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

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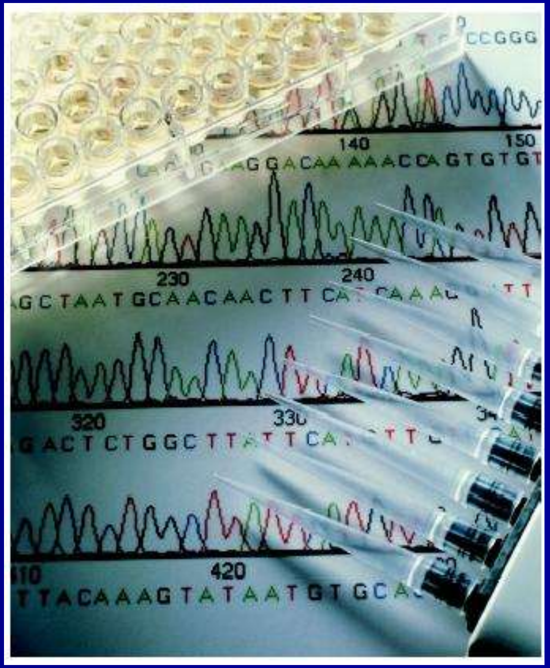


http://animalscience.ucdavis.edu/animalbiotech/

Overview

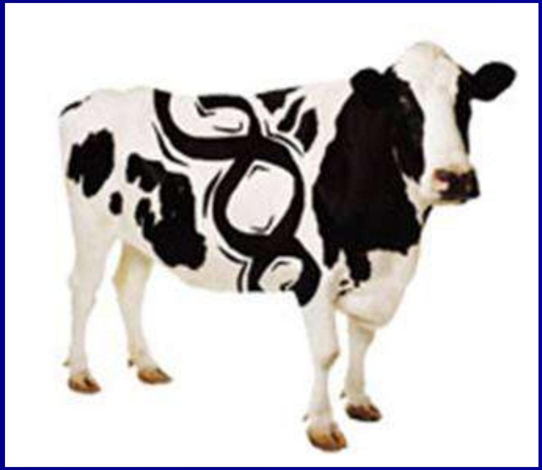
- Dairy Model
- What is different about beef?
- What do the data show?
- Implications?

Application of WGS in Dairy Cattle Has Been Successful

r_0

Validation:
New Progeny Tested Bulls

Training 1:
Old Progeny Tested Bulls



Training 2:
Old & New Progeny Tested Bulls

r_1

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 ΔG

$\Delta G = (i_m\ r_m + i_f\ r_f) / (L_m + L_f)$ genetic standard deviation/year

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

$= (2*0.6 + 0.8*0.6) / (2+2) \quad = \quad 0.42$ (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

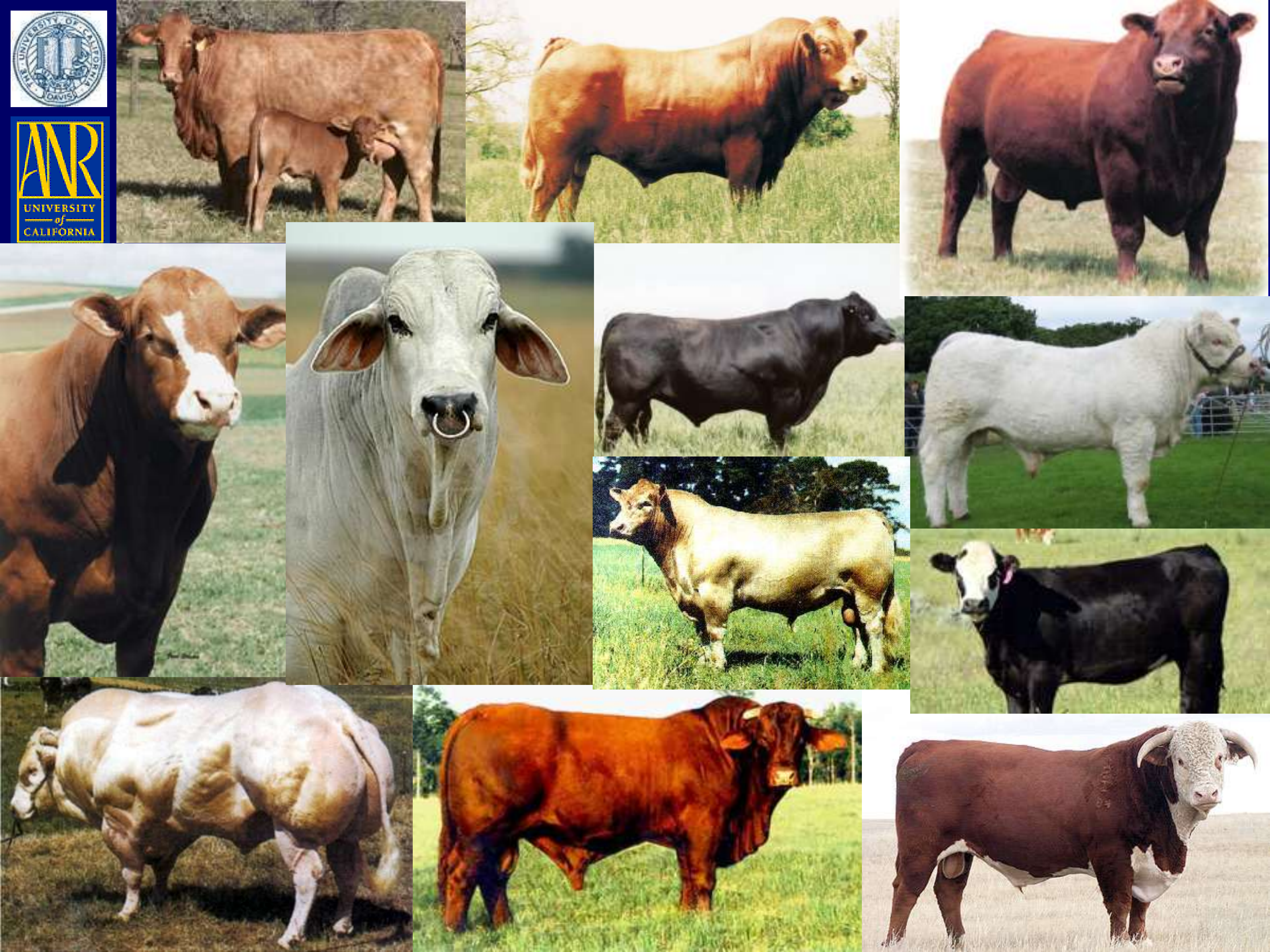
Rate of genetic gain ΔG

$\Delta G = (i_m\, r_m + i_f\, r_f)/\ (L_m + L_f)$ genetic standard deviation/year

