



Genetic Improvement of Beef Cattle: Current Practice and Future Prospects



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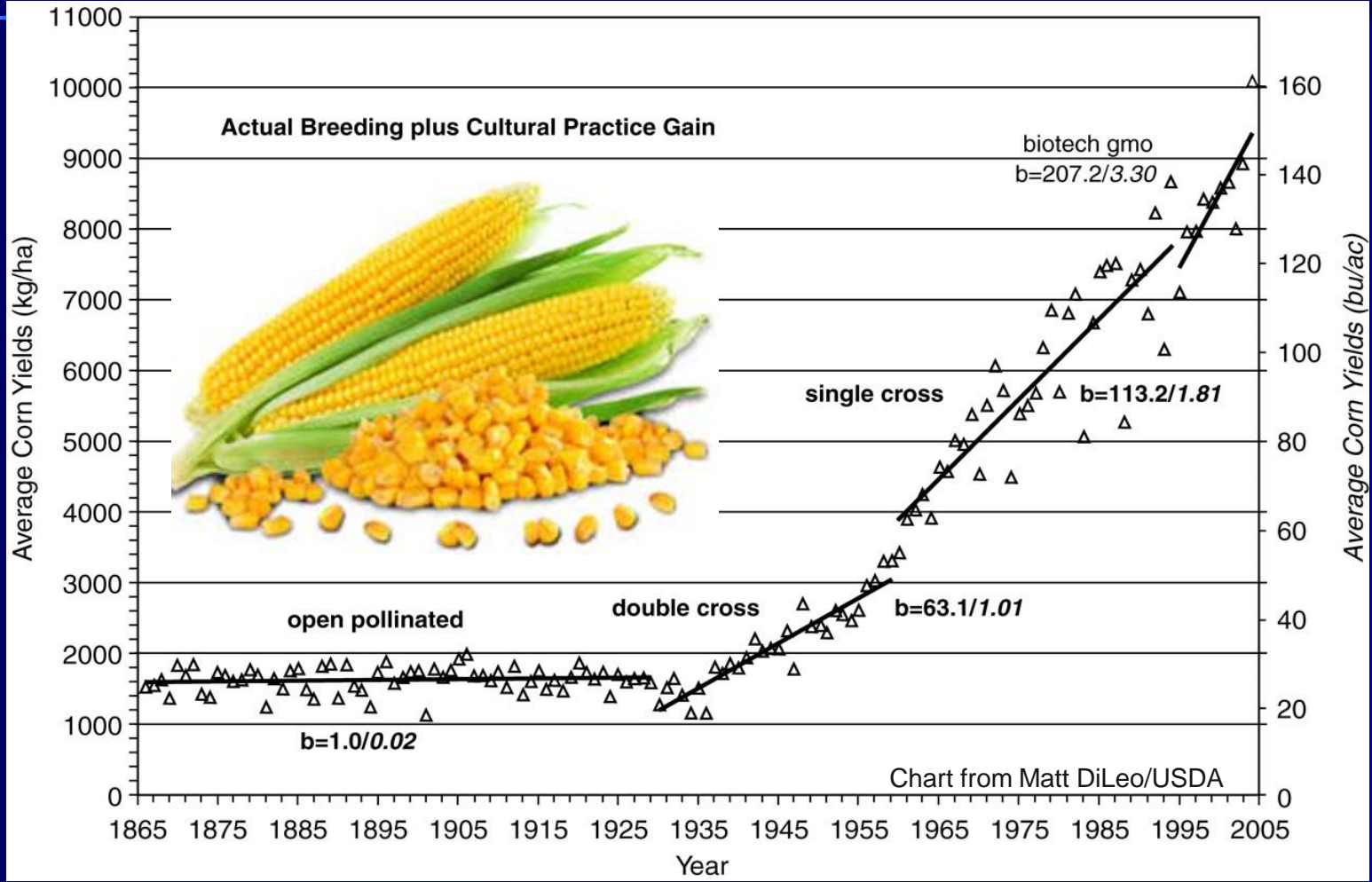


Animal breeders have used selection on phenotypes to great effect!





Plant and animal breeders have perhaps the most compelling sustainability story of all time

