

# Applications of Genomic Selection in (North American) beef cattle

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# Industry Structure

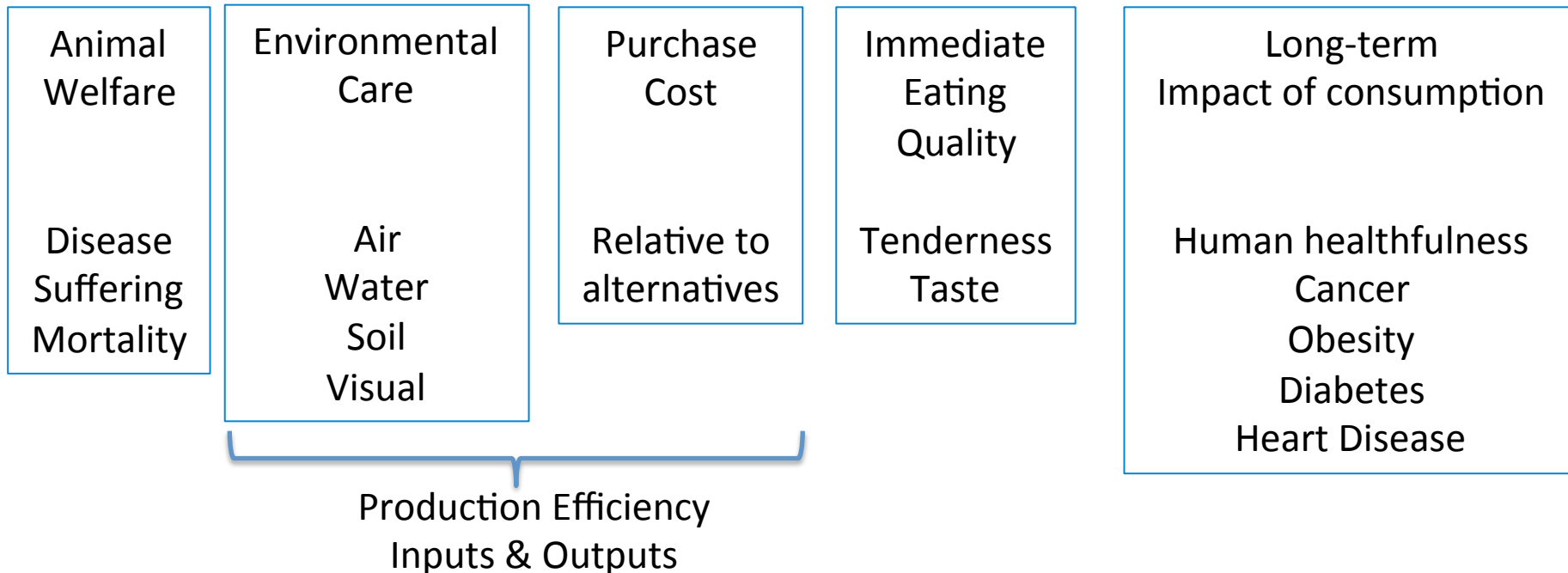
- Most cow-calf operations do not record pedigree nor individual animal performance
  - They represent about 29 million beef cows
    - And almost 6 million replacement heifers
  - Average herd size 40 cows
  - Predominantly natural mating
  - They represent the bull buying sector
    - At 1 bull per 15 cows there would be 2 million sires
    - At 4 year lifespan they buy 0.5 million bulls per year

# Bull breeding herds

- Most (but not all) bull breeders are affiliated with a breed association
- Breed associations maintain pedigrees, issue registration certificates and run “national” genetic evaluations at varying frequencies
- There are probably about 600,000 beef cattle registrations per year
  - American Angus Association registers 300,000

# The Big Picture

## Consumer Satisfaction



# Improving Consumer Satisfaction

## *Existing EBVs from NCE*

Animal Welfare	Environmental Care	Purchase Cost	Immediate Eating Quality	Long-term Impact of consumption
Disease Suffering Mortality	Air Water Soil Visual	Relative to alternatives	<b>Tenderness</b> Taste	Human healthfulness Cancer Obesity Diabetes Heart Disease
	Production Efficiency Inputs & <b>Outputs</b>			