= (2*0.8 + 0)/ (6+2) = 0.2 (progeny test)

= (2*0.6 + 0.8*0.6)/ (2+2) = 0.42 (genomic selection)

= (2*0.6 + 0.8*0.6)/ (.5+.5) = 1.68 (velogenetics) i.e. 8X

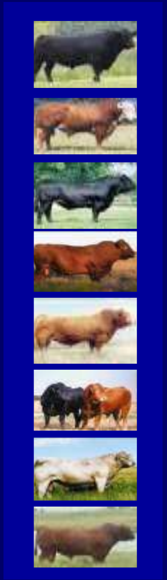

ANR
UNIVERSITY of CALIFORNIA

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 (eg Limousin)
- US MARC collection of some 2,000 recent AI bulls including 16 breeds (2000 bull project)



Angus	402	Brangus	68
Hereford	317	Beefmaster	64
Simmental	253	Maine-Anjou	59
Red Angus	173	Brahman	53
Gelbvieh	136	Chiangus	47
Limousin	131	Santa Gertrudis	43
Charolais	125	Salers	42
Shorthorn	86	Braunvieh	27

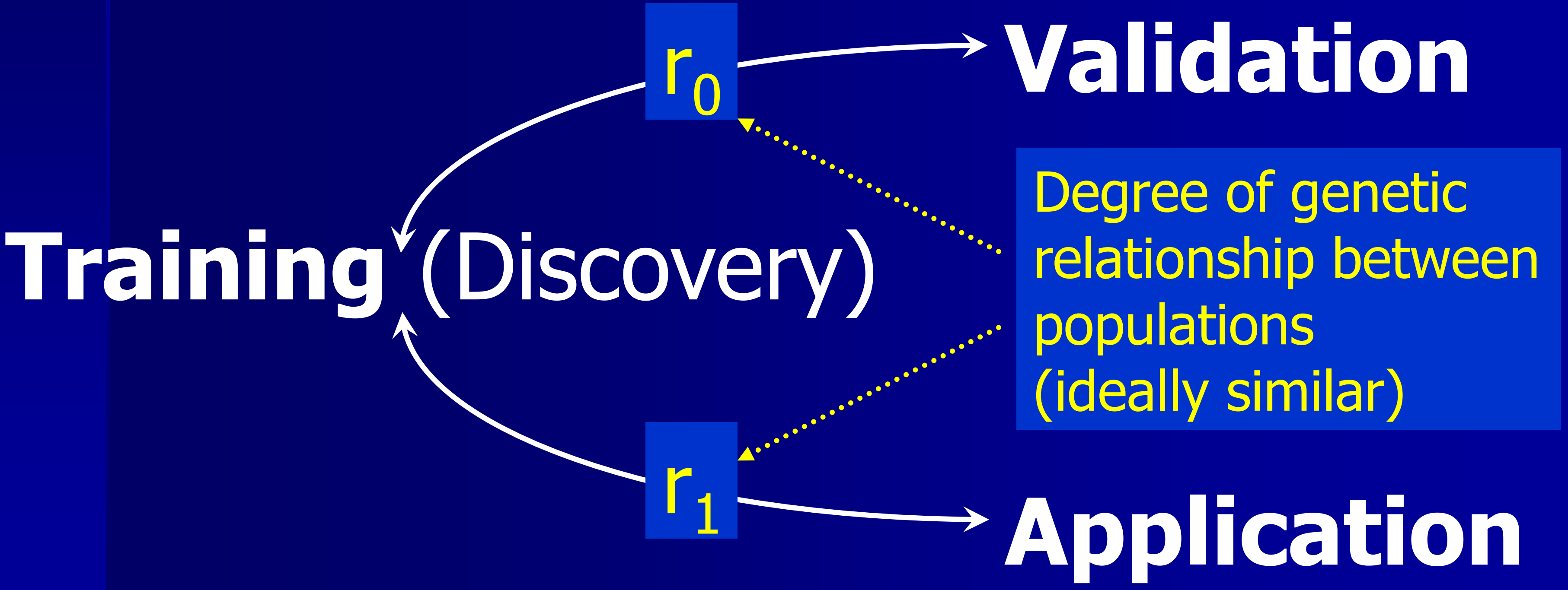
50k within-breed predictions

- 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

Validation: Purpose is to estimate the correlation between the prediction and the true genetic merit.



Validation

r_0

Training (Discovery)

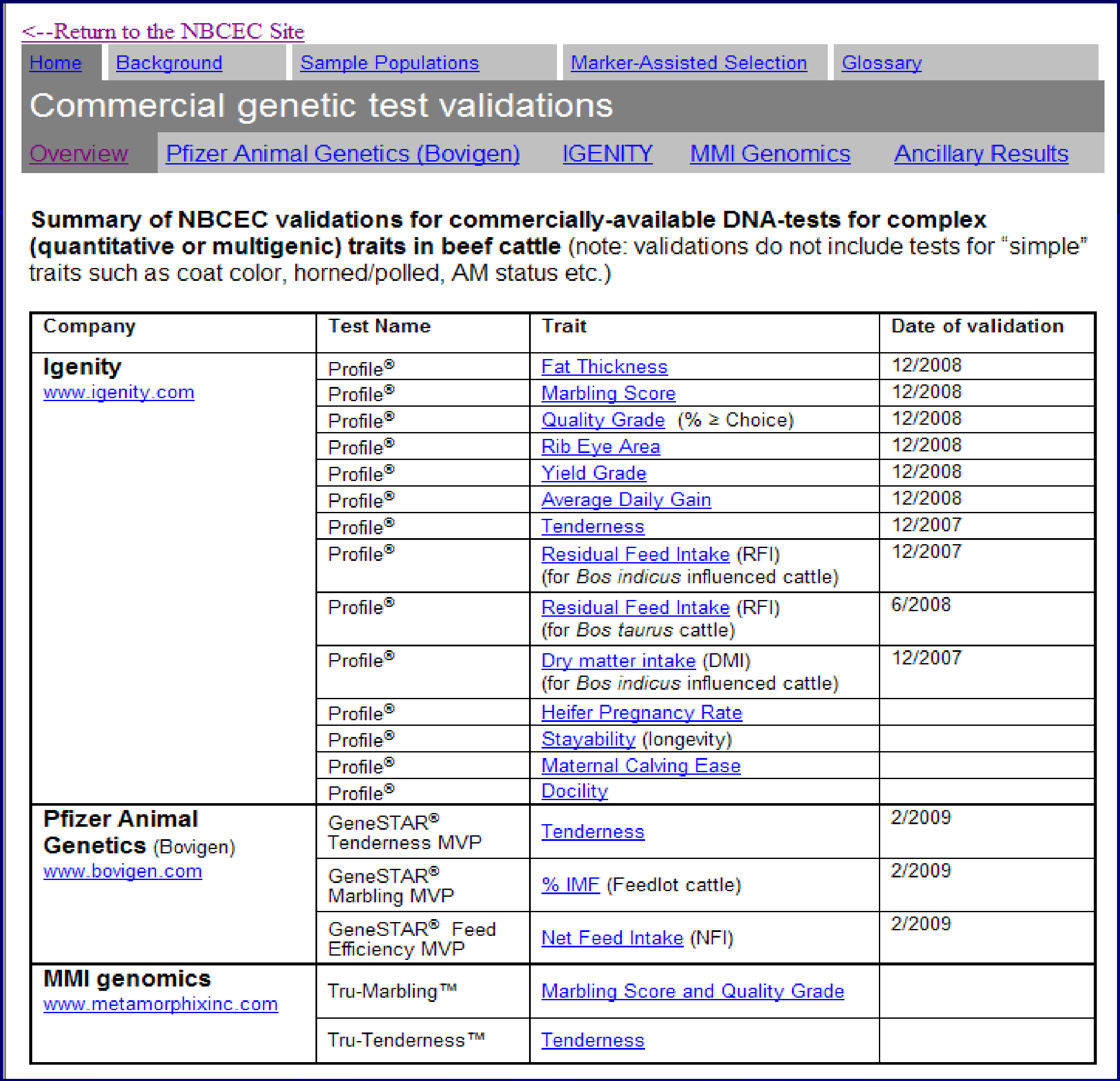
Degree of genetic relationship between populations (ideally similar)

