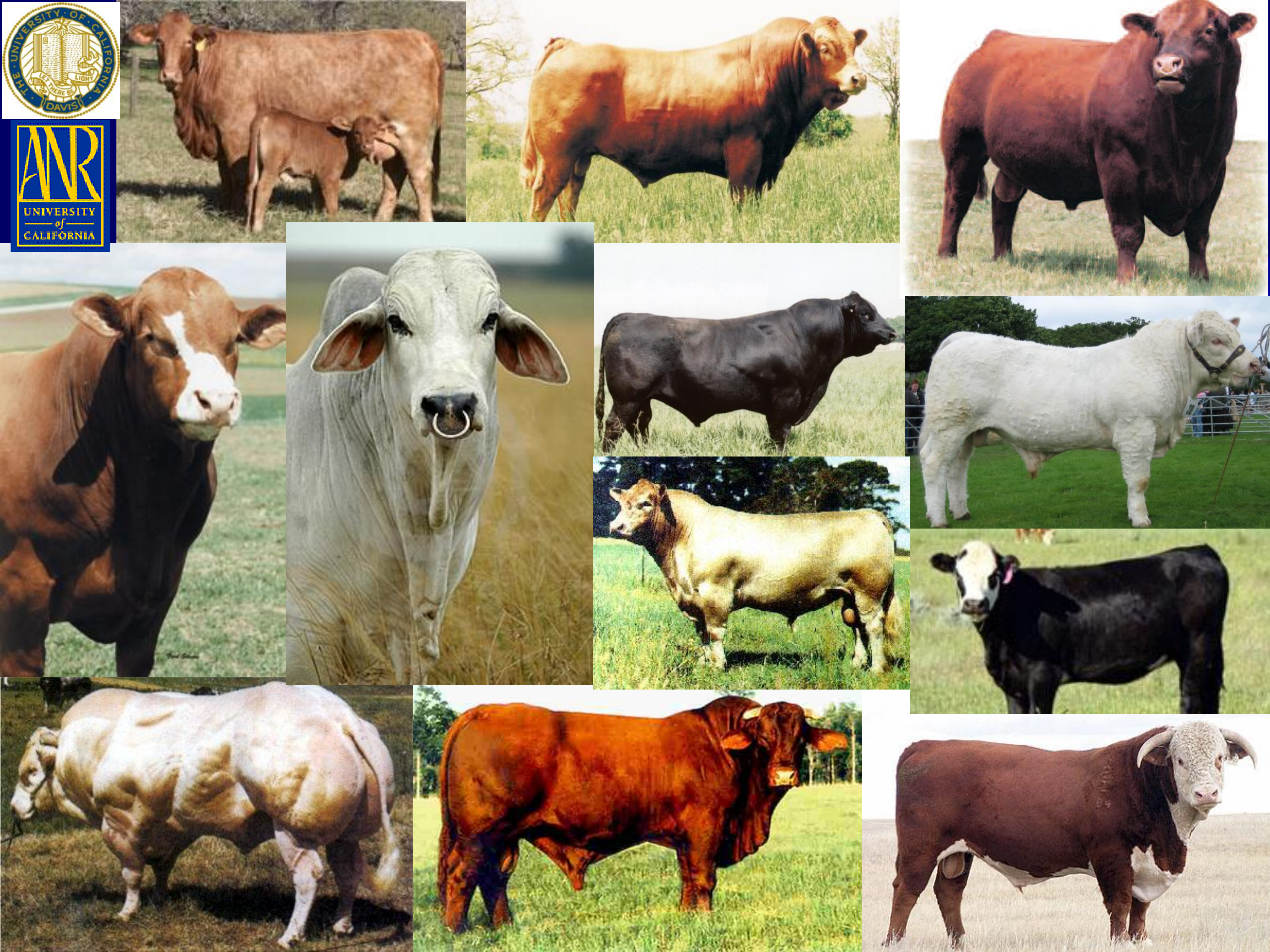
Mendelian Sampling

Reliability **0.65**

Dairy industry suited to WGS



- High use of AI
- Mostly 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



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

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– 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?

? Do predictions work across breeds?

? What is the value generated by the increased accuracy?

? Does this technology change optimal breeding program design?

What commercial products are out there for beef cattle producers?

GeneSTAR® SureTRAK® SireTRACE™ GeneSTAR®

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™

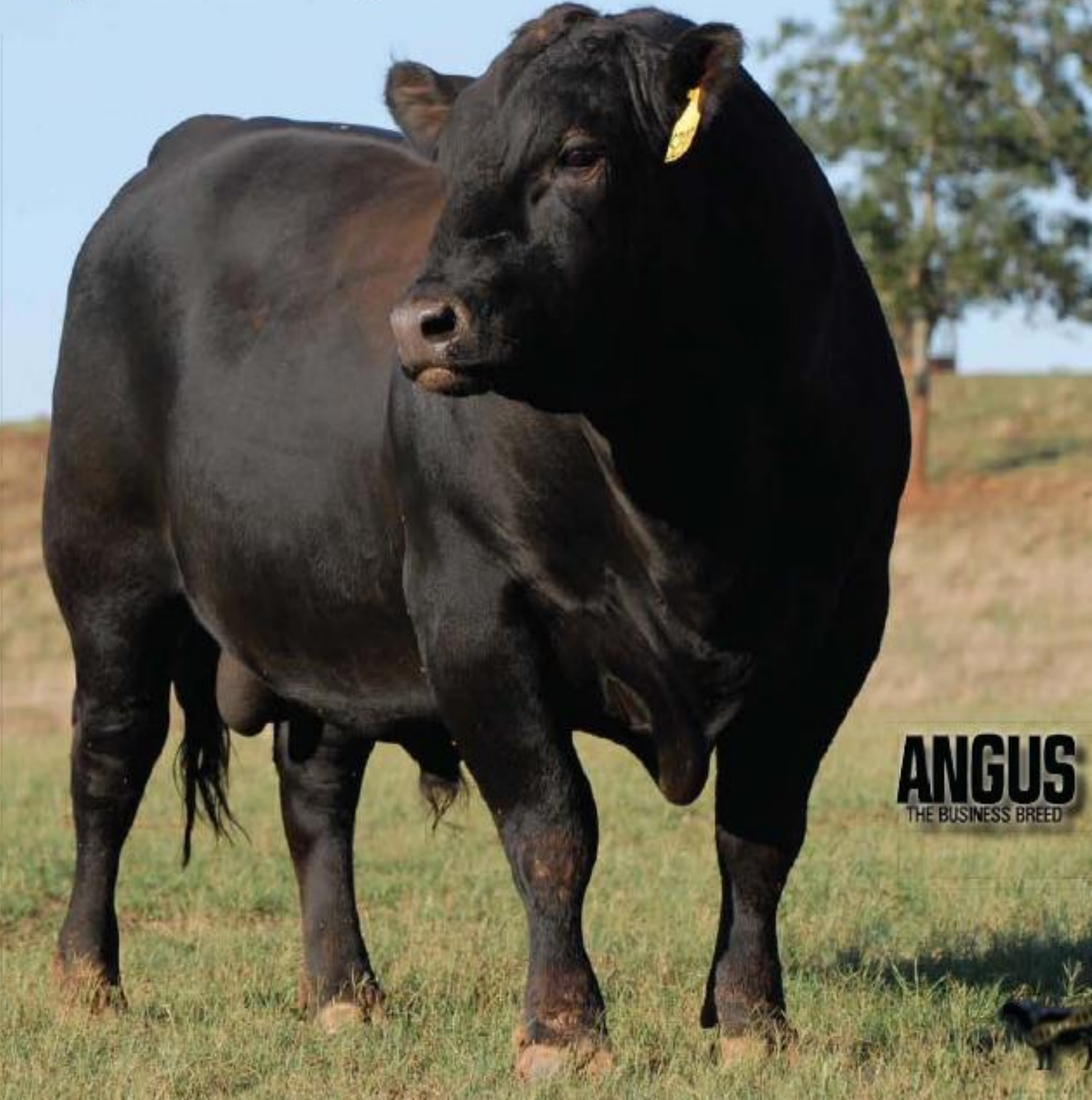
METAMORPHIX, INC.