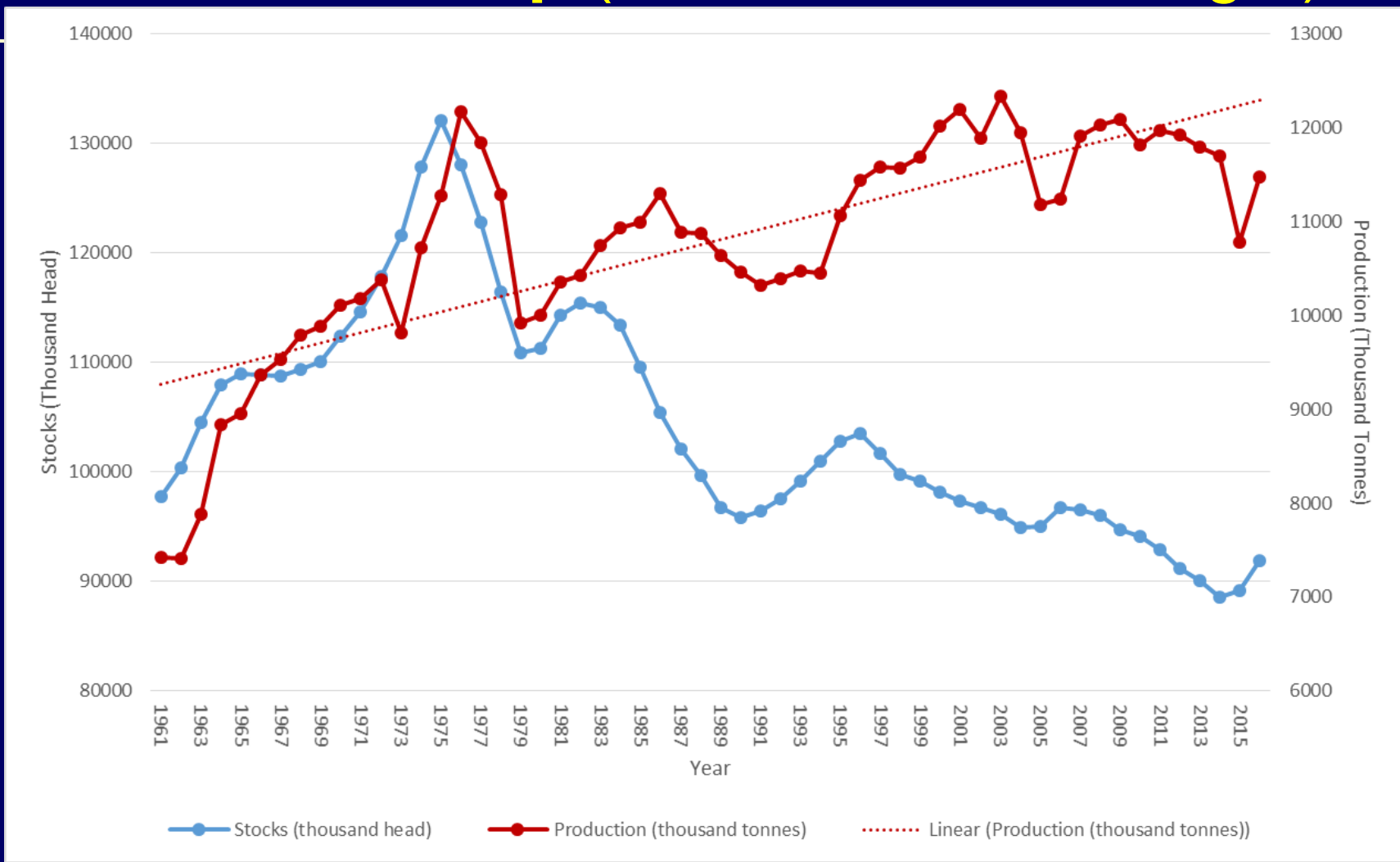


<https://grist.files.wordpress.com/2015/12/corn-hybrid-yields.jpeg>



US Cattle Inventory 1961 – 2015

Stocks Down ('000 Head; blue, left) vs. Production Up ('000 Tonnes; red, right)

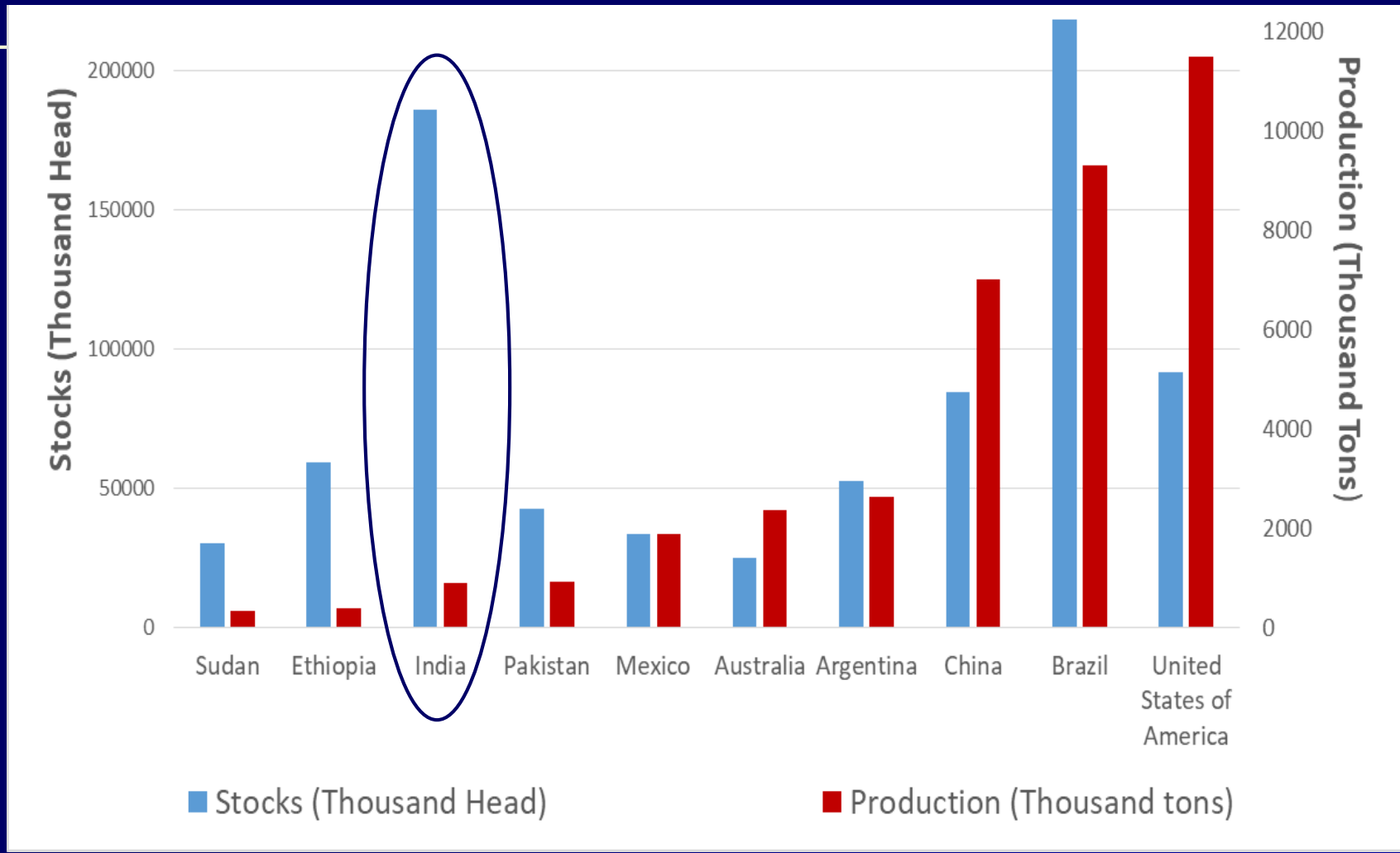




2016 Global Beef Production Numbers

Cattle numbers ('000 Head; blue, left)

vs. Beef production ('000 Tonnes; red, right)



A man in a white lab coat and purple bow tie stands against a black background, pointing his right arm upwards. In the background, there is a glowing green line graph on the left and a glowing white ring in the upper center. The word "SCIENCE" is written in large, bold, white letters with a black outline across the middle of the image.