r_1

Application

Slide courtesy of Marc Thallman, US MARC

www.nbcec.org

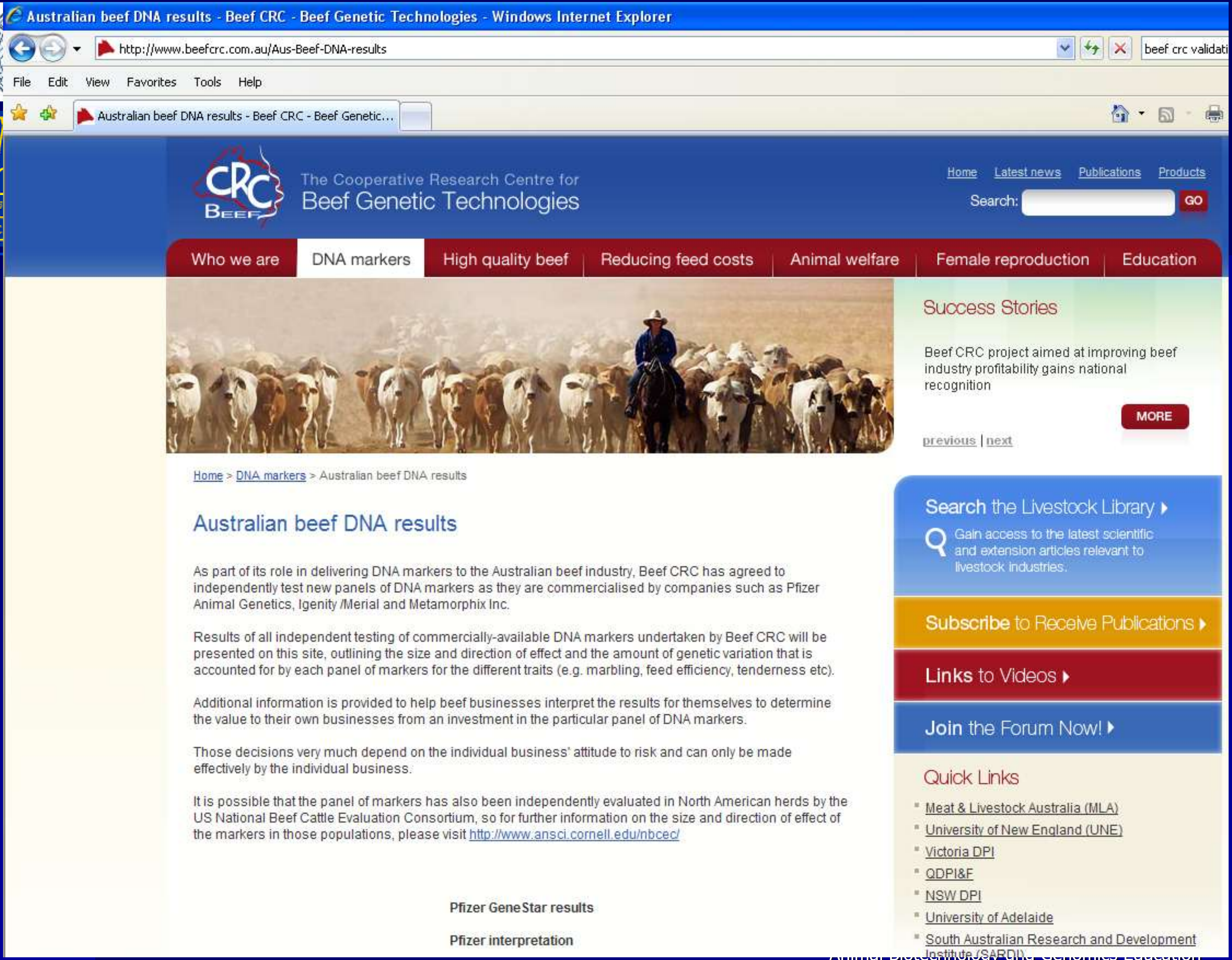


<--Return to the NBCEC Site

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/polled, AM status etc.)

Company	Test Name	Trait	Date of validation
Igenity www.igenity.com	Profile®	Fat Thickness	12/2008
	Profile®	Marbling Score	12/2008
	Profile®	Quality Grade (% ≥ Choice)	12/2008
	Profile®	Rib Eye Area	12/2008
	Profile®	Yield Grade	12/2008
	Profile®	Average Daily Gain	12/2008
	Profile®	Tenderness	12/2007
	Profile®	Residual Feed Intake (RFI) (for *Bos indicus* influenced cattle)	12/2007
	Profile®	Residual Feed Intake (RFI) (for *Bos taurus* cattle)	6/2008
	Profile®	Dry matter intake (DMI) (for *Bos indicus* influenced cattle)	12/2007
	Profile®	Heifer Pregnancy Rate	
	Profile®	Stayability (longevity)	
	Profile®	Maternal Calving Ease	
	Profile®	Docility	
Pfizer Animal Genetics (Bovigen) www.bovigen.com	GeneSTAR® Tenderness MVP	Tenderness	2/2009
	GeneSTAR® Marbling MVP	% IMF (Feedlot cattle)	2/2009
	GeneSTAR® Feed Efficiency MVP	Net Feed Intake (NFI)	2/2009
MMI genomics www.metamorphixinc.com	Tru-Marbling™	Marbling Score and Quality Grade	
	Tru-Tenderness™	Tenderness	



Success Stories

Beef CRC project aimed at improving beef industry profitability gains national recognition

Gain access to the latest scientific and extension articles relevant to livestock industries.