Calving Ease

Growth

Ultrasound REA, IMF, FAT

# Consumer Satisfaction

## *Existing EBVs from NCE*

## *Desired EBVs from new approaches*

Animal  
Welfare

Environmental  
Care

Purchase  
Cost

Immediate  
Eating  
Quality

Long-term  
Impact of consumption

Disease  
Suffering  
Mortality

Air  
Water  
Soil  
Visual

Relative to  
alternatives

Tenderness  
Taste

Human healthfulness  
Cancer  
Obesity  
Diabetes  
Heart Disease

Production Efficiency  
Inputs & Outputs

BRD  
Pinkeye  
Feed Intake

Calving Ease

GHG/CO2

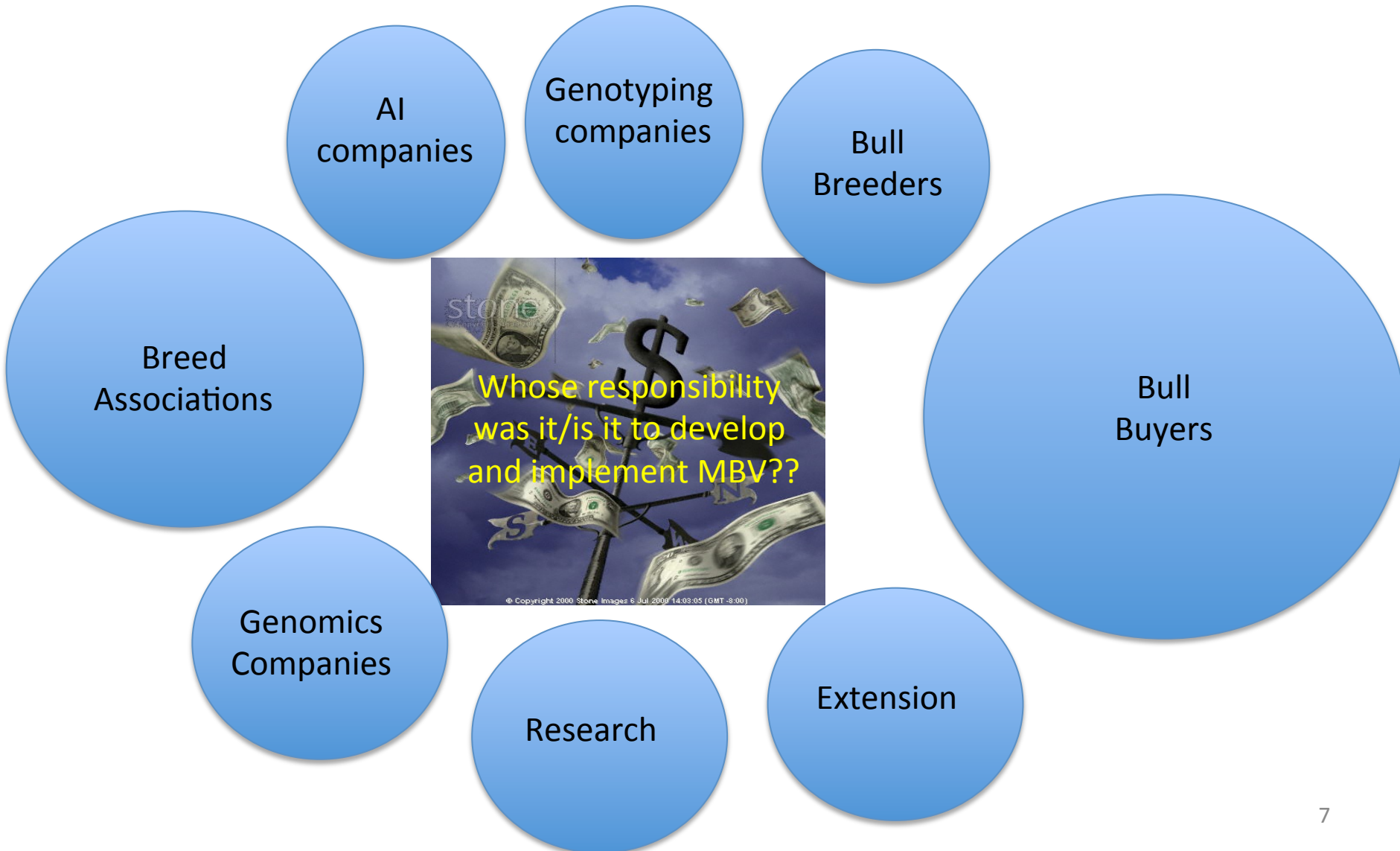
Growth

Reproduction

Ultrasound REA, IMF, FAT

Fatty Acids?  
Minerals?

# Industry Structure



# Current Genetic Evaluation

AHA  
Hereford

AAA  
Angus

AICA  
Charolais

ASA  
Simmental

RAAA  
Red Angus

NALF  
Limousin

AGA  
Gelbvieh

IBBA  
Brangus

Santa  
Gertrudis

Mostly  
purebred  
Some  
xbred  
carcass

Includes  
CHAxAAN

Only US  
purebred  
black

Mostly  
admixed  
Includes  
*Taurindicus*  
Simbrah etc

Red and  
Black and  
composites

Includes  
LimFlex  
(LIMxAAN)

Includes  
Balancer  
(GVHxAAN)

Composite  
3/8 & 5/8

Includes  
CAN  
ARG  
URG

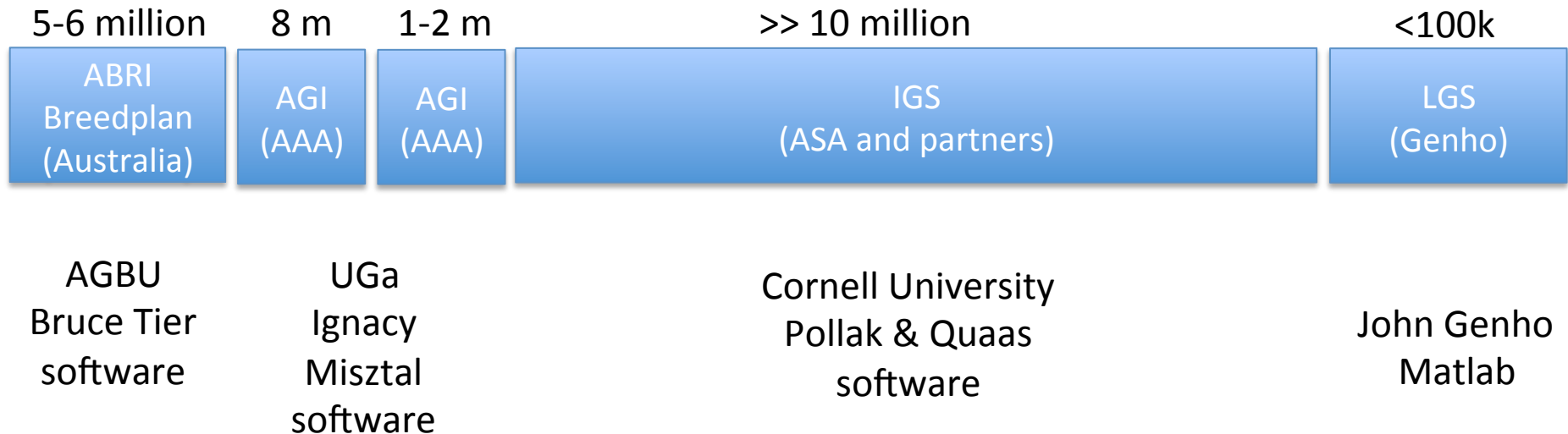
Includes USA, CAN (and elsewhere)