SCIENCE



Time line for beef breeding



Bull purchase/selection



Image adapted from "More Beef from Breeding" Workshop (2007). Meat and Livestock (MLA), Australia

Progeny born



Progeny slaughtered



Female progeny used for breeding





Practical Guide to Bull Buying



- Determine marketing strategy
 - Will heifers be retained?
- Determine management level
 - Nutrition
 - Labor
- Assure bulls are reproductively sound
 - BSE
- Check for structural soundness



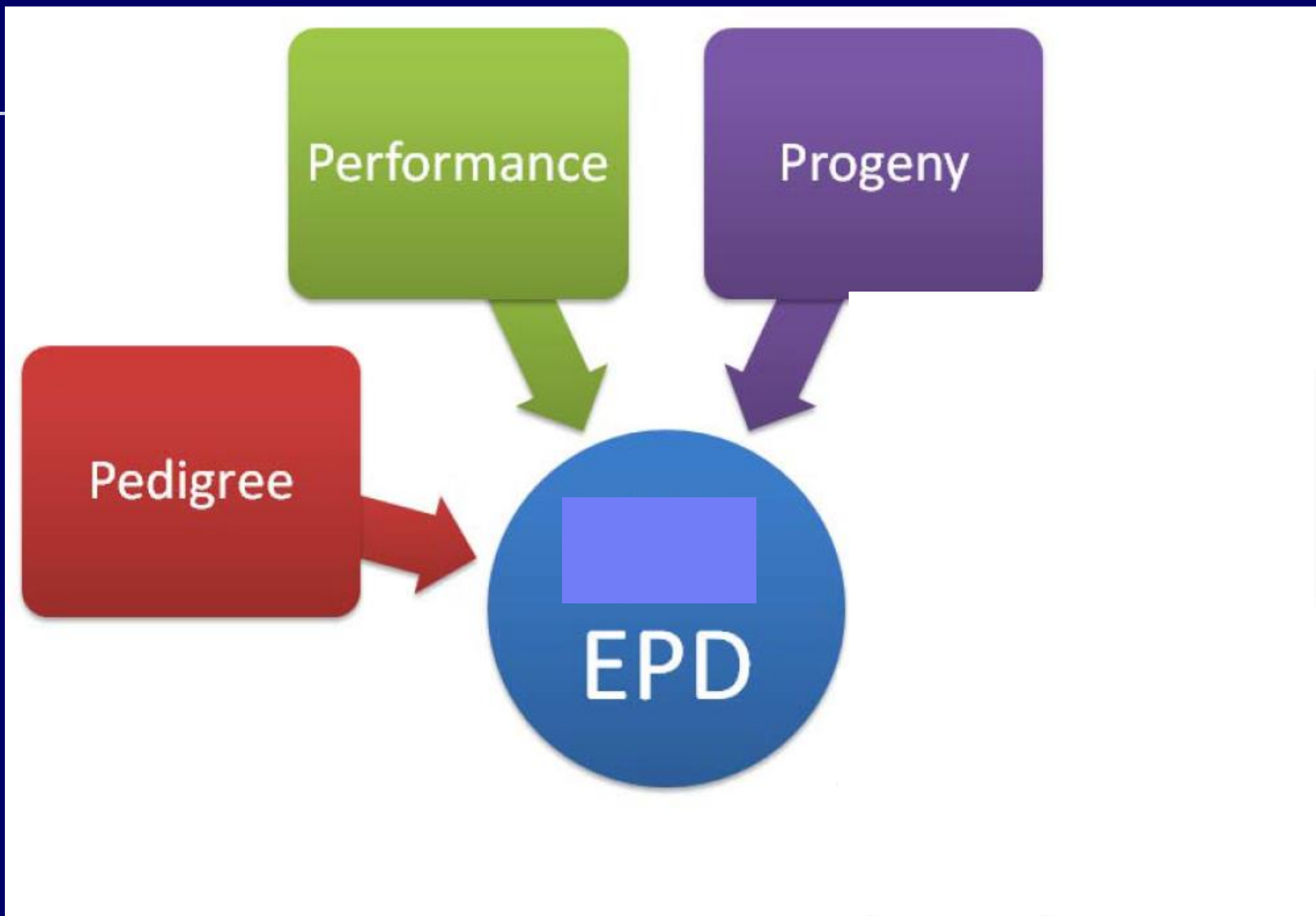
EPDs

- Best tool for selecting for performance traits
- Uses all information: actual measurement, relatives, environment, genomics
- Risk management tool





Information sources for EPDs





What EPDs are available?



EPD Definitions

	BULL A	BULL B
Calving ease direct	10	6
Birth weight	2.0	3.5
Weaning weight direct	20	22
Yearling weight	40	52
Yearling height	0.3	0.6
Milk	3	-2
Maternal weaning weight	13	9
Gestation length	-0.1	1.1
Calving ease maternal	4	6
Mature daughter height	0.5	1.0
Mature daughter weight	0	30
Scrotal circumference	0.1	-0.45
Heifer pregnancy	6	9
Udder	0.4	-0.1
Teat	0.5	0
Carcass weight	2.0	20
Percent retail cuts	0	0.2
Marbling	0	-0.3
IMF	3.0	1.0
Rib-eye area	0.06	1.6
Fat thickness	-0.01	-0.09
Rump fat thickness	-0.03	-0.10
Tenderness	-0.01	0.1
Days to finish	15	10
Residual average daily gain	-0.1	0.05
Residual feed intake	-0.05	0.10
Dry matter intake	0.2	0.4
Stayability	10	6
Maintenance energy	0	10
Docility	6	2

EPD



+65 lbs



+50 lbs

**Direct
weaning
weight**

**Expect the average difference in
offspring to be 15 pounds.**

EPD



+25 lbs



+15 lbs

**Direct
weaning
weight**

**Expect the average difference in
offspring of the sires daughters to
be 10 pounds.**

Calving Ease

- Bull – Calving Ease Direct
 - Heifers/Cows
 - Time spent with calving females
- Heifers – Calving Ease Maternal
 - If replacements are kept
 - Does not replace buying CED bull