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



ANGUS
THE BUSINESS BREED

Lead Today with 50K

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

Pfizer Animal Health
Animal Genetics

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

Black Angus Sire

G A R Predestined

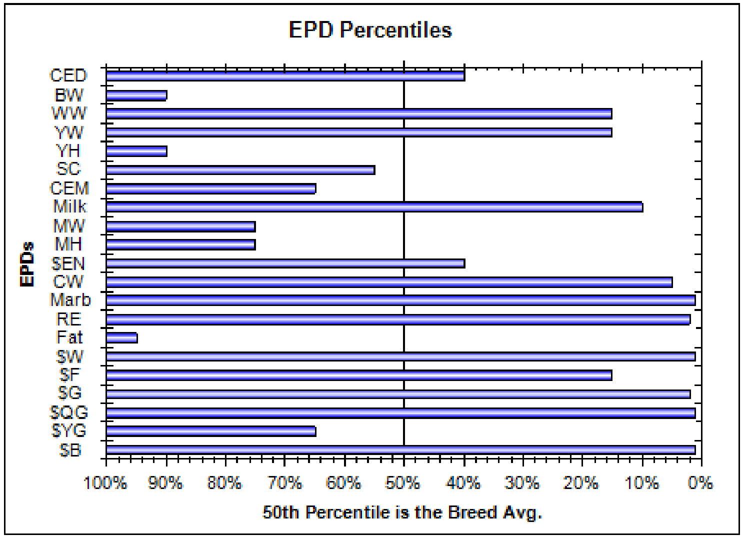
Reg. No.: 13395344
Calved: 8/16/1999
Tattoo: 5899
Semen: $25
Certificates: $20
Spring 2010 EPD

G A R Predestined:
From start to finish--conception to carcass--no other bull in the beef business today adds as much real value to cattle as Predestined. Ranking as the #1 bull for $B in the breed--our customers tell us that their Predestined-sired cattle return the most dollars to their pockets--they know that $B works. Unlike any other 036 son, Predestined tones down size, adds depth of flank, superior feet and legs and a pleasant disposition to his offspring. His conception rate is high and he's been a standout in timed-AI programs. His progeny look good--his bulls are thick and his heifers are fancy--and they always display additional shape and capacity. He ended 2006 as our top-seller and rightfully so--Predestined's many talents for creating value are for real.

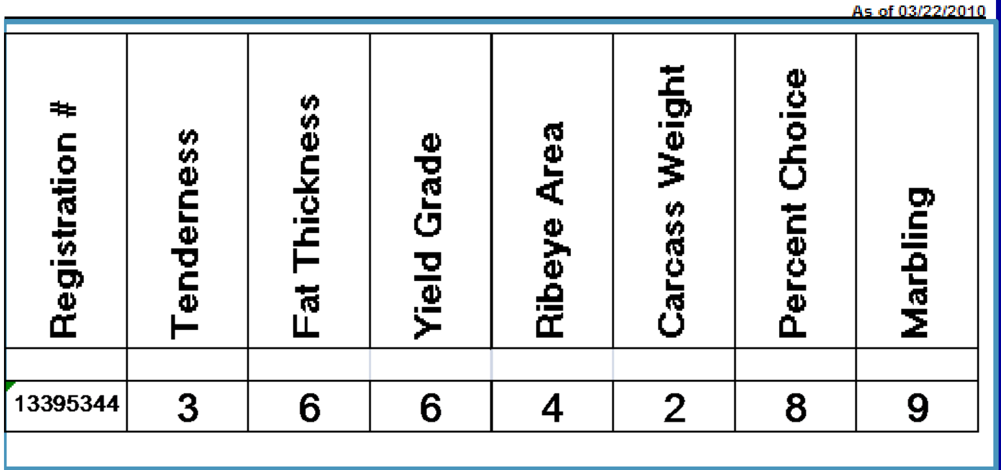
Production						Maternal					
CED Acc	BW Acc	WW Acc	YW Acc	YH Acc	SC Acc	CEM Acc	Milk Acc	MkH MkD	MW Acc	MH Acc	EN$
+7 .84	+4.1 .97	+53 .96	+99 .94	+0 .96	+.31 .95	+6 .80	+28 .85	345 1135	+13 .81	+.2 .81	+5.24

Carcass					Usnd	$Values					
CW Acc	Marb Acc	RE Acc	Fat Acc	Grp Prog	UGrp UProg	Wean	Feedlot	Grid	$QG	$YG	Beef
+26 .82	+1.07 .84	+.59 .82	+.046 .81	47 261	4269 11990	37.39	37.08	38.21	35.04	3.17	69.78

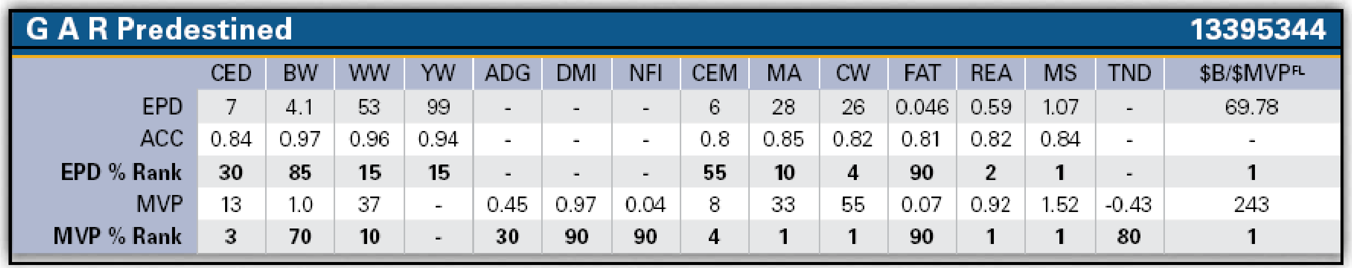
GeneSTAR										
	QG1	na	QG2	na	QG3	na	QG4	na	QG GPD	
	T1	★	T2	0	T3	0	-	-	T GPD	-0.35
	FE1	na	FE2	na	FE3	na	FE4	na	FE GPD	


EPD Percentiles

Current Sires Percent Breakdown


As of 03/22/2010

Registration #	Tenderness	Fat Thickness	Yield Grade	Ribeye Area	Carcass Weight	Percent Choice	Marbling
13395344	3	6	6	4	2	8	9