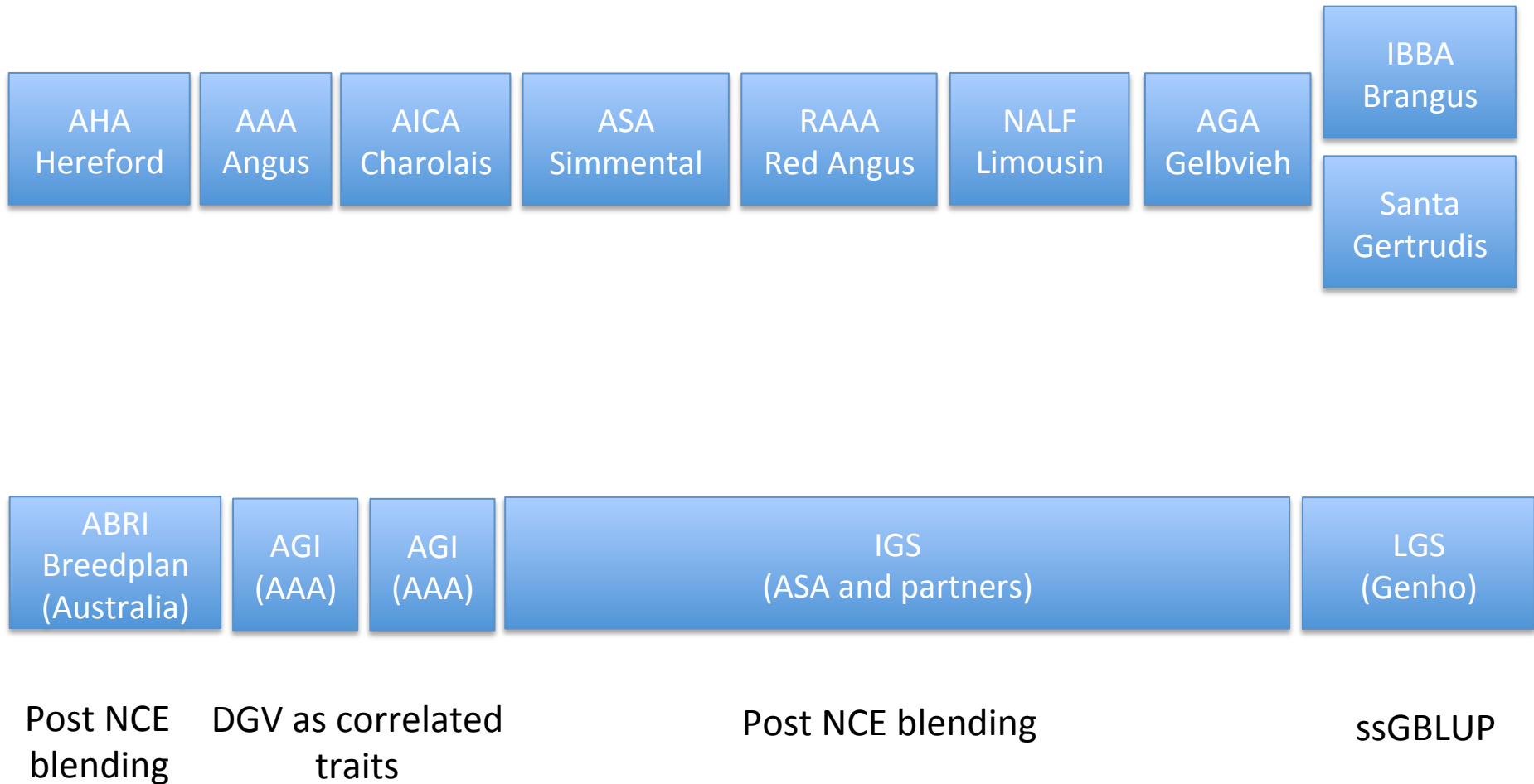
# Current Genetic Evaluation



“PACE”



# Current Genetic Evaluation



# Change in AHA Predictive Accuracy

Genetic Correlations Trait	2010 (800)	2011 (1,081)	2012 (1,081)	2013 (2,980)
Birth weight	0.40	0.43	0.52	0.68
Weaning wt	0.34	0.32	0.38	0.52
Yearling wt	0.33	0.30	0.44	0.60
Milk	0.21	0.22	0.26	0.37
Calving Ease D		0.43	0.42	0.68
Calving Ease M		0.18	0.20	0.51
Fat	0.43	0.40	0.44	0.48
Marbling	0.29	0.27	0.27	0.43
Ribeye Area	0.41	0.36	0.45	0.49
Scrotal Circum	0.25	0.28	0.27	0.43
Mature Cow wt				0.64
Average (% gVar)	0.33 (11%)		0.37 (13%)	0.52 (27%)

# Prediction of Shorthorn only from other Breeds

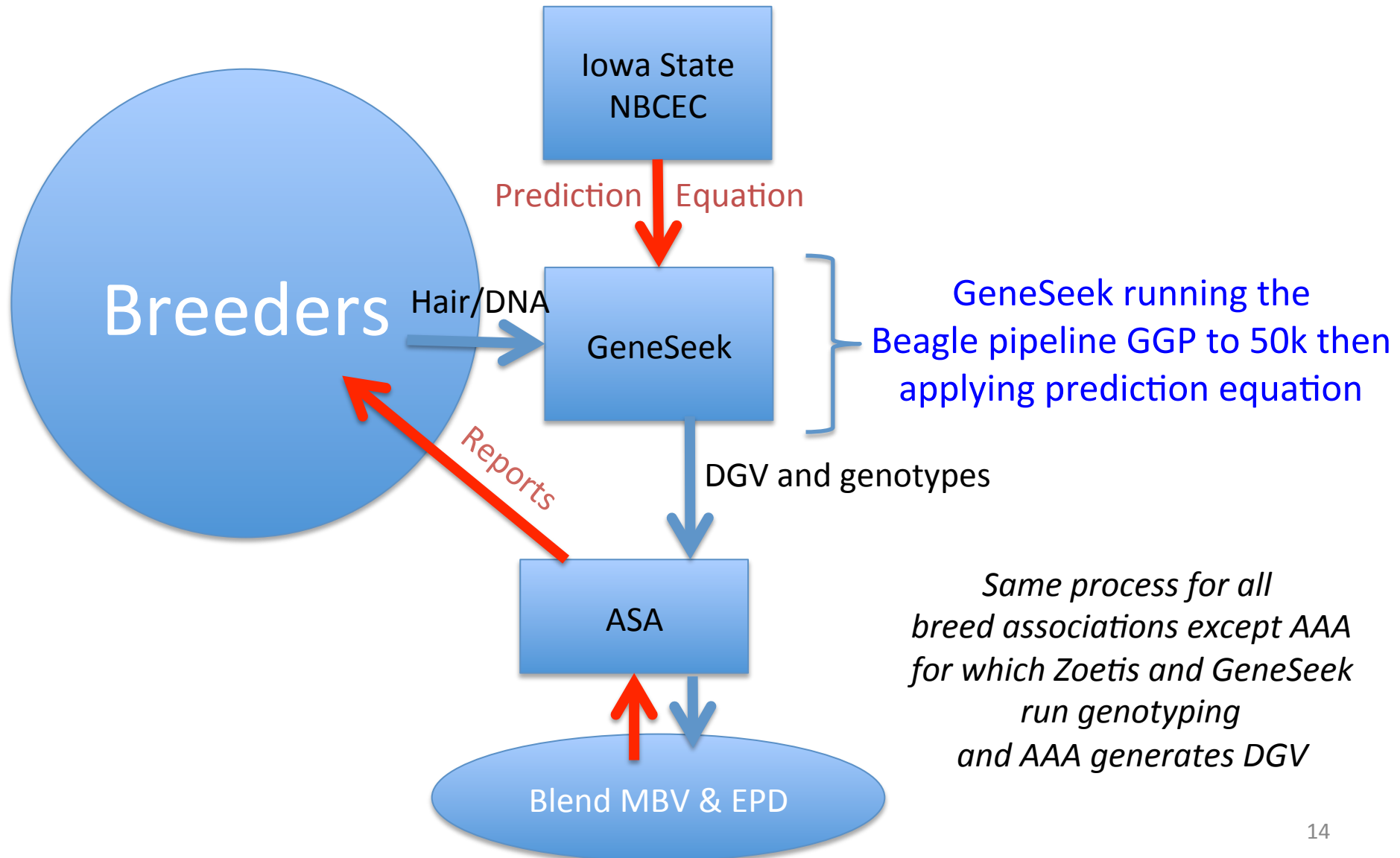
	Angus	Brangus	Gelbvieh	Hereford	Limousin	Red Angus	Simmental
Birth Weight	0.08	-0.05	0.09	0.23	0.18	0.40	0.37
Calving ease direct	0.05	-0.01	-0.16	0.17	0.15	0.23	0.30
Calving ease maternal	0.09	0.00		0.08	0.15	0.06	0.07
Carcass Weight	0.20	0.05	0.07		-0.10	0.23	0.20
Fat tickness	0.17	0.02		0.11		0.08	0.01
Milk	0.09	-0.04	0.16	-0.06	0.02	0.03	-0.06
Marbling	0.03	-0.04	0.11	-0.07	-0.08	0.09	0.17
Rib eye area	0.03	0.01	0.12	-0.07	-0.01	0.05	0.08
Weaning weight	0.12	-0.10	0.07	0.15	-0.02	0.15	0.09
Yearling weight	0.09	0.00	-0.08	0.14	0.02	0.13	0.13