Home > DNA markers > Australian beef DNA results

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, Igenity /Merial 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.ansci.cornell.edu/nbcec/

Pfizer GeneStar results

Pfizer interpretation

Quick Links

- Meat & Livestock Australia (MLA)
- University of New England (UNE)
- Victoria DPI
- QDPI&F
- NSW DPI
- University of Adelaide
- South Australian Research and Development Institute (SARDI)

Maybe Fisher was right.

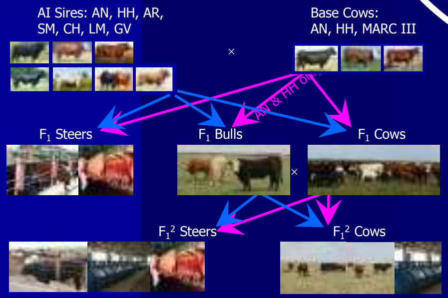
For most economic traits we need to track very many genes in order to explain a large part of the genetic variance.

2000 Bull Project

r$_0$

Validation:
2,000 Bull Project
International Collaboration

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



r$_1$

Application:
Seedstock Breeders

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

50k	Train in Multibreed Validate in Purebreed	Train in Purebreed Validate in Multibreed
50 QTL	0.39	0.42
100 QTL	0.29	0.31
250 QTL	0.25	0.28
500 QTL	0.20	0.30

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

Kizilkaya K. et al. (2009). Genomic prediction of simulated multi-breed and purebred performance using observed 50k SNP genotypes. Journal of Animal Science. *Submitted.*

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 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

D. J. Garrick and B. L. Golden. 2009. Producing and using genetic evaluations in today's U.S. beef. Journal of Animal Science

"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 ……..

Trait	Heritability
Carcass/end product	High
Skeletal measurements	High
Mature weight	High
Growth rate	Medium
Birth weight	Medium
Weaning weight	Medium
Yearling weight	Medium
Milk Production	Medium
Maternal ability	Low
Reproduction	Low
Health	Low
Cow longevity	Low
Overall cow productivity	Low

Accuracy of the prediction equation depends on:

$$\frac{Th^2}{N_e L}$$

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)