G A R Predestined 13395344

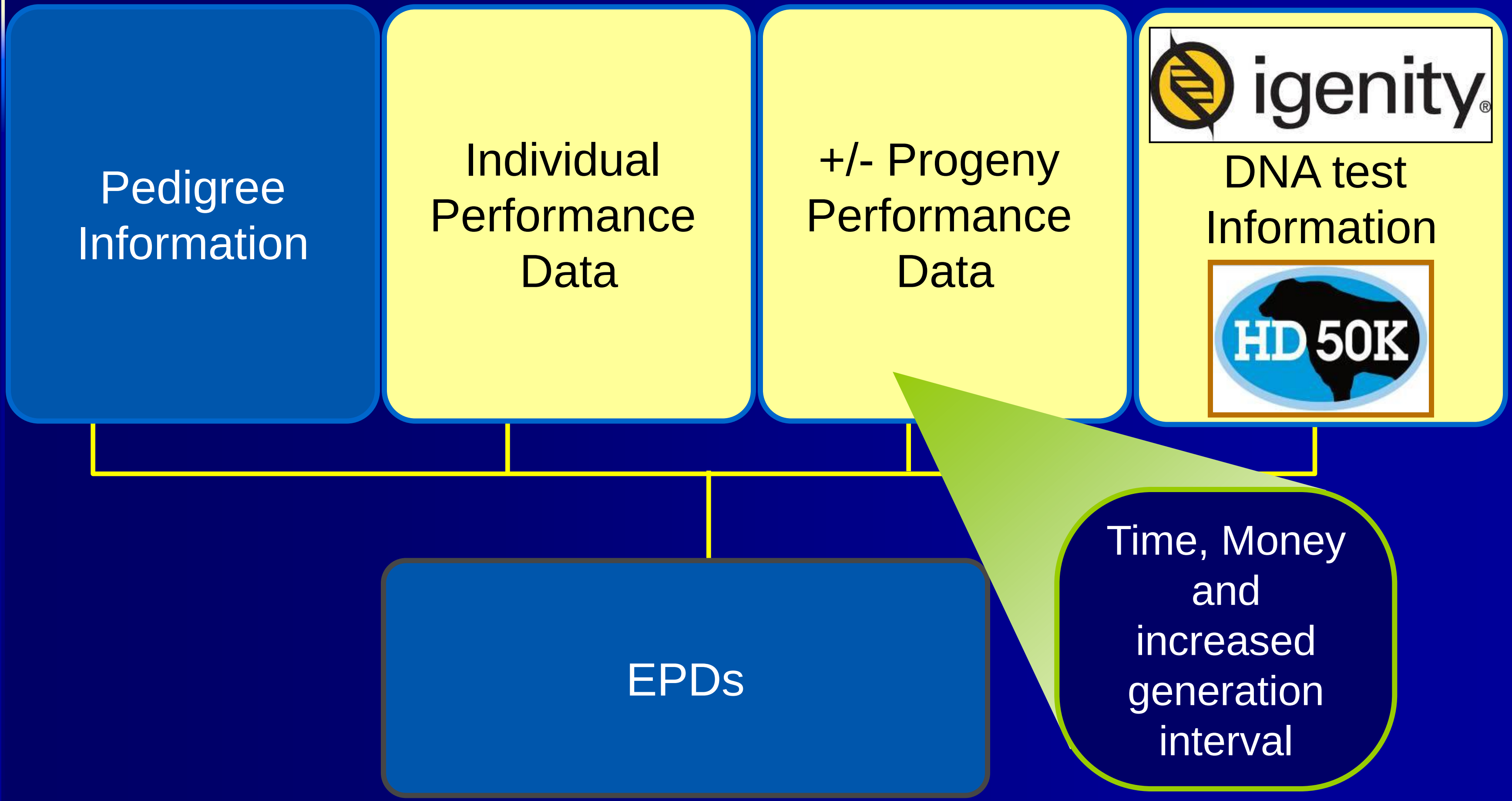
	CED	BW	WW	YW	ADG	DMI	NFI	CEM	MA	CW	FAT	REA	MS	TND	$B/$MVP^FL
EPD	7	4.1	53	99	-	-	-	6	28	26	0.046	0.59	1.07	-	69.78
ACC	0.84	0.97	0.96	0.94	-	-	-	0.8	0.85	0.82	0.81	0.82	0.84	-	-
EPD % Rank	**30**	**85**	**15**	**15**	**-**	**-**	**-**	**55**	**10**	**4**	**90**	**2**	**1**	**-**	**1**
MVP	13	1.0	37	-	0.45	0.97	0.04	8	33	55	0.07	0.92	1.52	-0.43	243
MVP % Rank	**3**	**70**	**10**	**-**	**30**	**90**	**90**	**4**	**1**	**1**	**90**	**1**	**1**	**80**	**1**

Simplot 9/25/2012

Need to integrate DNA information into National Cattle Evaluation (NCE)

“*information from DNA tests only has value in selection when incorporated with all other available forms of performance information for economically important traits in NCE, and when communicated in the form of an EPD with a corresponding BIF accuracy. For some economically important traits, 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 tests are another source of information to improve the accuracy of EPDs