Across breed prediction does not work if the breed is not in training

# Predictions in US Breeds

Trait	RedAngus (6,412)	Angus (3,500)	Hereford (2,980)	Simmental (2,800)	Limousin (2,400)	Gelbvieh (1,321)+
BirthWt	0.75	0.64	0.68	0.65	0.58	0.62
WeanWt	0.67	0.67	0.52	0.52	0.58	0.52
YlgWt	0.69	0.75	0.60	0.45	0.76	0.53
Milk	0.51	0.51	0.37	0.34	0.46	0.39
Fat	0.90	0.70	0.48	0.29		0.75
REA	0.75	0.75	0.49	0.59	0.63	0.61
Marbling	0.85	0.80	0.43	0.63	0.65	0.87
CED	0.60	0.69	0.68	0.45	0.52	0.47
CEM	0.32	0.73	0.51	0.32	0.51	0.62
SC		0.71	0.43		0.45	
<b>Average</b>	<b>0.67</b>	<b>0.69</b>	<b>0.52</b>	<b>0.47</b>	<b>0.57</b>	<b>0.56</b>

# Genomic Prediction Pipeline



# Selection Index Assumptions

$$\mathbf{Pb} = \mathbf{g}$$

$$\text{var} \begin{bmatrix} \widehat{u} \\ \widehat{m} \\ u \end{bmatrix} = \begin{bmatrix} r_p^2 & r_p^2 r_m^2 \\ r_p^2 r_m^2 & r_m^2 \\ r_p^2 & r_m^2 & 1 \end{bmatrix} \begin{bmatrix} r_p^2 \\ r_m^2 \\ 1 \end{bmatrix} \sigma_g^2$$

$$\text{var} \begin{bmatrix} u - \widehat{u} \\ m - \widehat{m} \end{bmatrix} = \begin{bmatrix} 1 - r_p^2 & (1 - r_p^2)(1 - r_m^2) \\ (1 - r_p^2)(1 - r_m^2) & 1 - r_m^2 \end{bmatrix},$$

# Blending

$$\widehat{u}_n = \frac{(1 - r^2) (\widehat{u}_p - \mu_{u_p}) + (1 - a^2) (\widehat{m} - \mu_m)}{1 - r^2 a^2}$$

$$Rel_n = 1 - \frac{(1 - r^2) (1 - a^2)}{1 - r^2 a^2}$$

where  $\widehat{u}_p$  is the previous national EBV with  $Rel_p = a^2$   
and  $\widehat{m}$  is the MBV (DGV) with genetic correlation  $r^2$



# Extended Blending

- Desirable for relatives of blended animals to benefit (in accuracy) from genotyping of their relatives – first extend the DGV to nongenotyped

Elements of inverse relationship matrix (sparse)

$$A^{11}u_1 = -A^{12}u_2$$

DGV of non-genotyped animals

DGV of genotyped animals

# Extended Blending

- Desirable for relatives of blended animals to benefit (in accuracy) from genotyping of their relatives – second compute their reliability
- Take advantage of partitioned matrix result

$$\mathbf{A}^{11} = (\mathbf{A}_{11} - \mathbf{A}_{12}\mathbf{A}_{22}^{-1}\mathbf{A}_{21})^{-1}$$

$$R_{DGV}^2 = \{diag[\mathbf{A}_{11}] - diag[(\mathbf{A}^{11})^{-1}]\} / diag[\mathbf{A}_{11}]$$

- Then blend nongenotyped relatives

# Properties of BLUP (1 of 2)

- Provided the model is correct:

$$\text{cov}(u, \hat{u}) = \text{var}(\hat{u})$$

Quantify from inverse MME  
Or approximate from MME

- Then

$$\beta_{u/\hat{u}} = \frac{\text{cov}(u, \hat{u})}{\text{var}(\hat{u})} = 1 \quad (\text{exactly})$$

*Although  $E[u] = 0$ ,  $E[u / \hat{u}] = \hat{u}$*

# Properties of BLUP (2 of 2)

- Provided the model is correct:

$$\text{cov}(u, \hat{u}) = \text{var}(\hat{u})$$

- Then

$$r_{u, \hat{u}} = \frac{\text{cov}(u, \hat{u})}{\sqrt{\text{var}(\hat{u}) \text{var}(u)}} = \sqrt{\frac{\text{var}(\hat{u})}{\text{var}(u)}}$$

- And

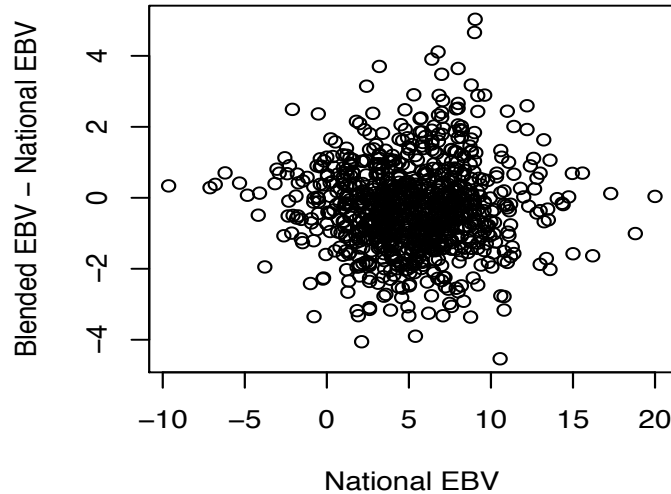
$$\text{var}(\hat{u}) = r_{u, \hat{u}}^2 \text{var}(u)$$

# Diagnostics of Good Behavior

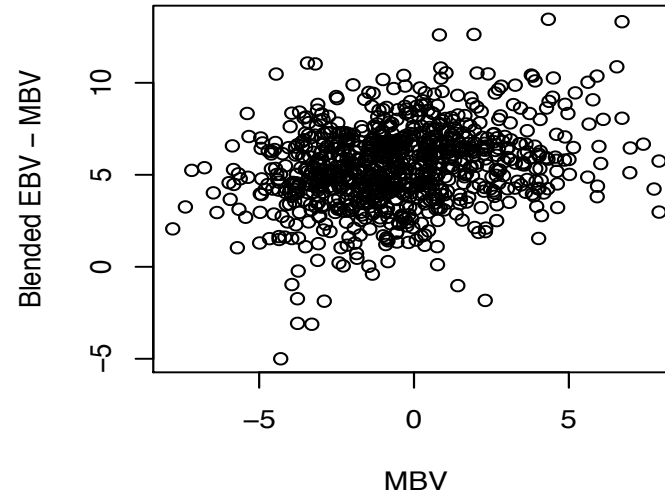
- Regression of more accurate (blended) on less accurate (EBV or MBV) should be 1
- Correlation of less accurate EBV with change in EBV (from less accurate to more accurate) should be zero