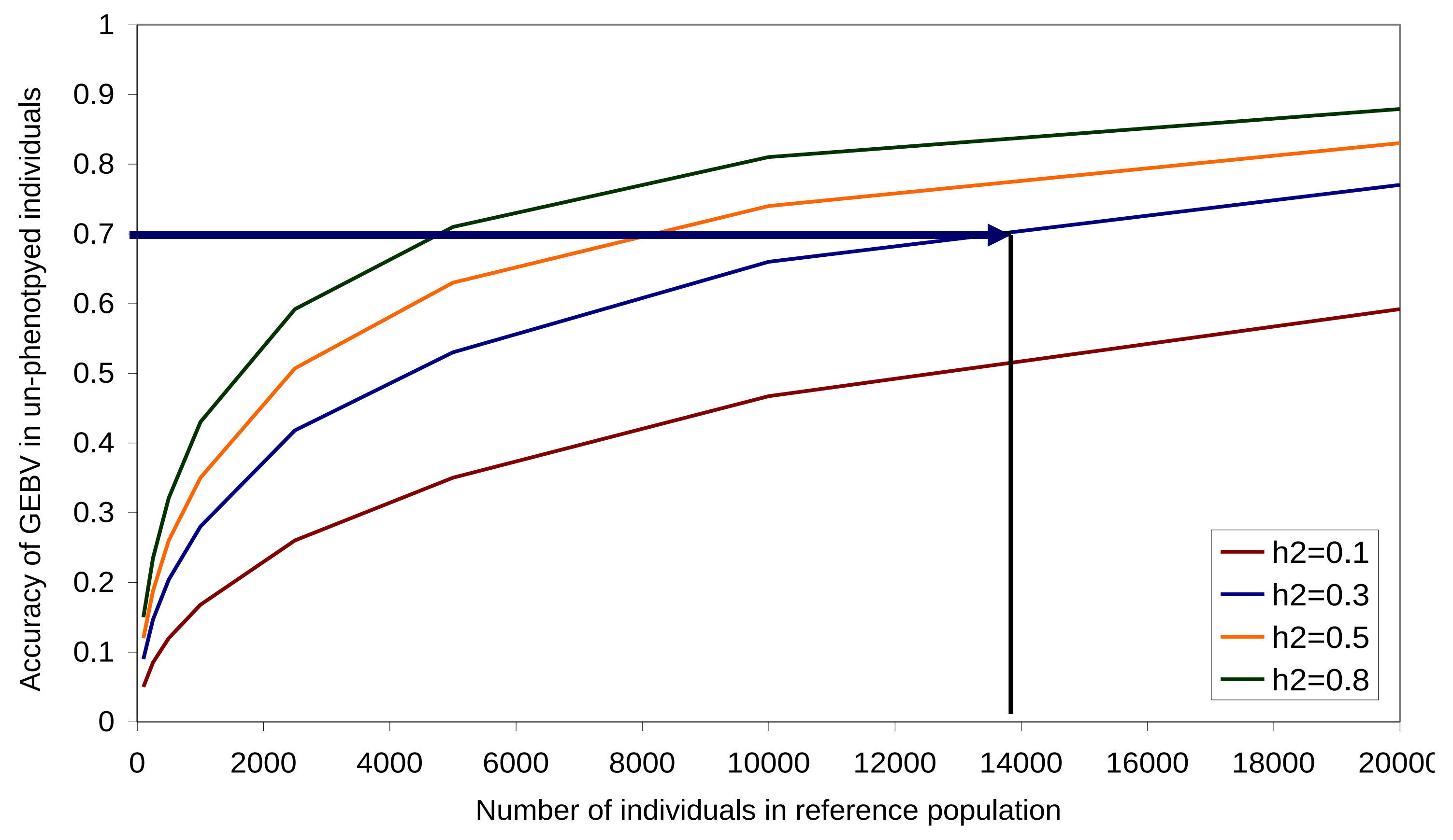
BOTTOM LINE

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

Modified from Goddard. (2009). BIF

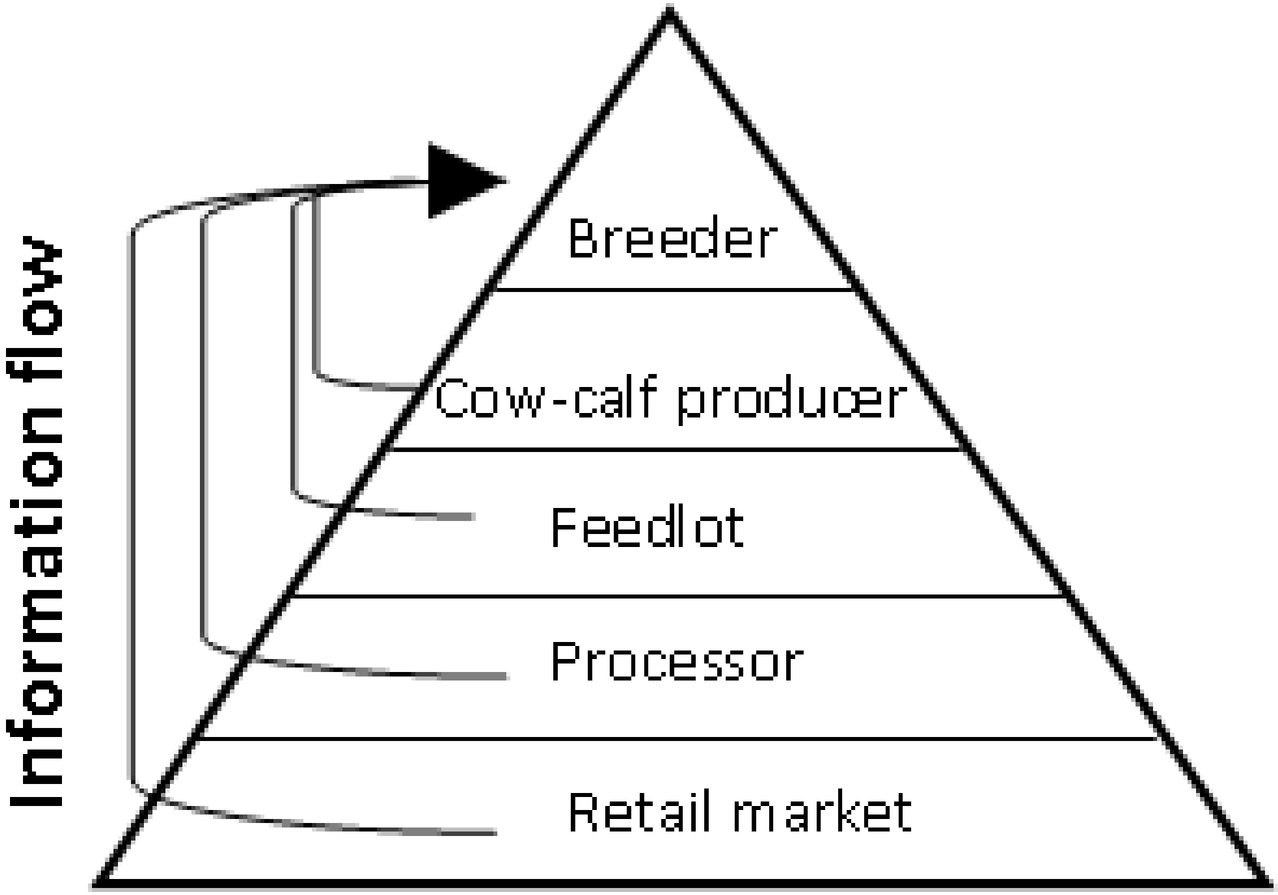
Effect of number of animals on accuracy of prediction equation

Mike Goddard. (2009) Beef Improvement Federation Meeting.



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

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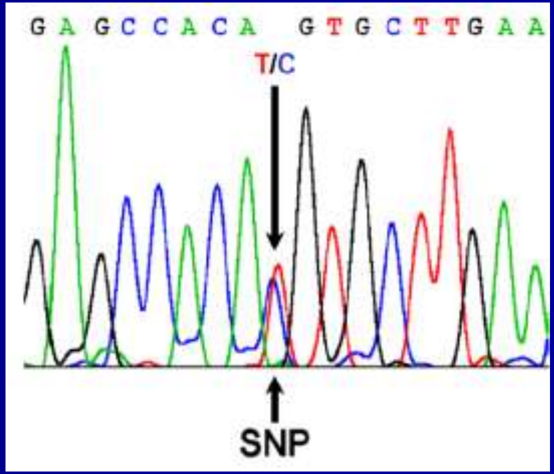


…and animal is then managed according to genetic potential.

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.

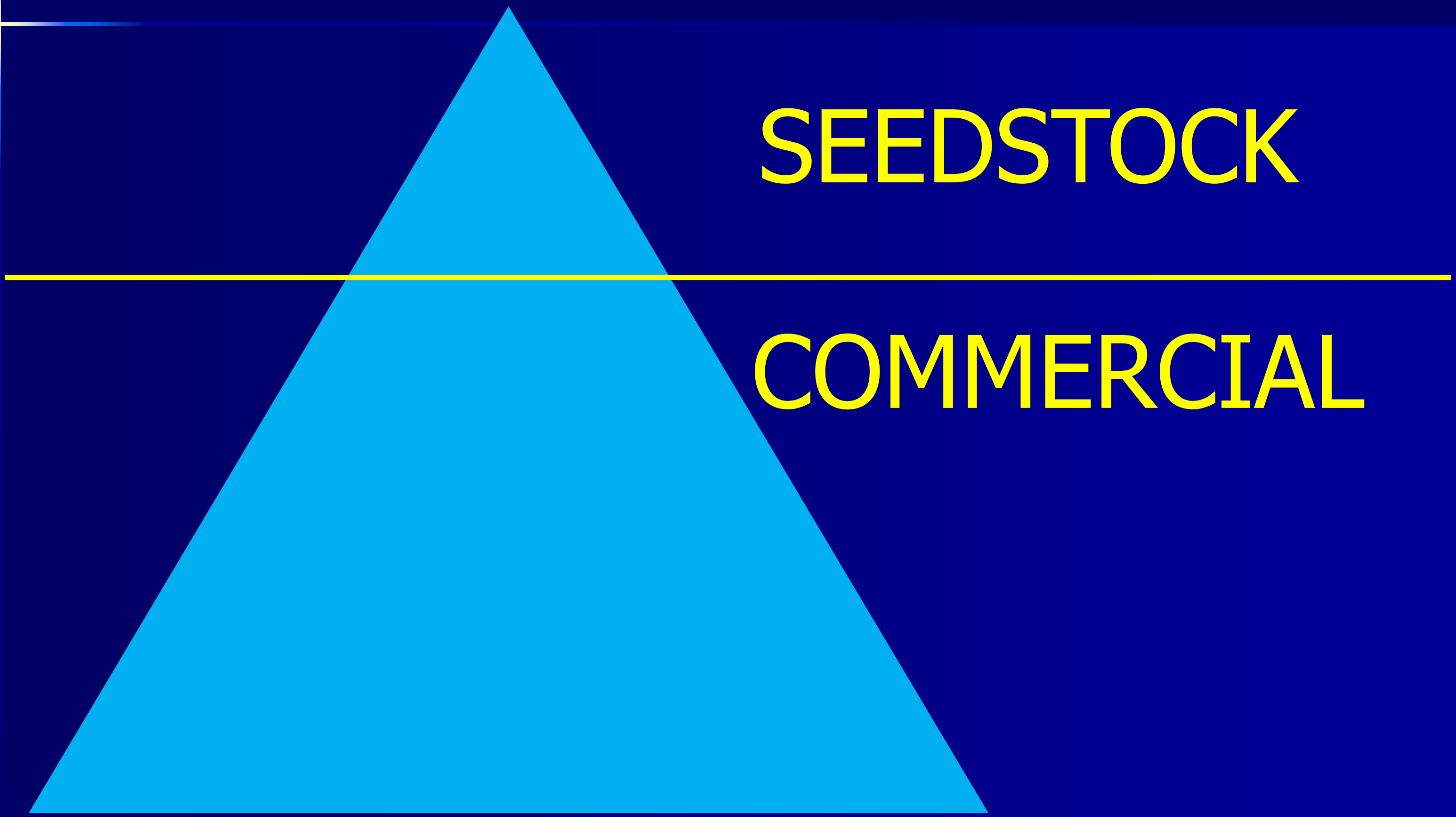
How can cattle producers benefit from genomic selection?