Pedigree Information

Individual Performance Data

+/- Progeny Performance Data

igenity

DNA test Information

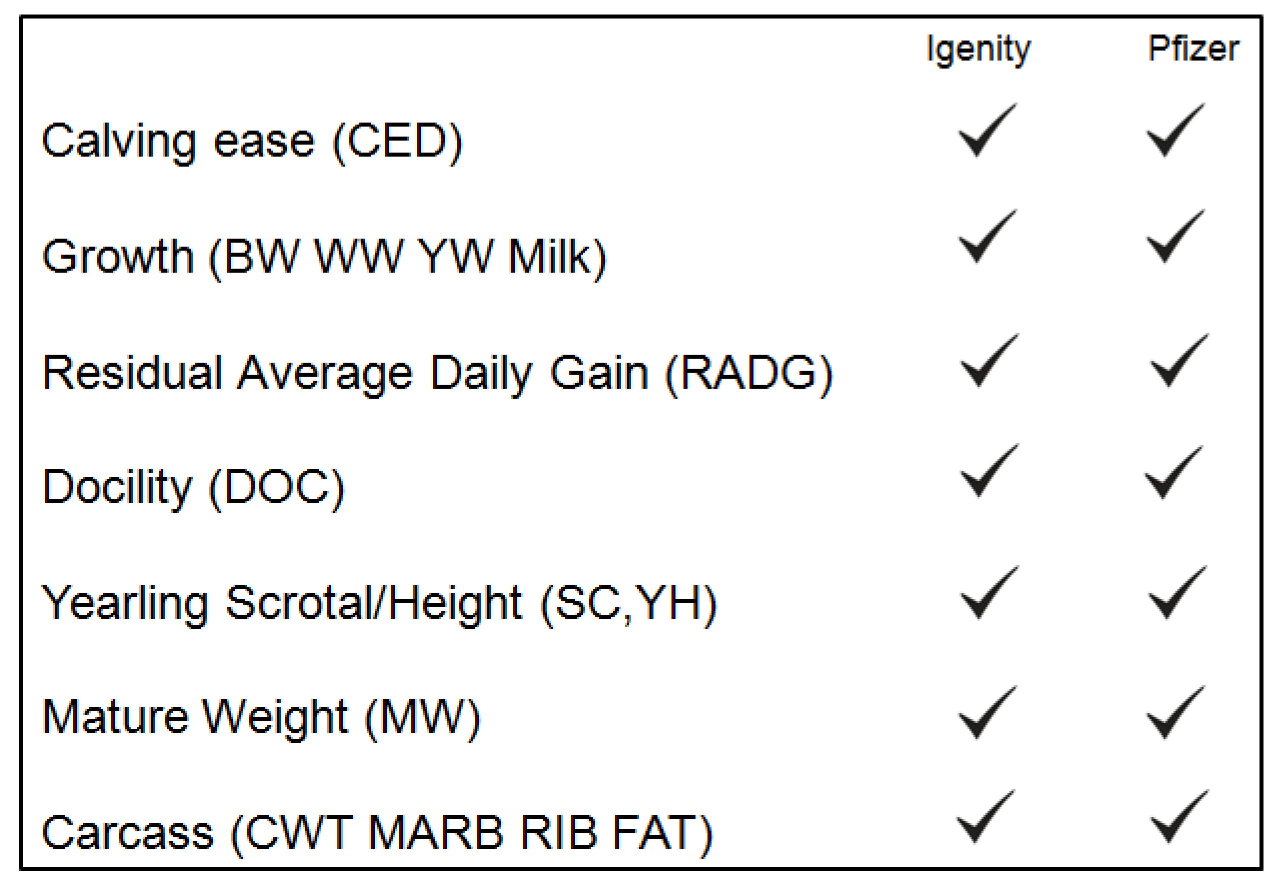
HD 50K

EPDs

Time, Money and increased generation interval

Modified from slide from Kent Anderson, Pfizer Animal Genetics, presented at BIF 2011

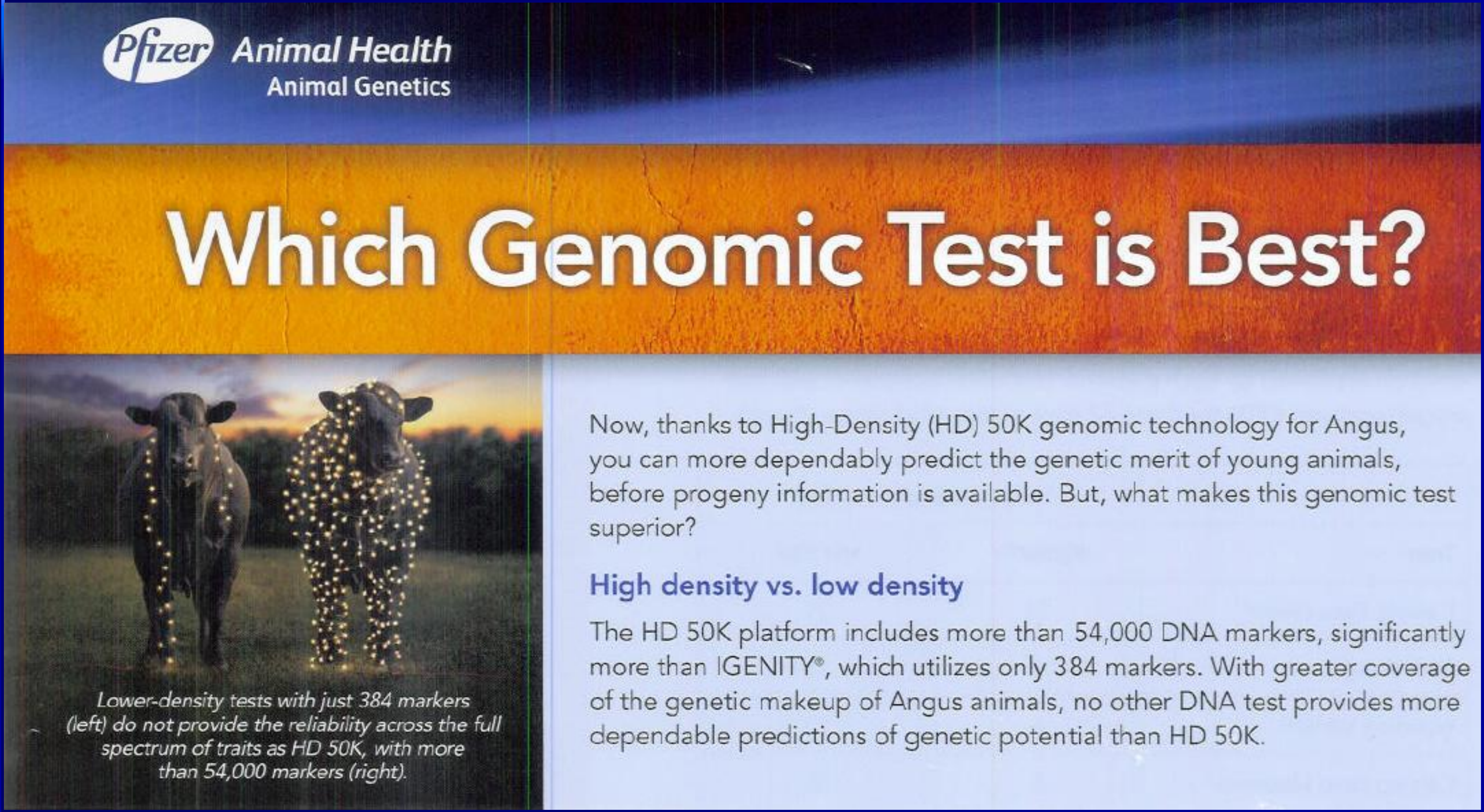
American Angus Association performs weekly evaluations with genomic data – recently updated to include new traits



	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)

So the question changed from “do they work (validation)” to “how well do they work (calibration or estimation of r_g)”?



Pfizer Animal Health
Animal Genetics

Which Genomic Test is Best?

Lower-density tests with just 384 markers (left) do not provide the reliability across the full spectrum of traits as HD 50K, with more than 54,000 markers (right).

Now, thanks to High-Density (HD) 50K genomic technology for Angus, you can more dependably predict the genetic merit of young animals, before progeny information is available. But, what makes this genomic test superior?

High density vs. low density

The HD 50K platform includes more than 54,000 DNA markers, significantly more than IGENITY®, which utilizes only 384 markers. With greater coverage of the genetic makeup of Angus animals, no other DNA test provides more dependable predictions of genetic potential than HD 50K.

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)