# Validation of Birth Weight (AHA)

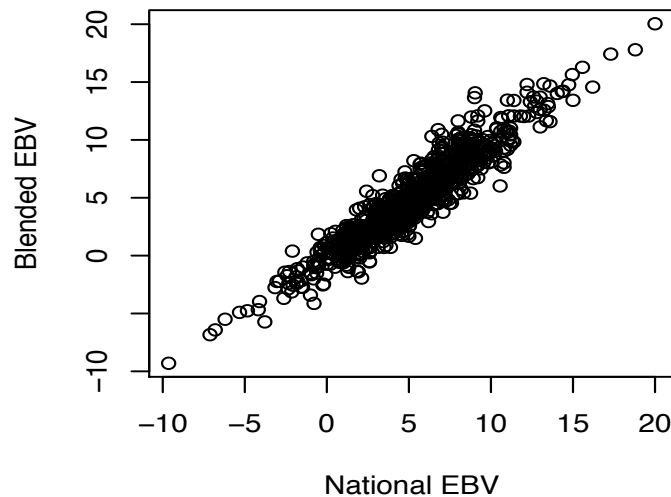
**CORR=0.01**



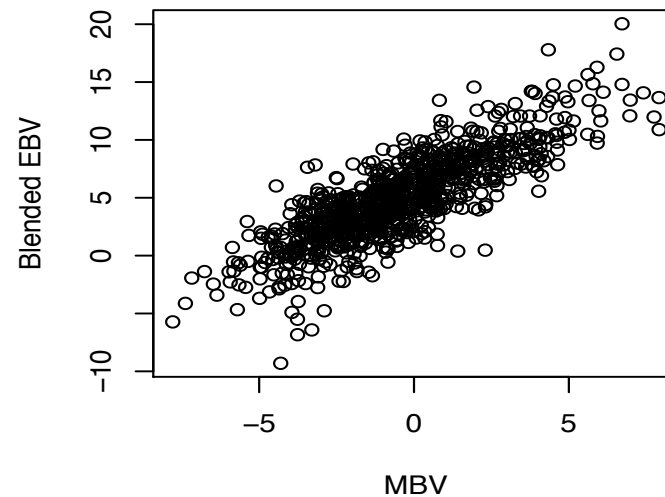
**CORR=0.26**



**SLOPE=1**

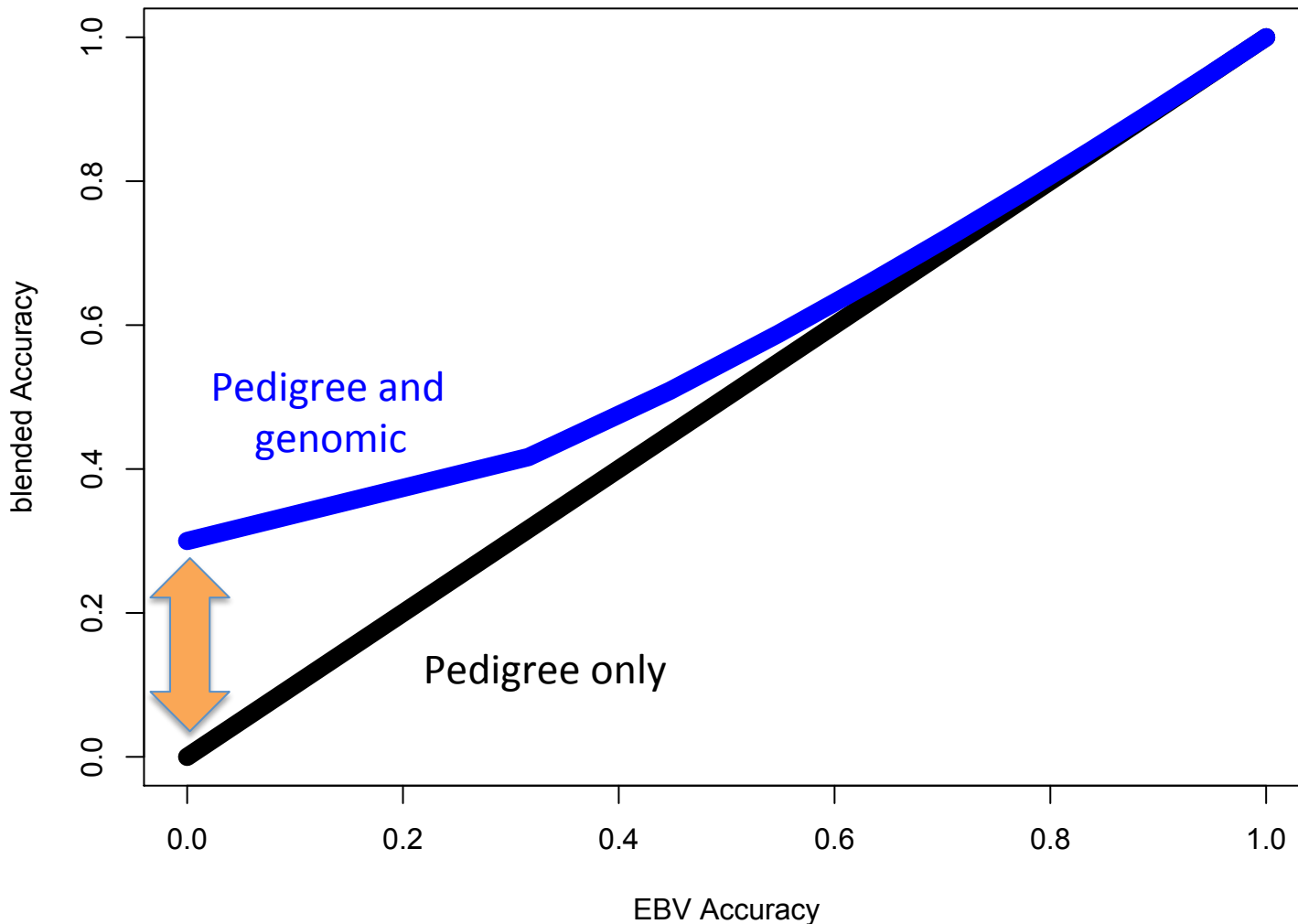


**SLOPE=1.22**



# Impact on Accuracy--%GV=10%

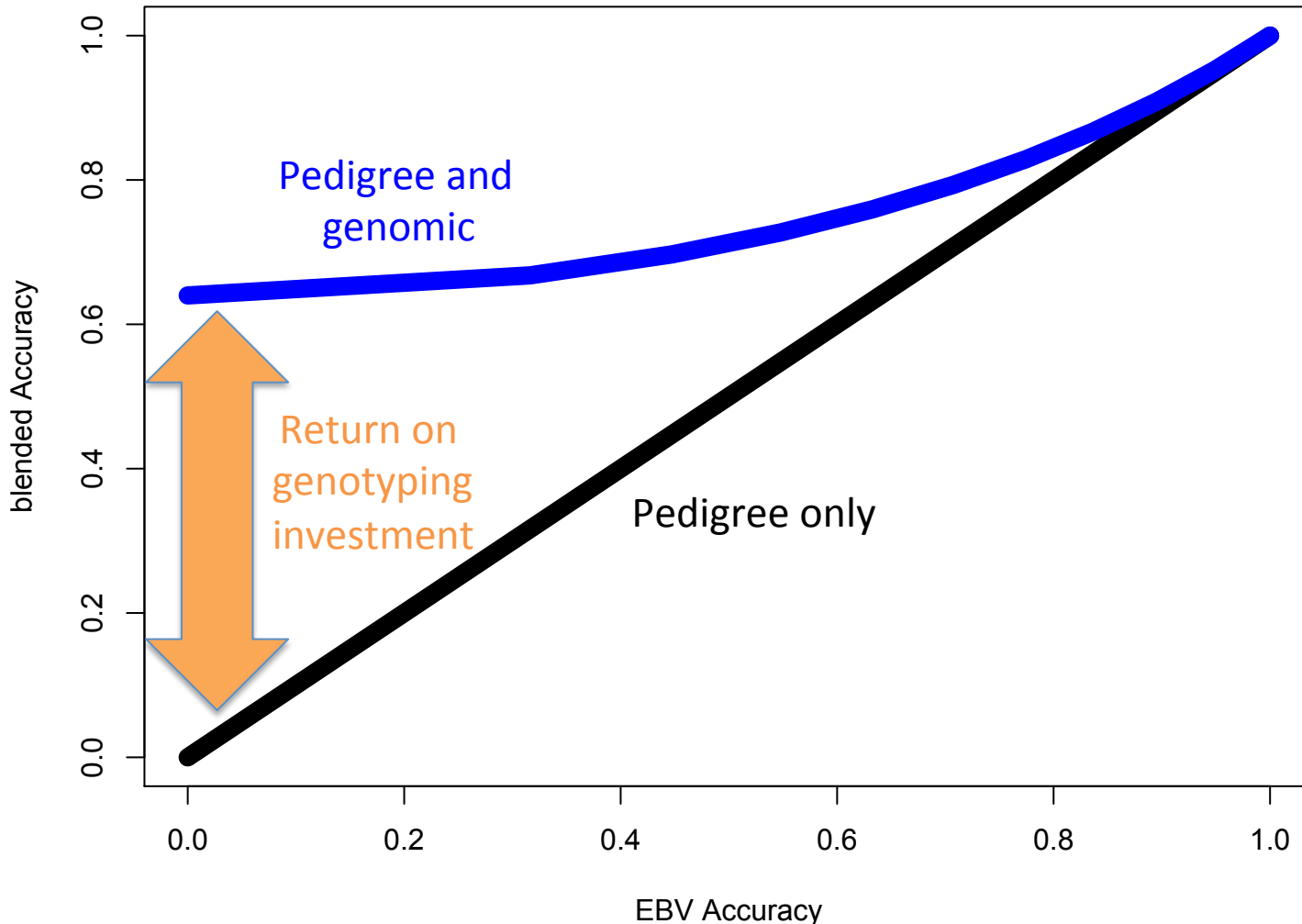
Genetic correlation=0.3



Blending will not improve the accuracy of a bull that already has a reliable EBV

# Impact on Accuracy--%GV=40%

Genetic correlation=0.64



Blended EBVs are equally likely to be better or worse than the preblended EBVs



# Genotype Counts in early 2014

Breed	9k	GGP-LD	50k	GGP-HD	BOS-1	700k HD	TOTAL
AAN		911	13,409	787		947	16,054
BRG			1,128	173		243	1,544
BSH			325			136	461
CHA			1,617			525	2,142
GVH	186	209	1,643	371	414	430	3,253