Be careful not to put too much emphasis on selection for calving ease

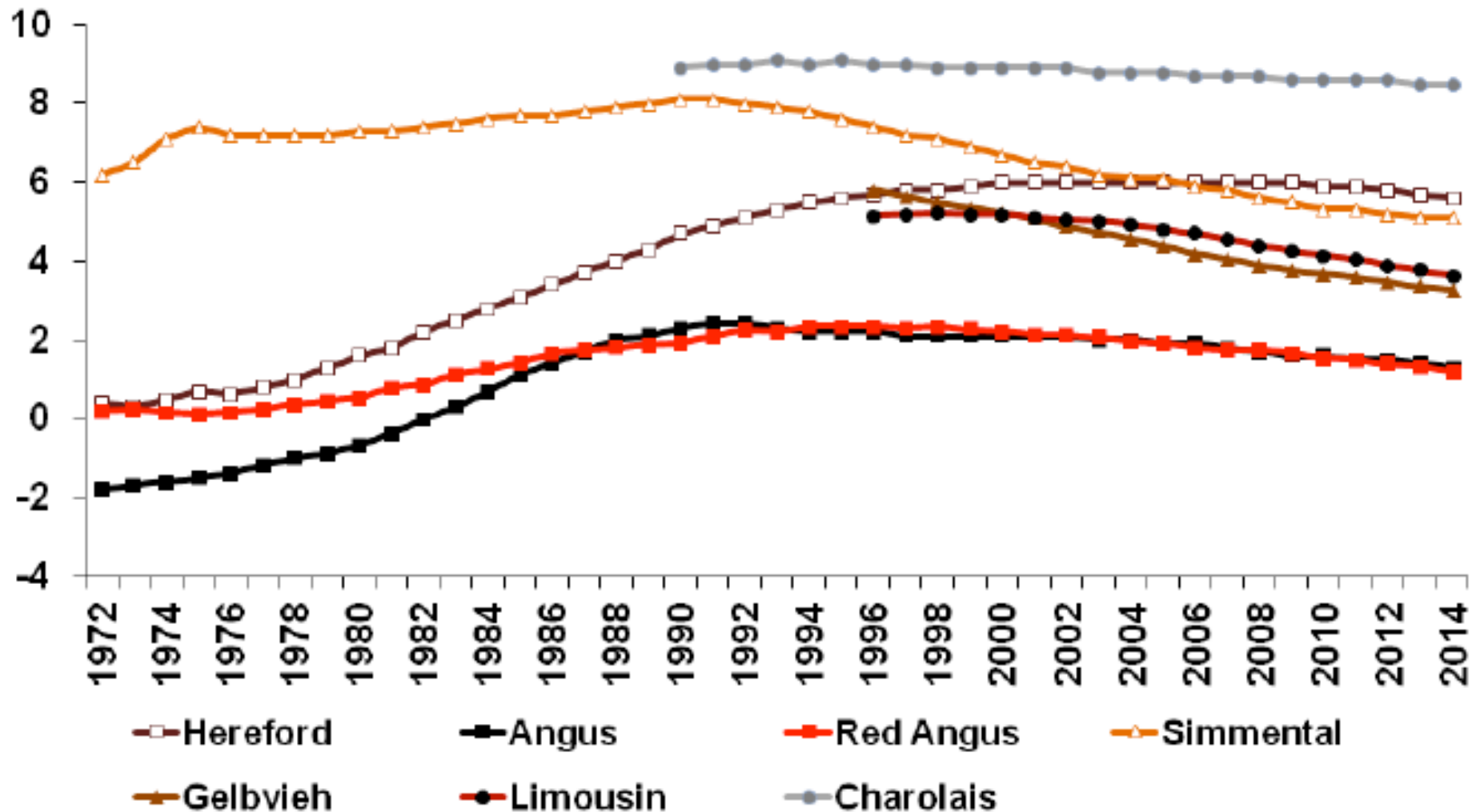


Smallest calf

An 850-pound Angus cow, owned by Paul Utz of Madison, Va., licks the face of her calf. Weighing 16 pounds at birth, the calf is the

world's smallest, according to officials at the Guinness Book of World Records. (AP Laser-photo)

Birth Weight Trends



Growth

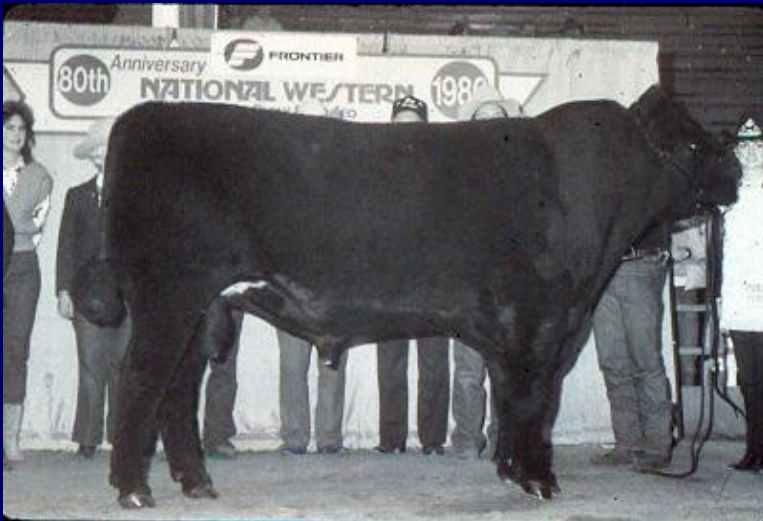
- Use EPD closest to marketing endpoint
 - Weaning Wt EPD
 - Yearling Wt EPD
 - Carcass Wt EPD
- Be aware of correlated traits
 - Milk
 - Mature Size
 - Calving Ease



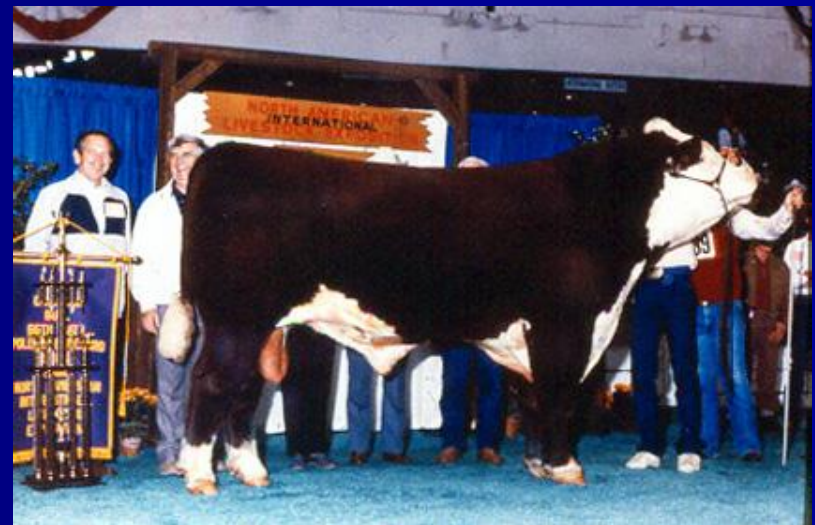
1953. Grand Champion Angus Female, International, 1953