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

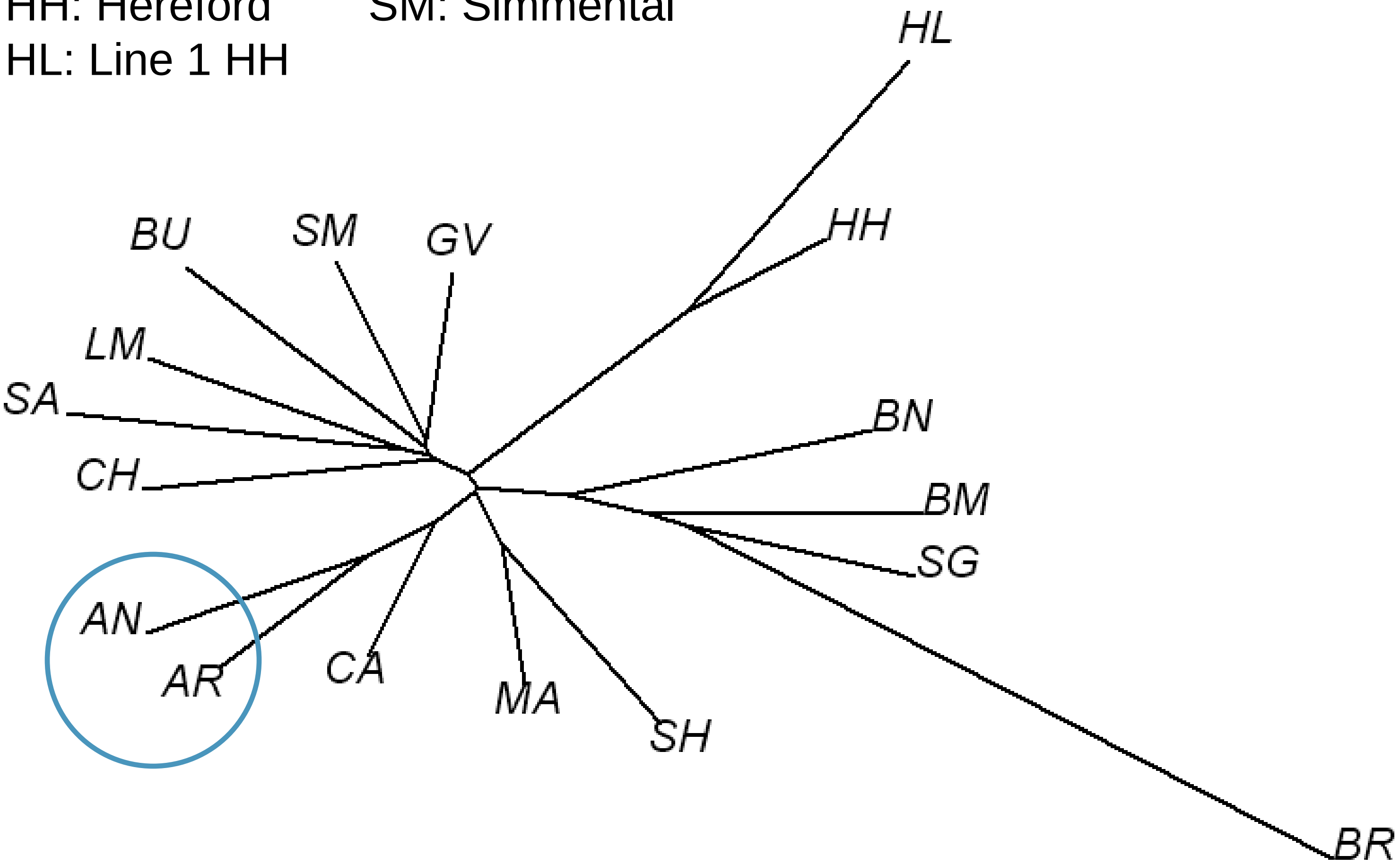
Angus = ASREML 5-fold validation Red Angus = correlation
Training on de-regressed EPDs Saatchi et al (GSE)

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

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

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 NCBEC, 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.

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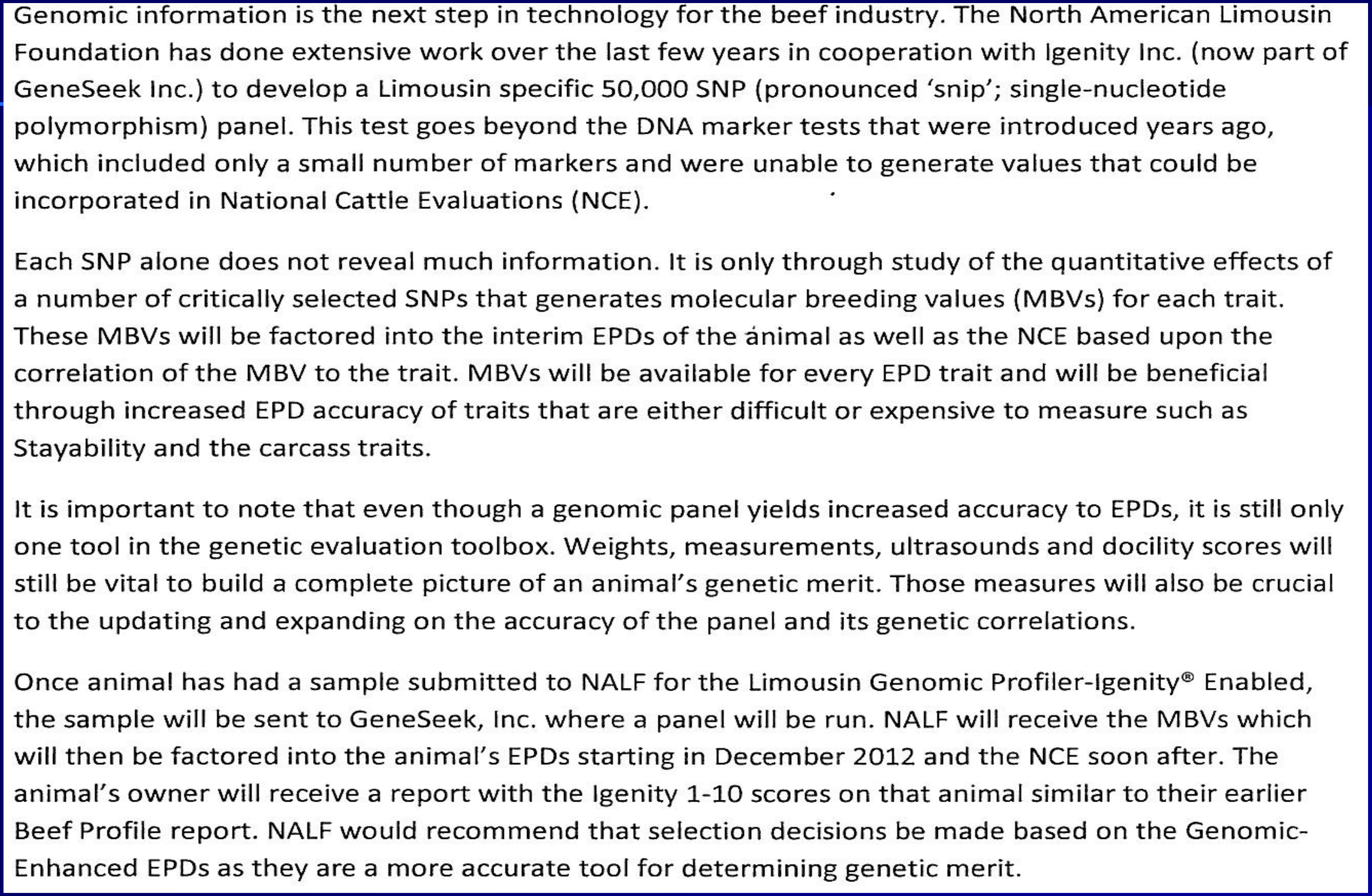
http://www.cattlenetwork.com/e-newsletters/drovers-daily/166794826.html

Limousin plans to start using DNA in EPDs in December 2012



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.