HER			7,064	1,887	471	850	10,272
LIM		429	3,420	8	461	675	4,993
NEL						2,571	2,571
RAN			1,931	1,183	226		3,340
RDP			1,394				1,394
SIM	5,223	7,026	6,501	1,347	1,601	674	22,372
TOTALS	5,409	8,575	38,432	5,756	3,173	7,051	68,396

*The amount of data has approximately doubled since then.....<sup>25</sup>*

# Lower Density Panels

AHA Predictive Accuracy 2,980 6-fold

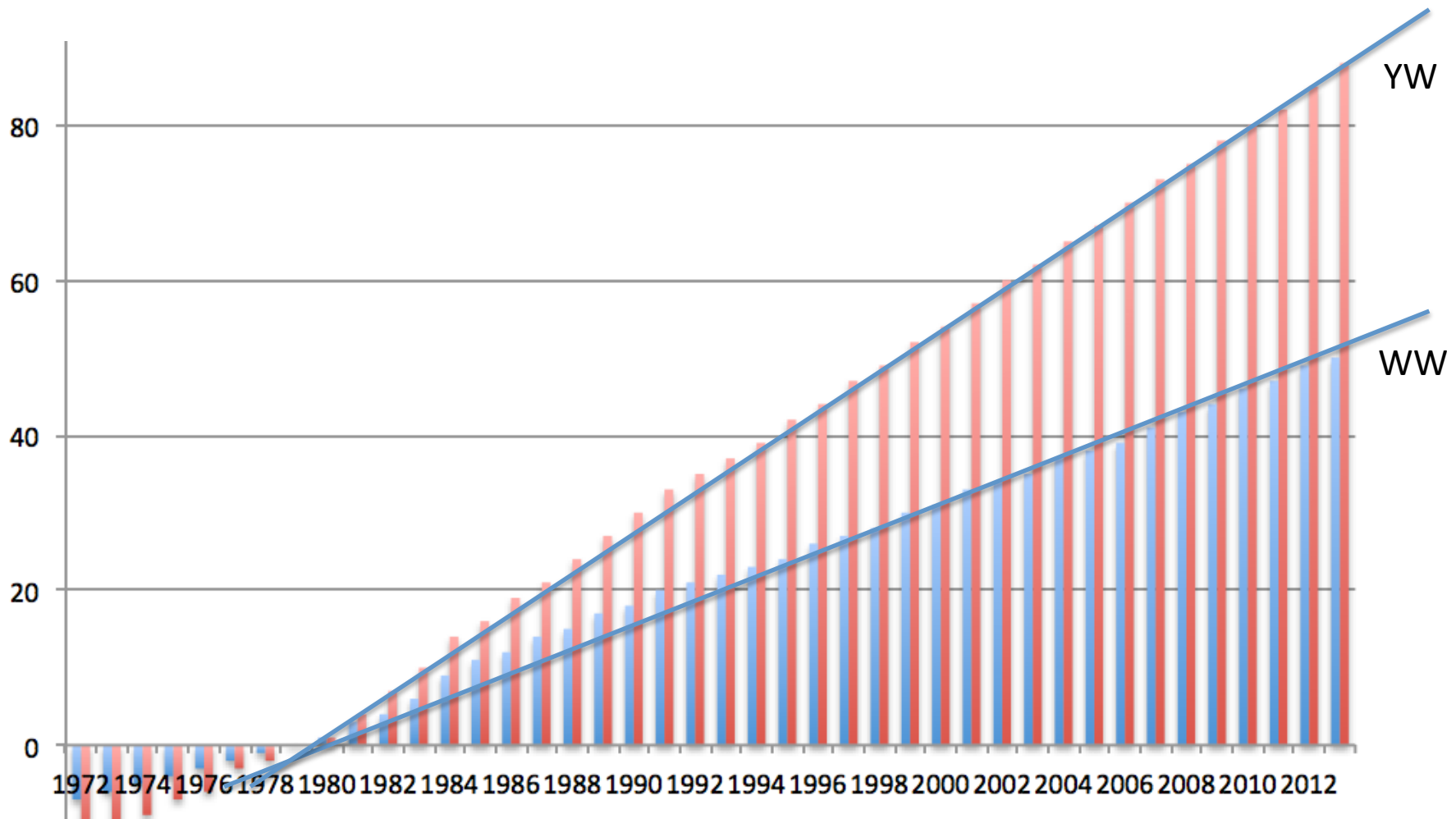
Trait	Actual	Imputed
Birth Weight	0.67	0.65
Calving Ease Direct	0.68	0.67
Calving Ease Maternal	0.51	0.50
Fat Thickness	0.47	0.46
Marbling	0.42	0.42
Mature cow weight	0.64	0.62
Rib Eye Muscle Area	0.49	0.46
Scrotal Circumference	0.43	0.42
Weaning Weight Direct	0.53	0.50
Weaning Weight Maternal	0.37	0.35
Yearling Weight	0.61	0.59
Mean	0.53	0.51