1950. Grand Champion Steer, International, weighing 1025 lbs



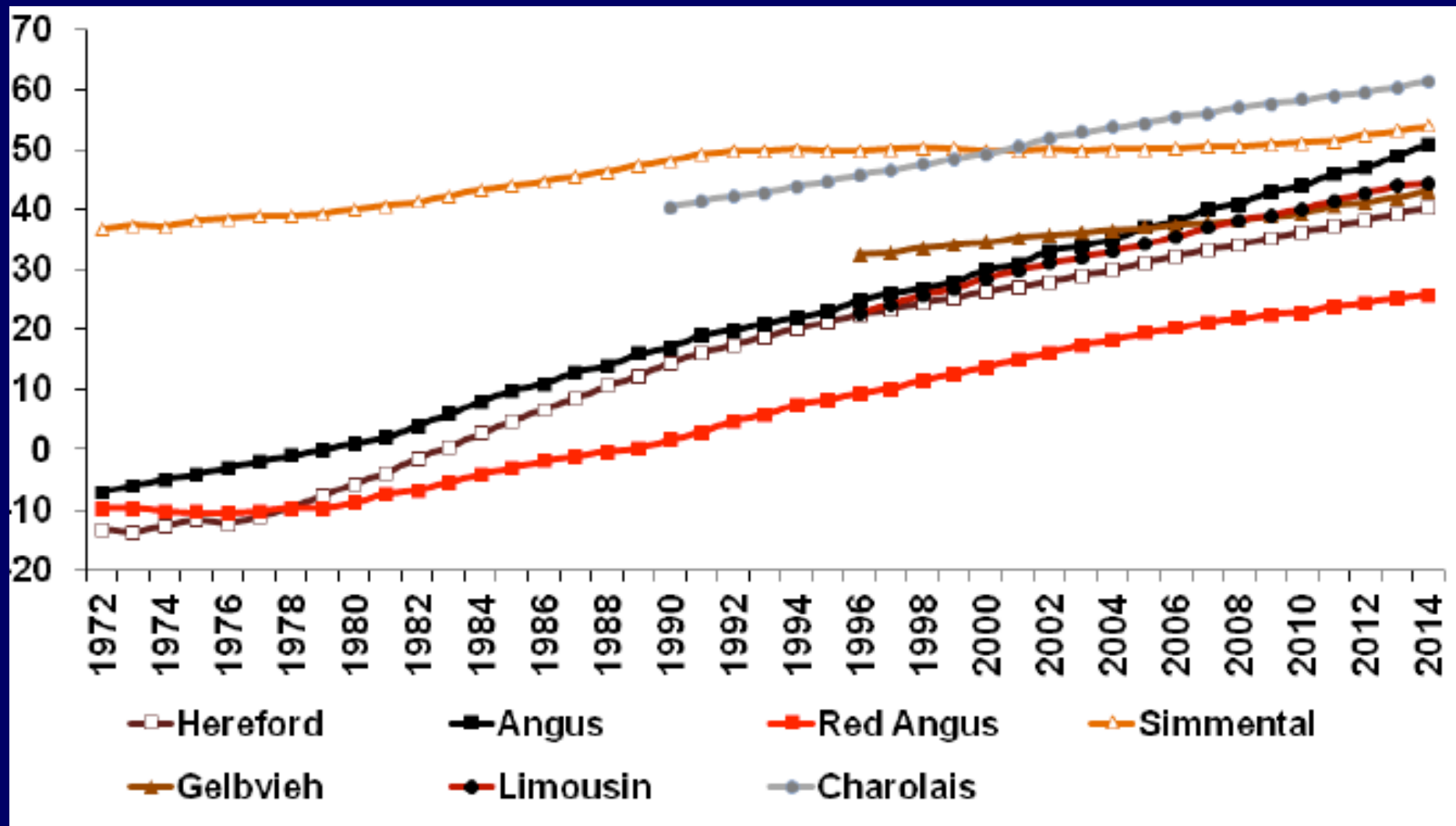
1986. "Coblepond New Yorker" weighed 2529 lbs and measured 65 inches tall at 35 mos. (Frame 10) when he was Denver Champion.



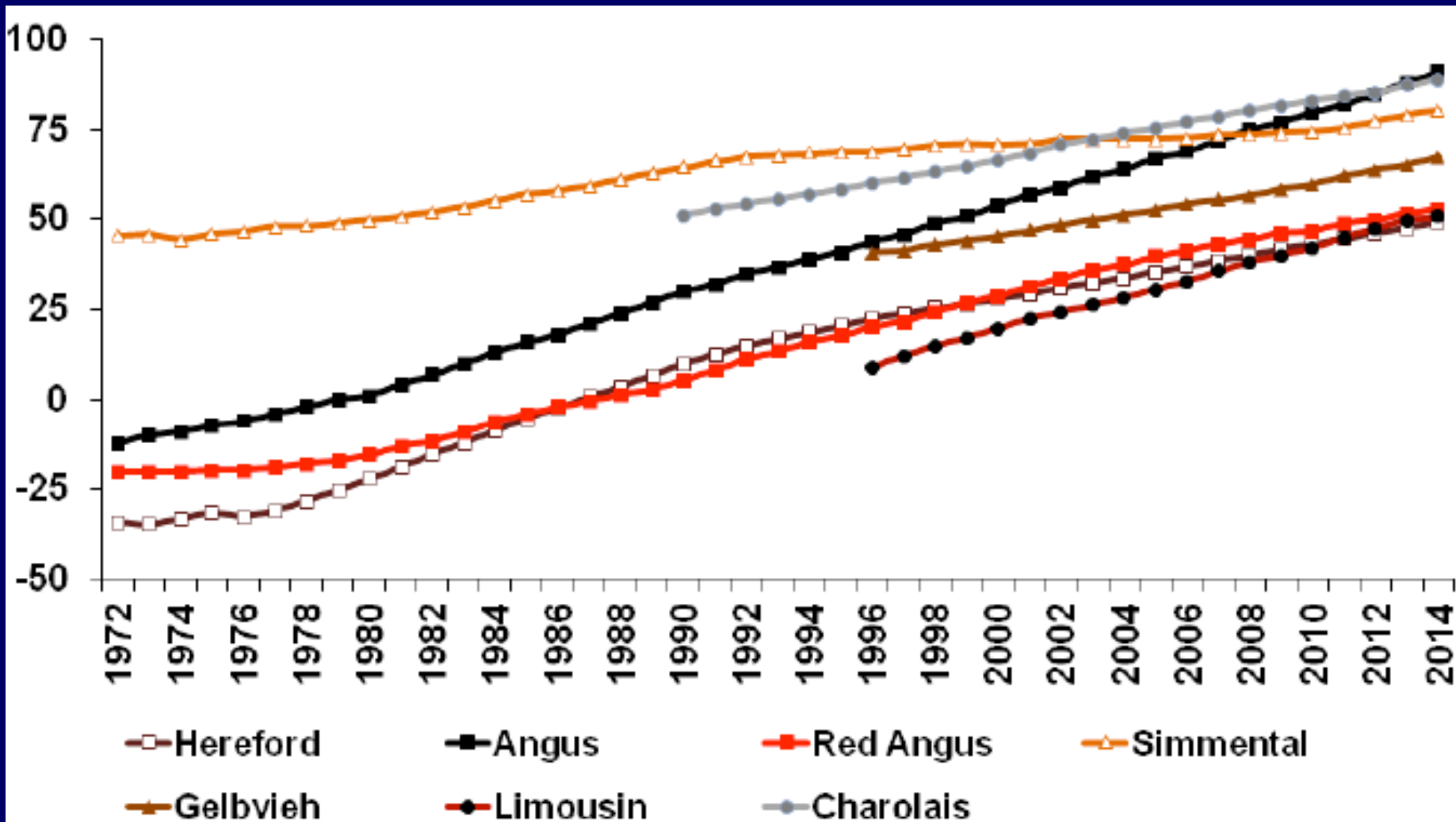
1988 Grand Champion Bull, National Polled Hereford Show (frame 10).