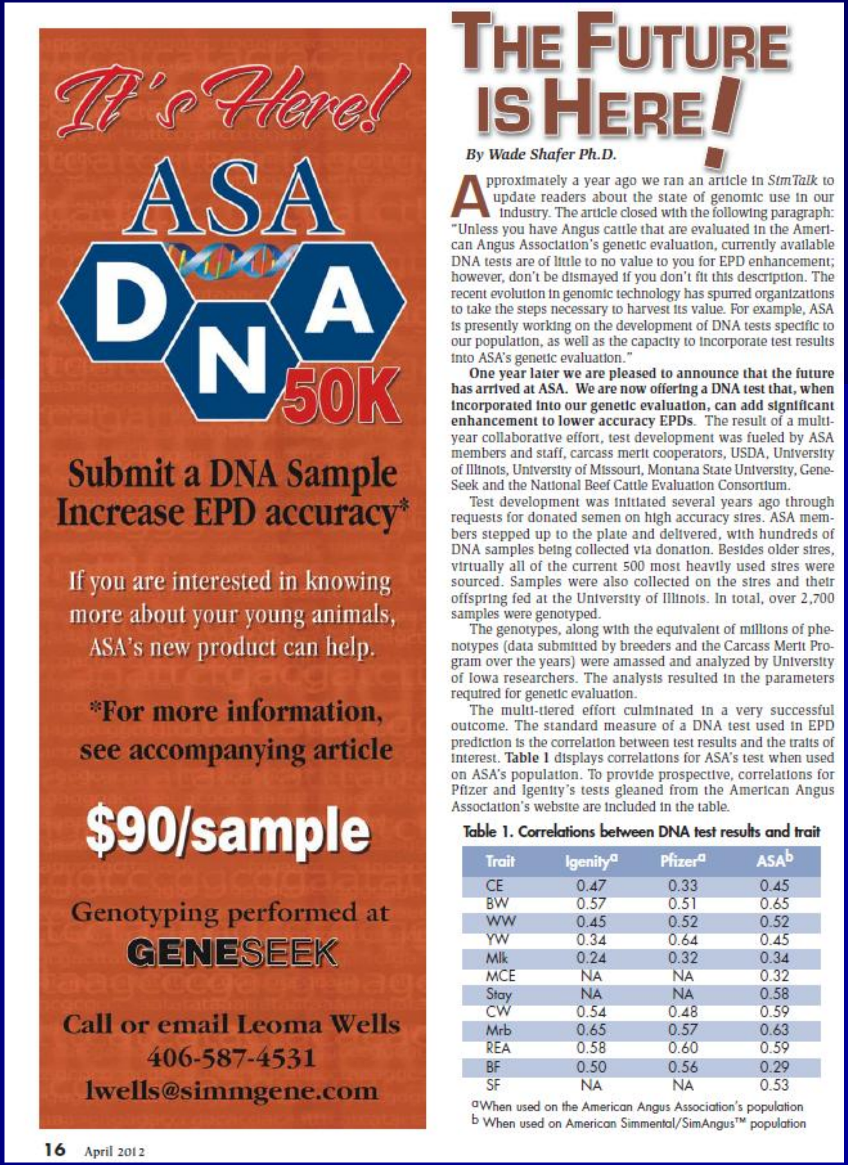
It is important to note that even though a genomic panel yields increased accuracy to EPDs, it is still only one tool in the genetic evaluation toolbox. Weights, measurements, ultrasounds and docility scores will still be vital to build a complete picture of an animal's genetic merit. Those measures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

Simmental

Trait	ASA r	(r²%)	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



It's Here!

ASA DNA 50K

Submit a DNA Sample
Increase EPD accuracy*

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

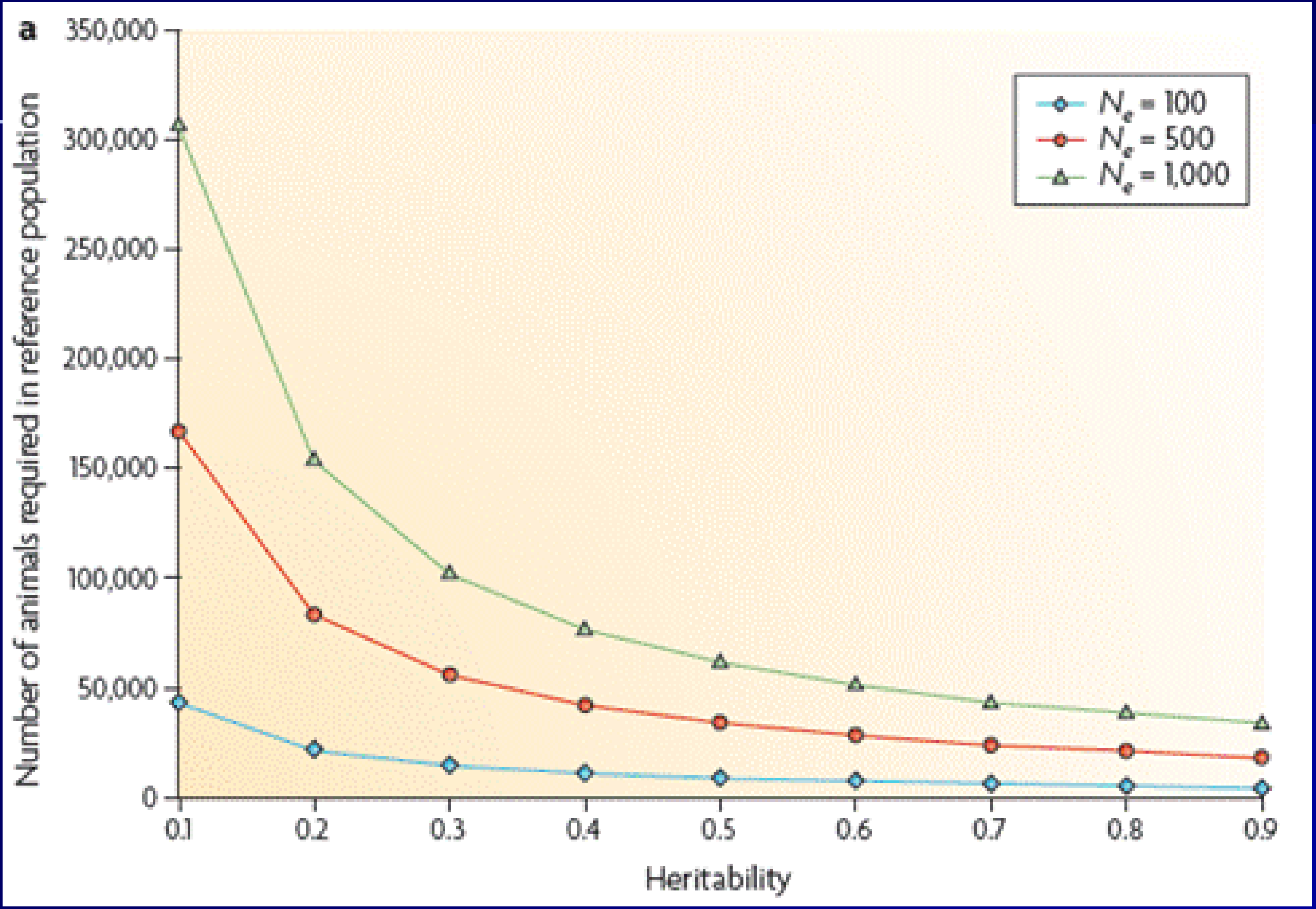
http://www.simmental.org/site/pdf/register/April%2012%20Register%20The%20Future%20is%20Here.pdf


The Future
NEXT EXIT

What is the opportunity?

- What is wrong with the current model
- What needs to happen to make it better
- Is Simplot well-positioned to make this happen
  - How many animals
  - What traits
- Is there sufficient value to make this viable?

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



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.