Rate of genetic gain ΔG

$\Delta G = (i_m\ r_m + i_f\ r_f) / (L_m + L_f)$ 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

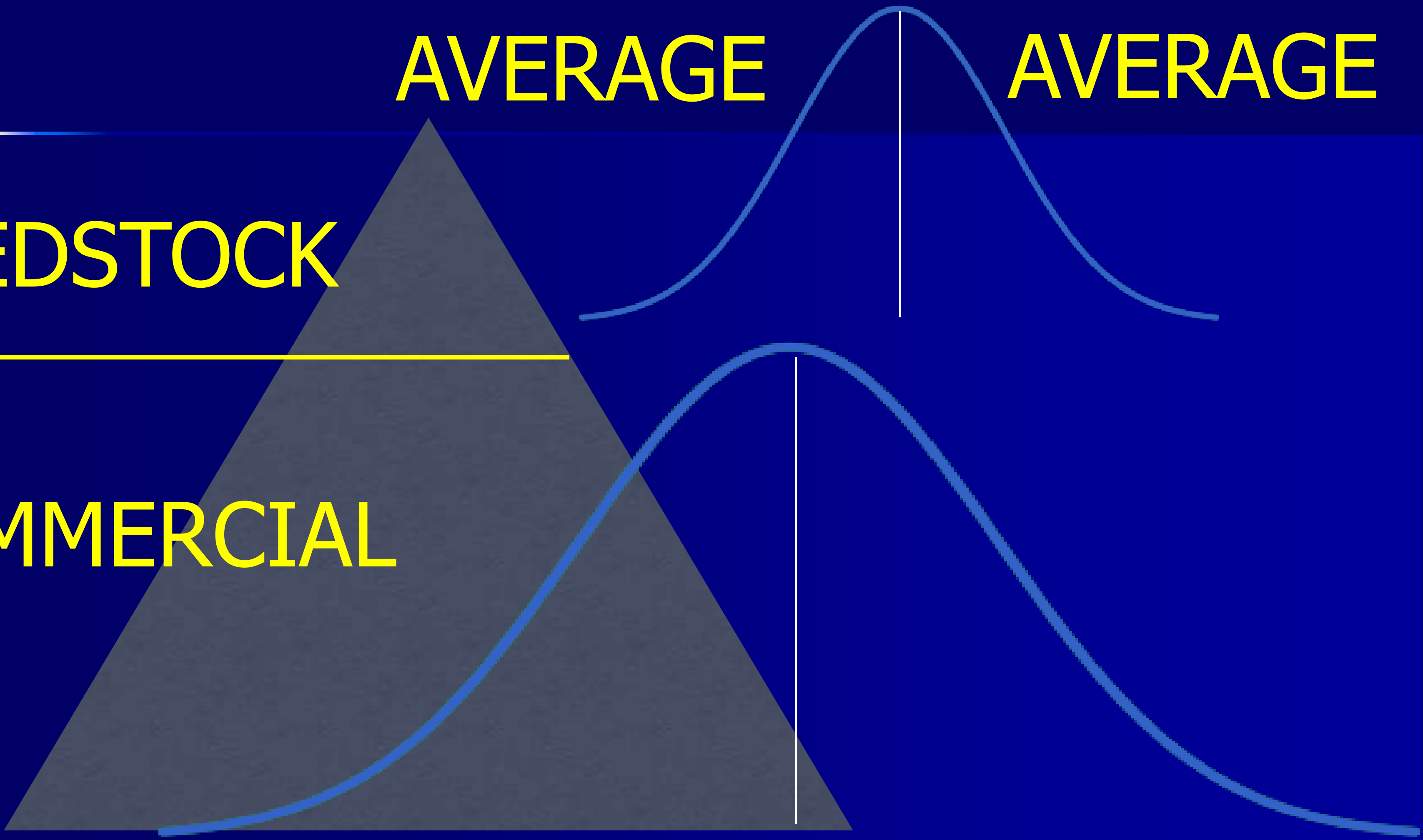
May see development of herd bulls from commercial sector