Images from Harlan Ritchie's historical review of type
<https://www.msu.edu/~ritchih/historical/cattletype.html>

Weaning Weight Trends



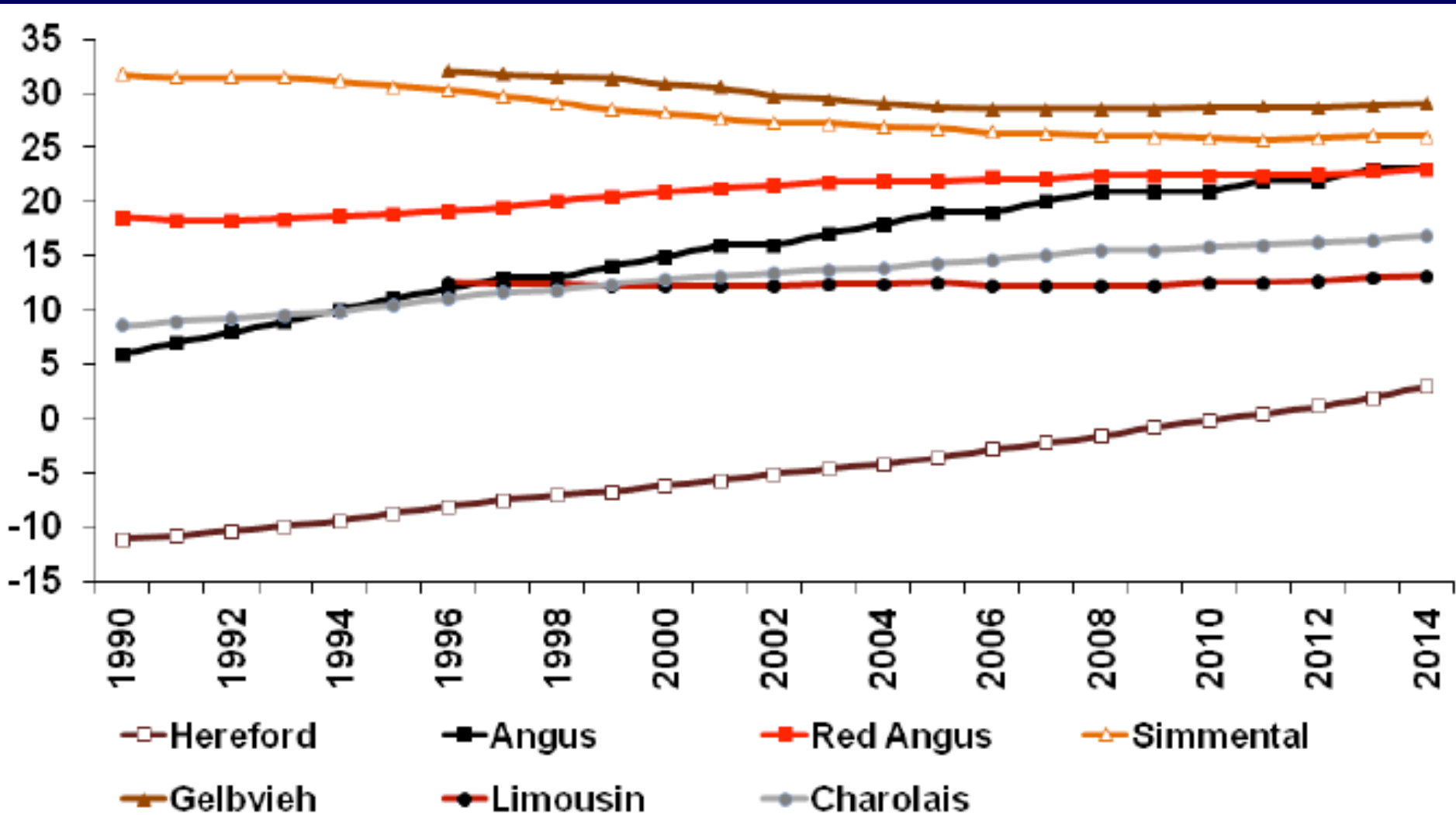
Yearling Weight Trends



Maternal

- Milk
- Reproduction
 - Heifer Pregnancy
 - 30-Month Pregnancy
 - Stayability
 - Sustained Cow Fertility

Milk Trends





When making selection decisions to improve fertility – which group of cattle should selection focus upon?