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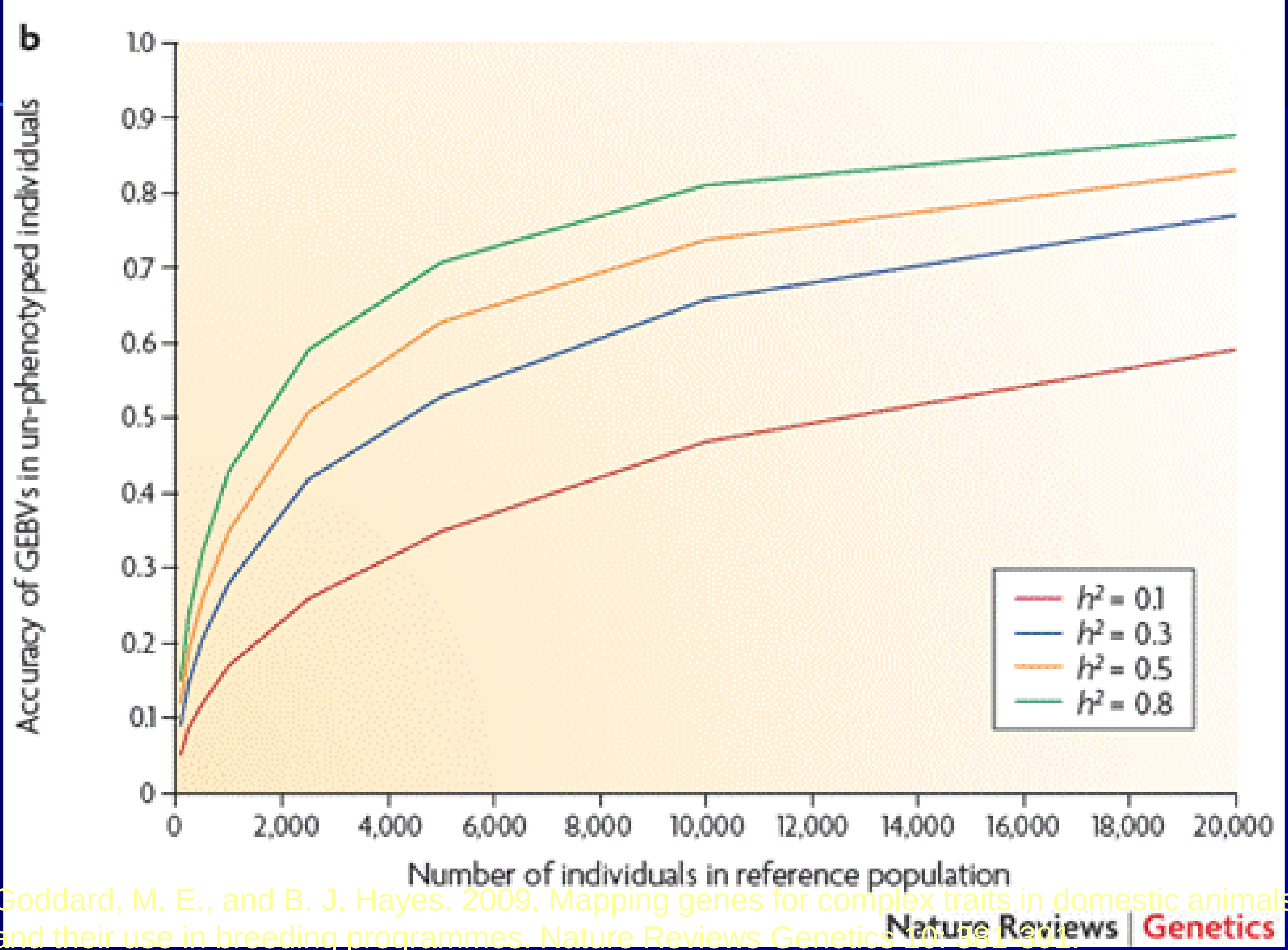

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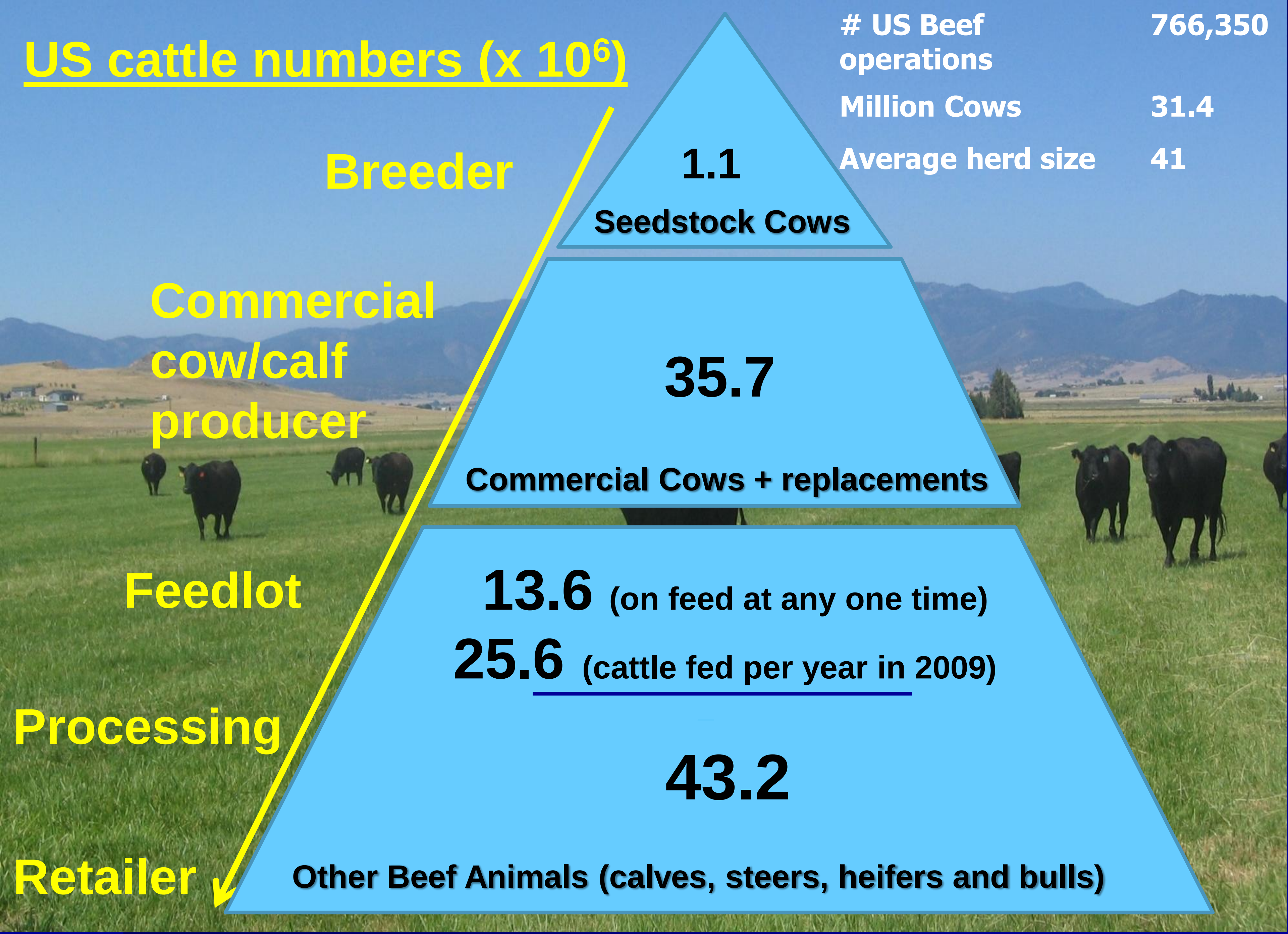
US cattle numbers (x 10^6)

# 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)

Potential uses of genomic information for beef sectors

ONLY THESE SECTORS PRODUCE NEW ANIMALS

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

What will the future look like?