Actual = 50k  
Imputed = 10k  
(from GGP-LD)

# Who is being genotyped?

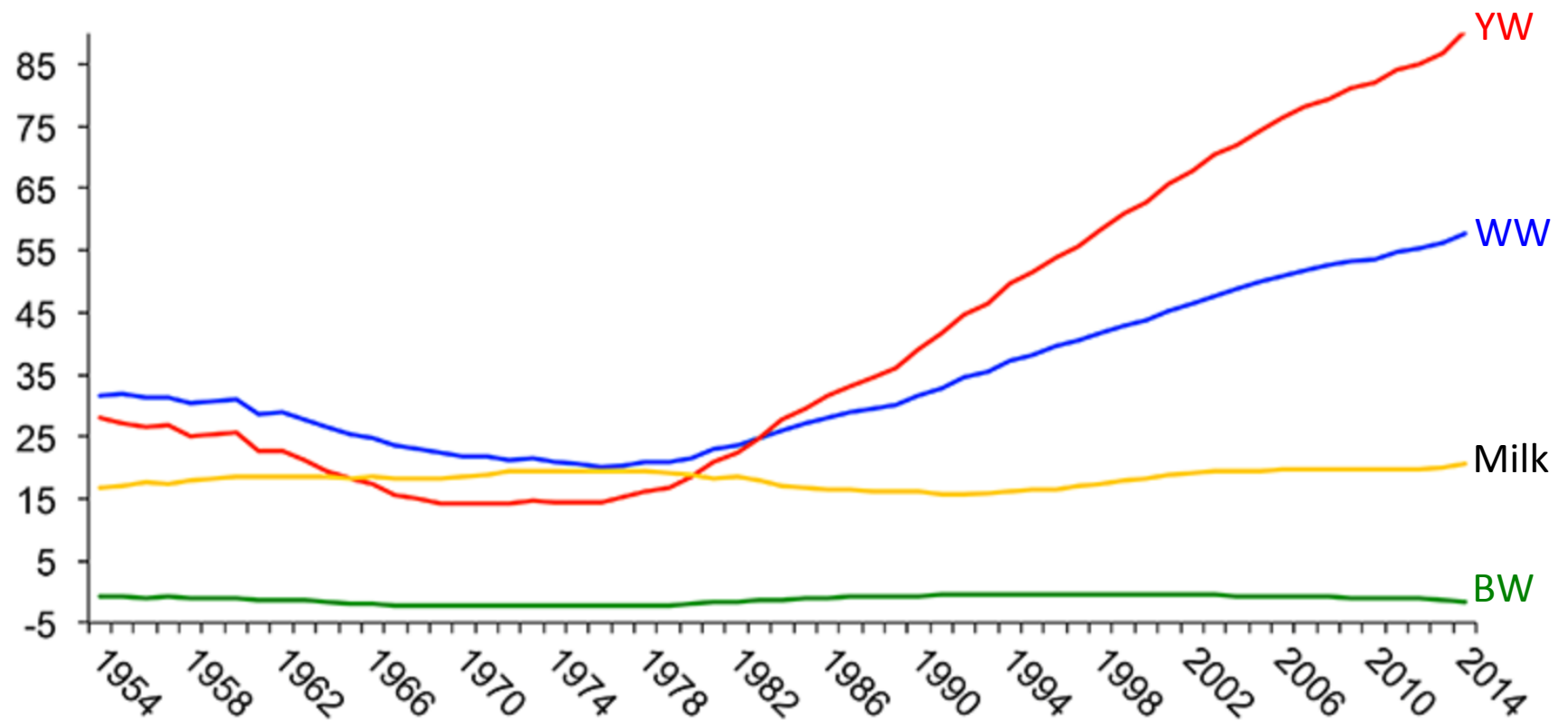
- Originally primarily widely-used AI sires
- Augmented with sires used in herds that wanted to predict young animals
- Just a few of the most promising young bulls
- Now often all the sale bulls and some heifers being genotypes
- But what is the impact of genotyping on  $\Delta G$ ?

# (Black) Angus Genetic Trends

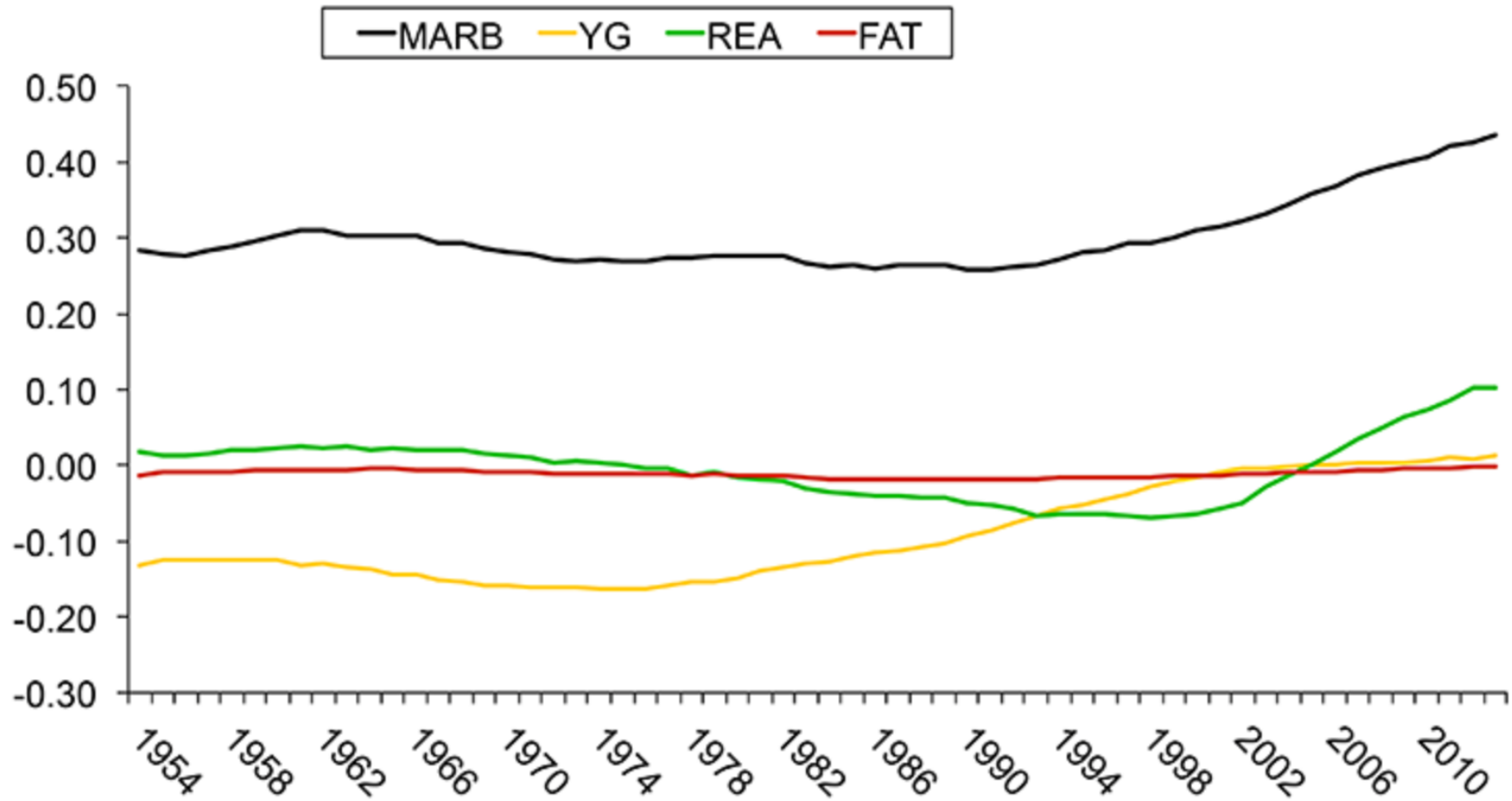


No evidence any technology over the last 35 years has changed  $\Delta G$ !