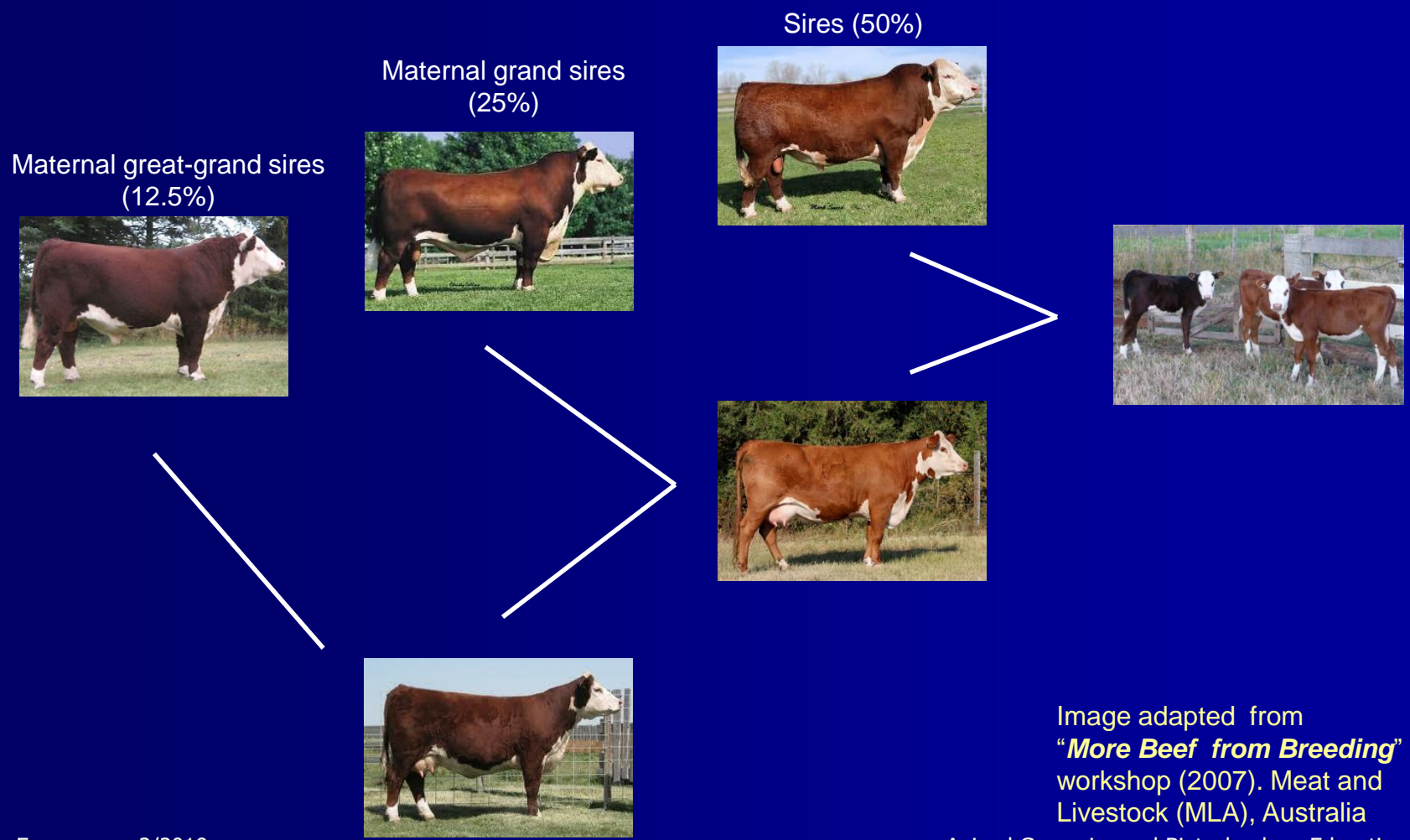
1. Bulls
2. Cows
3. Heifers





Genetic composition of the herd:

87% of genetic composition of calf crop is determined by the sires used over the last 3 generations



Carcass

- Carcass Wt EPD
- Quality Factors
 - Marbling EPD
 - % IMF EPD
- Yield Factors
 - Fat EPD
 - Ribeye Area EPD

Other

- Disposition
 - Docility EPD
- Scrotal Circumference
 - SC EPD
 - Actual Measurement
- Color/Horned-Polled
 - Homozygous vs Double bred
 - Carrier

30

PVF Insight 12

S A V Brilliance

PVF Missie

Triple C Majic Man

NB Magic Sugar

NB Sugar & Spice

CE	BW	WW	YW	MCE	Milk	MWW	Marb	REA	API
14	-0.6	62	104	8	30	61	0.27	1.2	131

2018 Purebred Simmental Percentile Table

	%	API	TI	CE	BW	WW	ADG	YW	MCE	MLK	MWW	STY	DOC	CWT	YG	MRB	BF	REA	SF
Purebred	1	163.73	86.19	18.4	-2.4	85.8	0.30	131.1	15.7	32.7	68.5	19.3	15.2	53.8	-0.49	0.49	-0.100	1.17	-0.51
Fullblood	2	159.11	84.28	17.4	-1.9	83.3	0.29	126.8	14.9	31.4	66.8	18.5	14.7	50.9	-0.46	0.45	-0.094	1.12	-0.48
Simbrah	3	156.19	83.07	16.8	-1.6	81.7	0.28	124.1	14.3	30.5	65.6	17.9	14.4	49.0	-0.45	0.42	-0.091	1.09	-0.47
Hybrid	4	153.99	82.16	16.3	-1.4	80.5	0.27	122.1	13.9	29.9	64.8	17.5	14.2	47.6	-0.44	0.40	-0.088	1.07	-0.46
	5	152.20	81.42	15.8	-1.2	79.5	0.27	120.4	13.6	29.4	64.1	17.2	14.0	46.5	-0.43	0.39	-0.086	1.05	-0.45
	10	146.07	78.87	14.5	-0.5	76.2	0.25	114.7	12.4	27.6	61.7	16.0	13.3	42.5	-0.40	0.33	-0.079	0.98	-0.42
	15	141.93	77.16	13.6	-0.1	73.9	0.24	110.9	11.6	26.4	60.1	15.2	12.9	39.9	-0.38	0.30	-0.074	0.94	-0.40
Top Fifty Sires	20	138.63	75.79	12.9	0.3	72.1	0.23	107.8	11.0	25.4	58.9	14.6	12.5	37.8	-0.37	0.27	-0.070	0.90	-0.39
	25	135.81	74.63	12.3	0.6	70.6	0.22	105.2	10.5	24.6	57.8	14.1	12.2	36.0	-0.35	0.24	-0.067	0.87	-0.37
Possible Change	30	133.26	73.57	11.7	0.9	69.2	0.22	102.8	10.0	23.9	56.8	13.6	11.9	34.4	-0.34	0.22	-0.063	0.84	-0.36
	35	130.92	72.60	11.2	1.1	68.0	0.21	100.7	9.5	23.2	55.9	13.1	11.7	32.9	-0.33	0.20	-0.061	0.82	-0.35
	40	128.68	71.67	10.7	1.3	66.7	0.20	98.6	9.1	22.5	55.0	12.7	11.5	31.4	-0.32	0.18	-0.058	0.80	-0.34
	45	126.53	70.78	10.3	1.6	65.6	0.20	96.6	8.7	21.9	54.2	12.3	11.2	30.1	-0.31	0.16	-0.056	0.77	-0.33
	50	124.40	69.90	9.8	1.8	64.4	0.19	94.6	8.3	21.3	53.4	11.9	11.0	28.7	-0.30	0.14	-0.053	0.75	-0.32
	55	122.27	69.02	9.3	2.0	63.2	0.18	92.6	7.9	20.7	52.6	11.5	10.8	27.3	-0.29	0.12	-0.050	0.73	-0.31
	60	120.12	68.13	8.9	2.3	62.1	0.18	90.6	7.5	20.1	51.8	11.1	10.5	26.0	-0.28	0.10	-0.048	0.70	-0.30
	65	117.88	67.20	8.4	2.5	60.8	0.17	88.5	7.1	19.4	50.9	10.7	10.3	24.5	-0.27	0.08	-0.045	0.68	-0.29
	70	115.54	66.23	7.9	2.7	59.6	0.16	86.4	6.6	18.7	50.0	10.2	10.1	23.0	-0.26	0.06	-0.043	0.66	-0.28
	75	112.99	65.18	7.3	3.0	58.2	0.16	84.0	6.1	18.0	49.0	9.7	9.8	21.4	-0.25	0.04	-0.040	0.63	-0.27
	80	110.17	64.01	6.7	3.3	56.7	0.15	81.4	5.6	17.2	47.9	9.2	9.5	19.6	-0.23	0.01	-0.036	0.60	-0.25
	85	106.87	62.64	6.0	3.7	54.9	0.14	78.3	5.0	16.2	46.7	8.6	9.1	17.5	-0.22	-0.02	-0.032	0.56	-0.24
	90	102.73	60.93	5.1	4.1	52.6	0.13	74.5	4.2	15.0	45.1	7.8	8.7	14.9	-0.20	-0.05	-0.027	0.52	-0.22
	95	96.60	58.39	3.7	4.8	49.3	0.11	68.8	3.0	13.2	42.7	6.6	8.0	10.9	-0.17	-0.11	-0.020	0.45	-0.19
	Avg	124.40	69.90	9.8	1.8	64.4	0.19	94.6	8.3	21.3	53.4	11.9	11.0	28.7	-0.30	0.14	-0.053	0.75	-0.32