“It is perhaps the cumulative value derived from using DNA test information for multiple purposes (traceability, parentage, genetic defects, selection for difficult to measure traits, marker-assisted management, product differentiation), in combination with the rapidly-declining cost of genotyping, that will ultimately push the economics of DNA-based technologies over the tipping point towards more widespread industry adoption”

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

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)

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

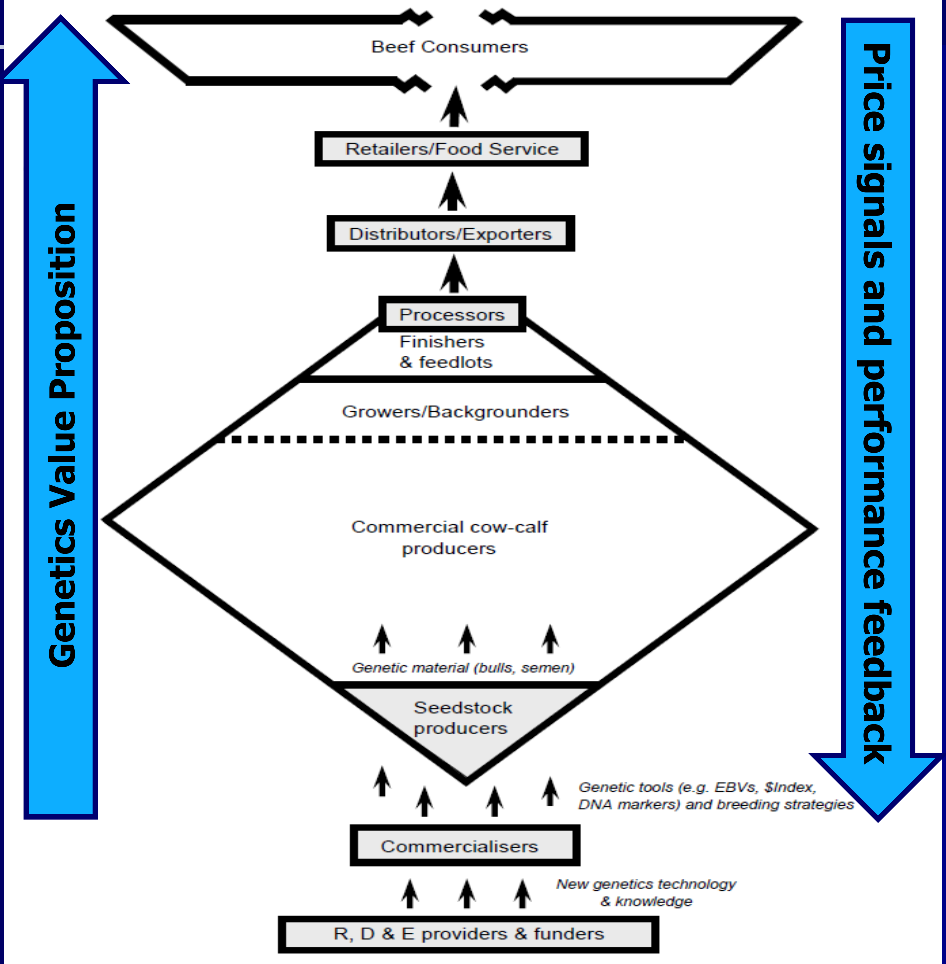
- **Identification of molecular markers to improve fertility of beef cattle** (Thomas, CO) – finished 12/2011
  - >10,000 DNA samples and phenotypes on heifers
- **BIGS – Bioinformatics to implement genomic selection** (Garrick/Snelling/Golden)/ **Enhanced Bioinformatics to implement genomic selection (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

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



Genetics Value Proposition

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

Price signals and performance feedback

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 .

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)
Nucleus seedstock/AI bulls	Full genome sequence	$250
Seedstock/bull multiplier	HD 770 K genotype	$50
Registered females and stock bulls for commercial sector	50K genotype + parentage + single gene traits/recessives	$25
Commercial cattle – Marker-assisted management (MAM), replacement heifer selection	Imputation LD chip + parentage + single gene traits/recessives	$10
Feedlot cattle purchasing, sorting and marker-assisted management (MAM)	Access genotypes from supplier (subset of LD imputation chip).	<$1
Traceability for voluntary labelling e.g. Angus beef	Access genotypes from supplier (subset of LD imputation chip).	<$1
Traceability for disease outbreak/contaminated meat	Access genotypes from supplier (subset of LD imputation chip).	<$1

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

CONCLUSION: Ramifications of DNA-enabled selection

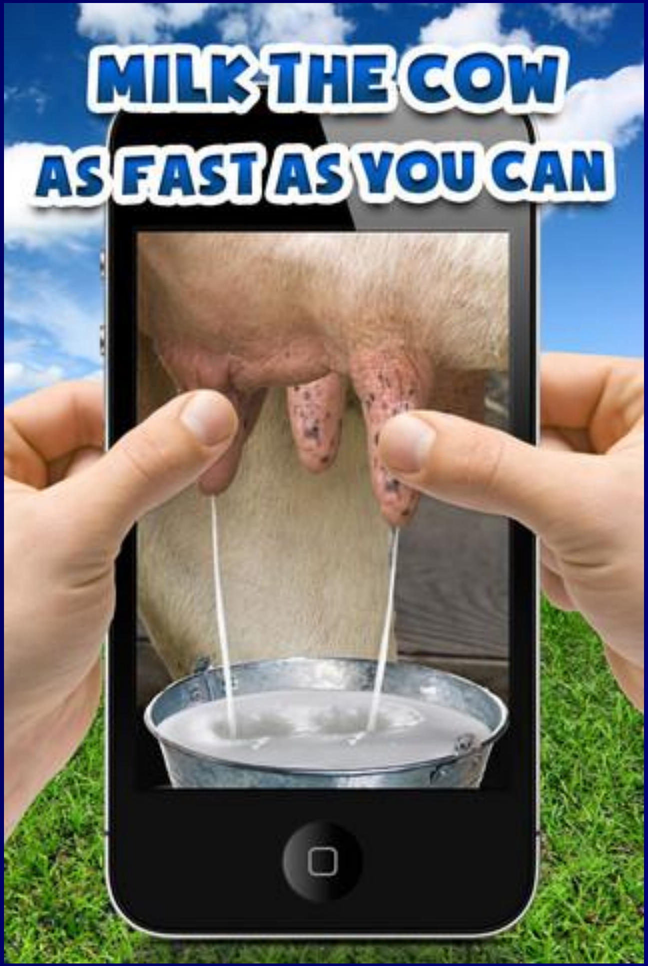
- The benefits of genomic selection are best captured in well-structured industries that are already making significant genetic progress
- May encourage more vertical integration to collect phenotypes to enable predictions for ERTs for all sectors
- May see genetic evaluations developed for novel traits – if large enough populations can be amassed and data shared
- May see breeds/countries start to share data – especially with HD chips and whole genome sequencing
- Will beef follow the pig/poultry model of vertically-integrated breeding companies owning all sectors?

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. 2011. Where in the beef cattle supply chain might DNA tests generate value? Animal Production Science. 52(3) 185-196.

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.

United States Department of Agriculture

National Institute of Food and Agriculture

Questions?