SEEDSTOCK

COMMERCIAL

Modified from Garrick. (2008). BIF



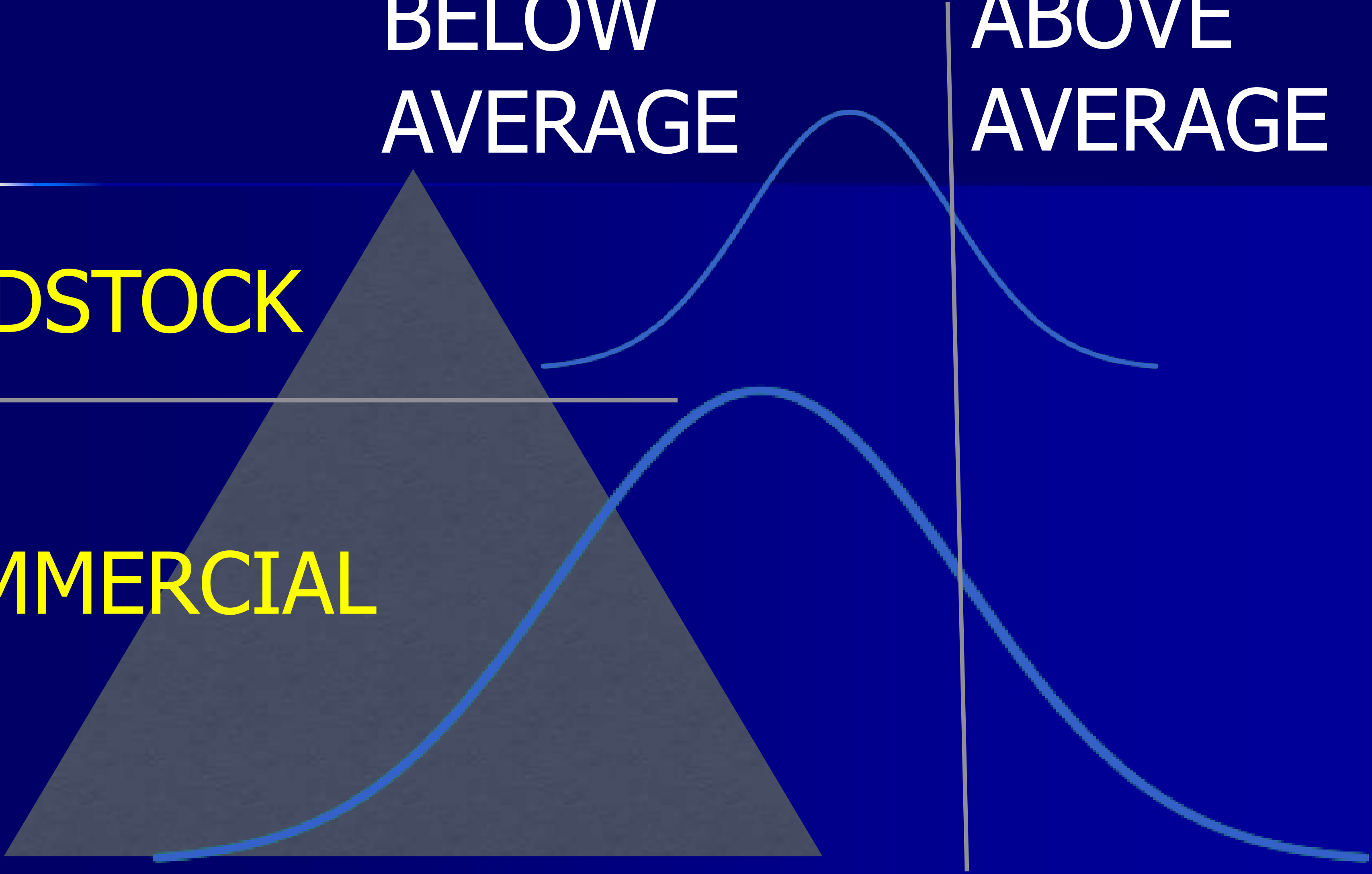
BELOW AVERAGE

ABOVE AVERAGE

SEEDSTOCK

COMMERCIAL

Modified from Garrick. (2008). BIF



BELOW AVERAGE

ABOVE AVERAGE

SEEDSTOCK

COMMERCIAL

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?

Developing genomic resources for whole genome selection. J. C. McEwan. 2007. Proceedings of the New Zealand Society of Animal Production.67:148-153.

"*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

Stakeholders in NCE

- Breed Associations
- Bull Breeders
- Bull Buyers
- AI Companies
- EPD Servicing Entities
- Researchers interested in NCE
- Others (BIF, NBCEC, Cooperative Extension)

Current Business Model

Cash

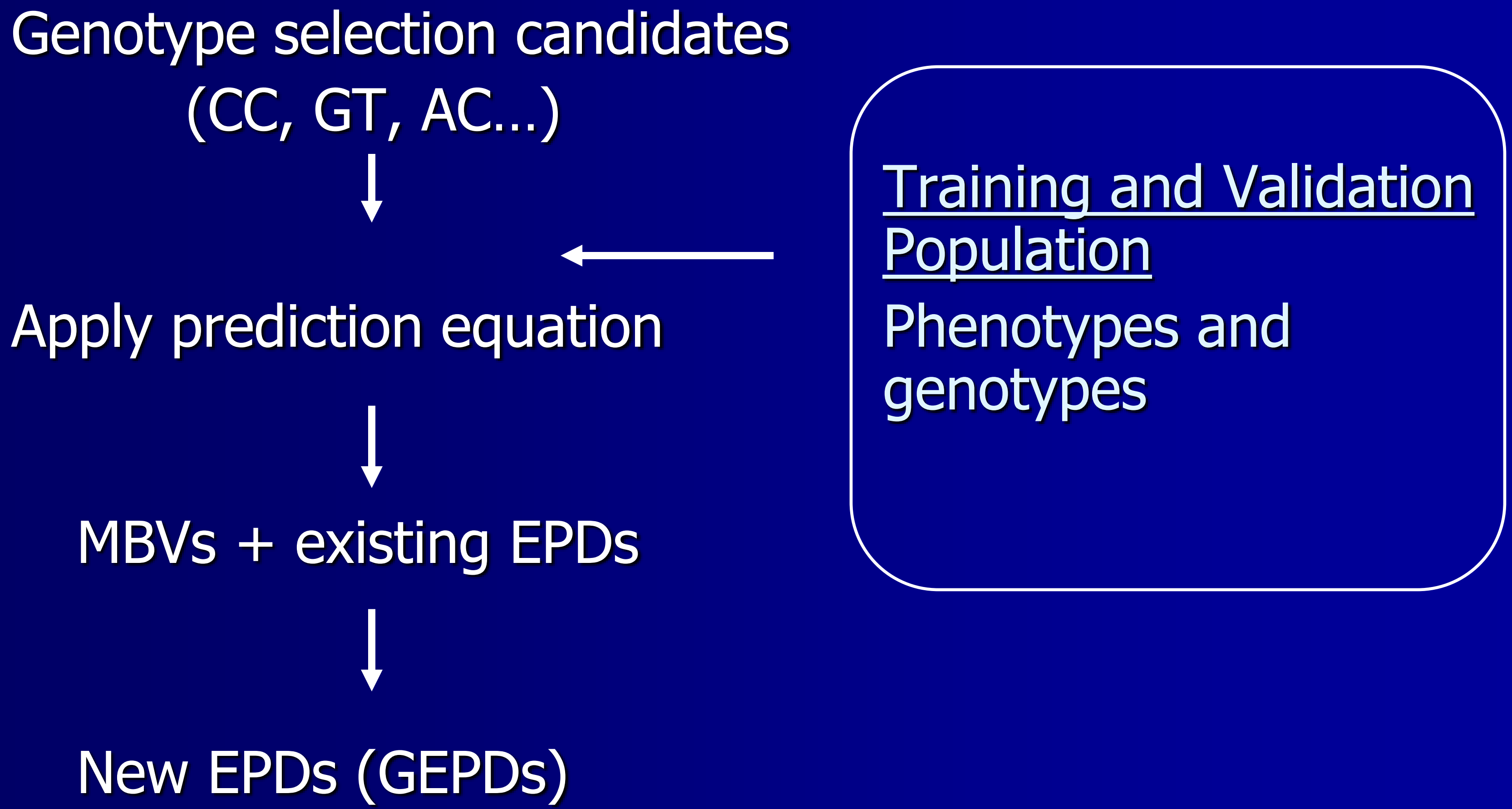
- Bull breeders collect data at own expense
- Bull breeders pay Breed Associations
- Breed Associations pay Service entity