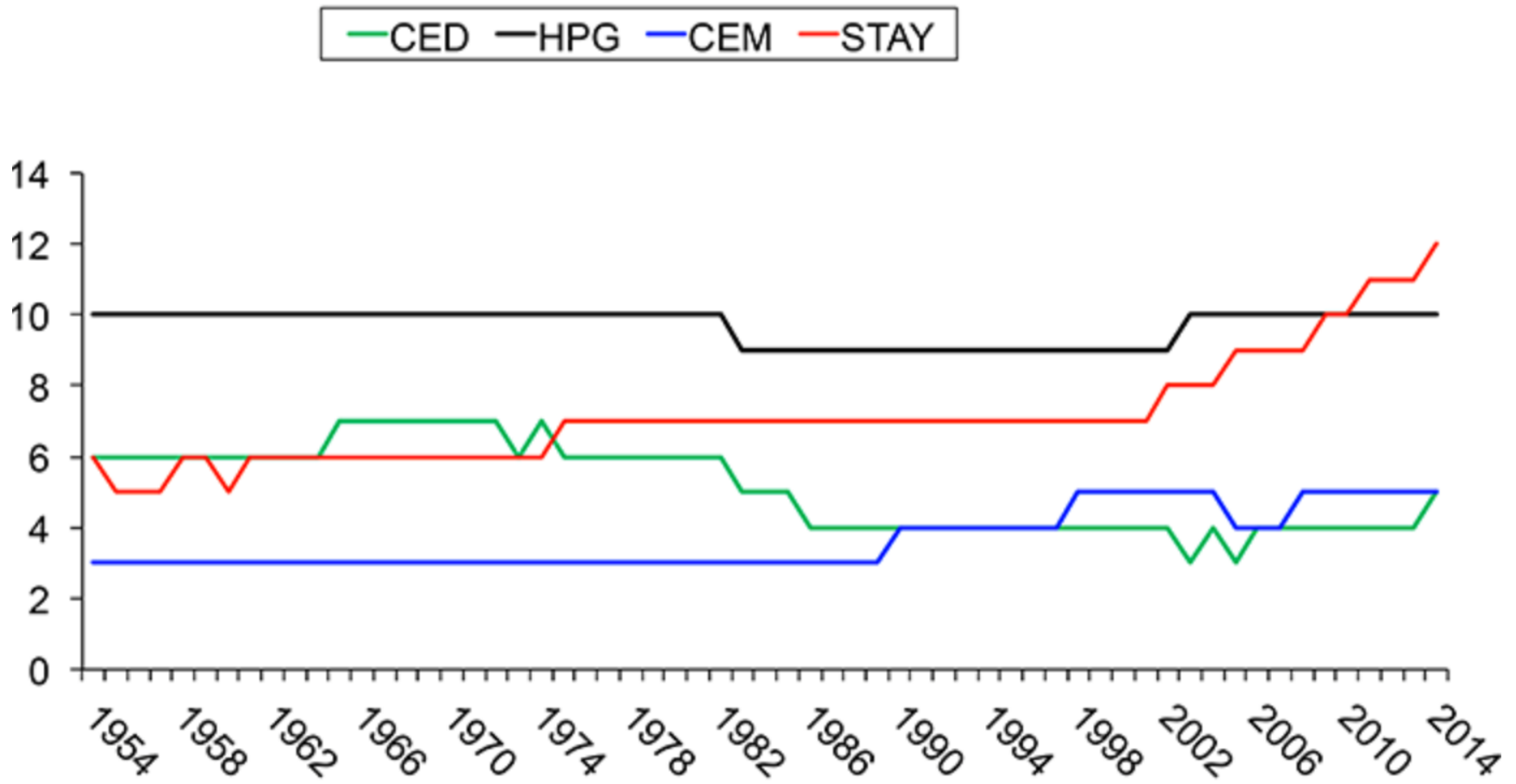
# Red Angus Association Genetic Trends



# Red Angus Carcass Genetic Trends



# Red Angus Reproductive Genetic Trends



# Future Developments - GBS

Trait	Black Angus	Hereford	Gelbvieh	Limousin	Red Angus	Simmental	Trait Average
Birth weight	93	84	81	76	100	93	87
Calving ease D.	85	90	85	93	96	91	90
Calving ease M.	88	72	90	90	89	84	85
Carcass weight	91	-	90	92	87	87	89
Fat thickness	81	83	70	-	57	105	79
Heifer Preg	-	-	-	-	108	-	108
Marbling	95	73	87	71	95	99	87
Milk	89	69	87	112	52	98	85
Post-wean ADG	101	78	77	73	85	73	81
Rib eye area	85	83	51	79	99	92	82
Stayability	-	-	-	-	94	88	91
Weaning eight	91	84	87	77	84	91	86
Yearling weight	97	84	91	80	84	83	86
Breed Average	91	80	81	84	87	90	86

GeneSeek

Pre-production  
genotyping-by-  
sequencing  
panel

Relative Efficiency (correlation reduced panel/correlation 50k) for 1k panel targeting QTL



# Summary

- What are the opportunities for the use of genomic selection in beef cattle
  - Huge opportunities for traits not easily improved by conventional selection
    - Unfortunately, these traits are not practical for implementing genomic selection without massive phenotyping and industry re-organisation
  - Some opportunities to screen bulls for sale
    - But this may not improve the bull breeding business
  - Some opportunities to improve bull fathers

# Summary

- How is genomic selection used in beef cattle?
  - Using combined panel that can simultaneously
    - Determine or verify parentage
    - Screen various recessive conditions
    - Impute to panels used to predict the routinely evaluated traits produced by National Cattle Evaluation
  - Hard to determine the extent intensities of selection or generation intervals of various selection pathways are being altered
  - Potential to increase selection of unregistered animals and erode the demand for bulls from bull breeding herds

# Summary

- What are the challenges for further advancing the use of genomic selection in beef cattle?
  - The value proposition is poorer than in other industries
  - Works better for some traits than others
  - The regression of phenotype on DGV is often  $<1$ 
    - Poorly evaluated animals may have large  $\text{var}(\hat{u})$

# Need Better Tools

- The genome is heterogeneous and quality of marker panels is poor in some genomic locations
  - Imputation limited by quality of actual genotypes
- The reference (sequence) genome has limitations
  - Need long reads eg PAC Bio
  - May need breed specific reference
  - Need more and better annotation
- Need to discover more causal mutations

# Need More Data

- More phenotypes and genotypes!
  - Both nature and scope