Non cash

- pedigree/performance data for the collective benefit
- Researchers improve analyses motivated by data

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”***

Wiggans et al. 2008. Genomic Evaluations in the United States and Canada: A collaboration. ICAR.

New stakeholders and new questions raised by evaluation system using WGS

Stakeholders in WGS

- Genotyping Companies
- Genomics Companies
- Owners/Controllers of Training datasets
- Breed Associations
- EPD Servicing Entities
- AI Companies
- Bull Breeders
- Bull Buyers
- Researchers interested in NCE
- Others (BIF, NBCEC, Cooperative Extension)

Future Business Model ??

- Development of training data
- Genotyping/analysis costs
- Servicing (EPDs, MGVs, merged combination)
- How are bull breeders rewarded for better EPDs
- Does data get shared for collective benefit
- Researchers participate/improve analyses motivated by $$

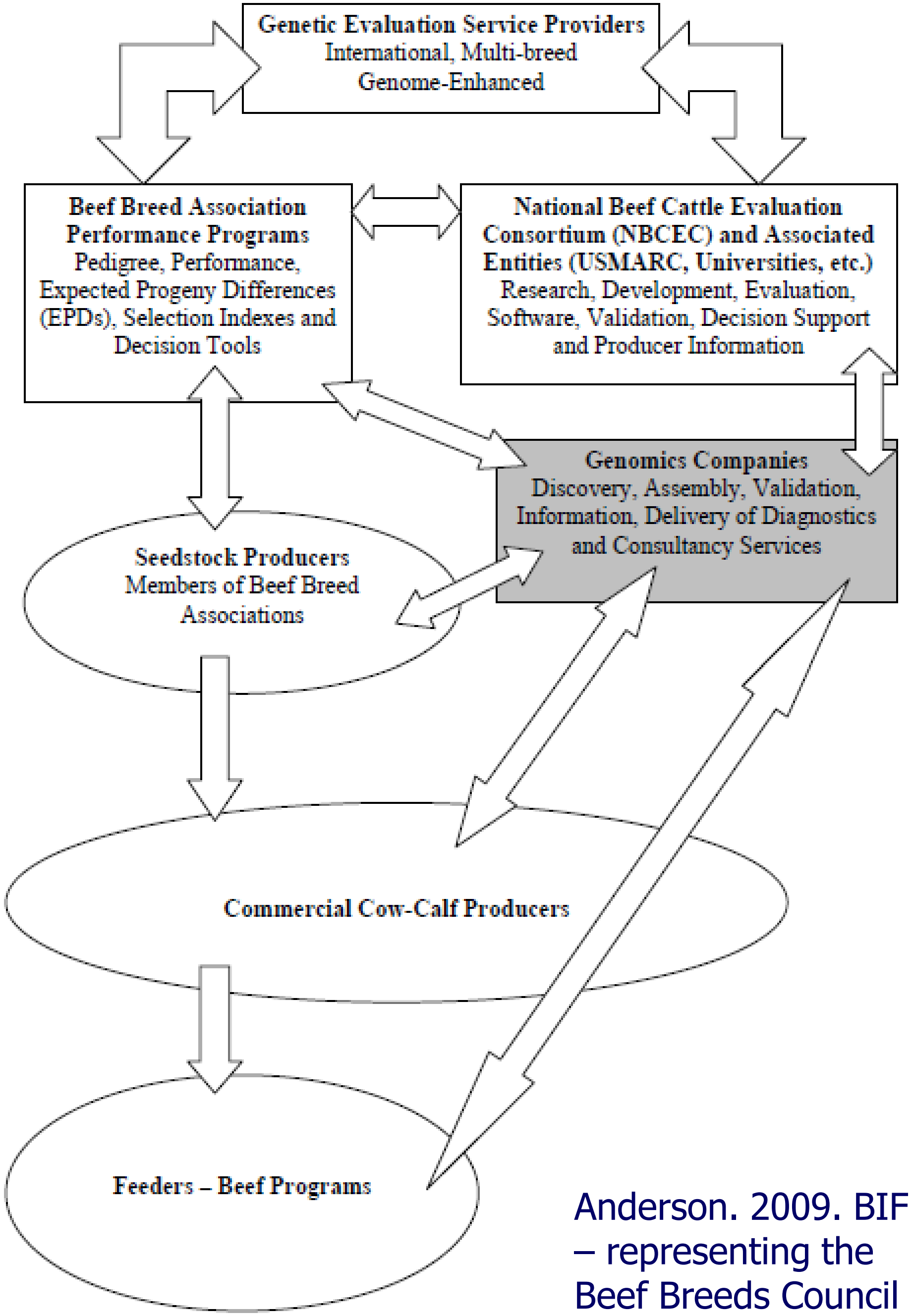
Modified from Garrick. (2008). BIF

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!



Genetic Evaluation Service Providers
International, Multi-breed
Genome-Enhanced

Beef Breed Association Performance Programs
Pedigree, Performance, Expected Progeny Differences (EPDs), Selection Indexes and Decision Tools

National Beef Cattle Evaluation Consortium (NBCEC) and Associated Entities (USMARC, Universities, etc.)
Research, Development, Evaluation, Software, Validation, Decision Support and Producer Information

Genomics Companies
Discovery, Assembly, Validation, Information, Delivery of Diagnostics and Consultancy Services

Seedstock Producers
Members of Beef Breed Associations

Commercial Cow-Calf Producers

Feeders – Beef Programs

Anderson. 2009. BIF – representing the Beef Breeds Council

Questions ?