Production									Maternal						
CED	BW	WW	YW	RADG	DMI	YH	SC	DOC	HP	CEM	Milk	MkH	MW	MH	EN\$
Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	Acc	MkD	Acc	Acc	
+19	-3.6	+53	+98	+.22	+.19	+.6	+.50	+14	+13.4	+18	+28	5	+14	+0	-9.09
.75	.85	.79	.64	.46	.46	.64	.69	.55	.29	.22	.28	5	.47	.23	

Carcass					Usnd	\$Values					
CW	Marb	RE	Fat	Grp	UGrp	Wean	Feedlot	Grid	\$QG	\$YG	Beef
Acc	Acc	Acc	Acc	Prog	UProg						
+32	-.04	+.55	+.085	5	13	62.55	60.09	-1.35	2.6	-3.95	77.15
.50	.54	.52	.49	12	34						

Accuracy	Production									Maternal					Carcass			
	CED	BW	WW	YW	RADG	DMI	YH	SC	Doc	HP	CEM	Milk	MW	MH	CW	Marb	RE	Fat
.05	9.7	2.55	14.9	24.3	.092	.730	.42	.76	16.7	7.7	10.4	9.5	38	.54	20	.29	.30	.041
.10	9.2	2.42	14.1	23.0	.087	.691	.40	.72	15.8	7.3	9.9	9.0	36	.51	19	.28	.28	.039
.15	8.7	2.28	13.3	21.7	.082	.653	.38	.68	14.9	6.9	9.2	8.5	34	.49	18	.26	.27	.037
.20	8.2	2.15	12.6	20.5	.077	.614	.35	.64	14.0	6.5	8.8	8.0	32	.46	17	.25	.25	.034
.25	7.7	2.02	11.8	19.2	.073	.577	.33	.60	13.2	6.1	8.2	7.5	30	.43	16	.23	.23	.032
.30	7.2	1.88	11.0	17.9	.068	.538	.31	.56	12.3	5.7	7.7	7.0	28	.40	15	.22	.22	.030
.35	6.7	1.75	10.2	16.6	.063	.500	.29	.52	11.4	5.3	7.1	6.5	26	.37	14	.20	.20	.028
.40	6.2	1.61	9.4	15.4	.058	.462	.26	.48	10.5	4.9	6.6	6.0	24	.34	13	.18	.19	.026
.45	5.6	1.48	8.6	14.1	.053	.423	.24	.44	9.7	4.5	6.0	5.5	22	.31	12	.17	.17	.024
.50	5.1	1.34	7.9	12.8	.048	.385	.22	.40	8.8	4.1	5.5	5.0	20	.29	11	.15	.16	.022
.55	4.6	1.21	7.1	11.5	.044	.346	.20	.36	7.9	3.7	4.9	4.5	18	.26	10	.14	.14	.019
.60	4.1	1.08	6.3	10.2	.039	.308	.18	.32	7.0	3.3	4.4	4.0	16	.23	9	.12	.12	.017
.65	3.6	.94	5.5	9.0	.034	.269	.15	.28	6.1	2.9	3.8	3.5	14	.20	7	.11	.11	.015
.70	3.1	.81	4.7	7.7	.029	.231	.13	.24	5.3	2.4	3.3	3.0	12	.17	6	.09	.09	.013
.75	2.6	.67	3.9	6.4	.024	.192	.11	.20	4.4	2.0	2.7	2.5	10	.14	5	.08	.08	.011
.80	2.1	.54	3.1	5.1	.019	.154	.09	.16	3.5	1.6	2.2	2.0	8	.11	4	.06	.06	.009
.85	1.5	.40	2.4	3.8	.015	.115	.07	.12	2.6	1.2	1.6	1.5	6	.09	3	.05	.05	.006
.90	1.0	.27	1.6	2.6	.010	.077	.04	.08	1.8	.8	1.1	1.0	4	.06	2	.03	.03	.004
.95	.5	.13	.8	1.3	.005	.038	.02	.04	.9	.4	.5	.5	2	.03	1	.02	.02	.002

Historically not all cattle breeding objectives have been economic



Photo taken in 1949 at Red Bluff Bull Sale, CA.
Kindly provided by Cathy Maas from Crowe Hereford Ranch, Millville, CA.



Selection Index

- Allows comparison on single value
- Weights traits according to economic importance
- Selection index
$$= a_1EPD_1 + a_2EPD_2 + \dots + a_kEPD_k$$

Selection Index

- Easy to use, selection based on one value
- Should be aware of EPD in index that is not of value to your beef operation
- If missing relevant EPDs, use SI in tandem with those EPDs



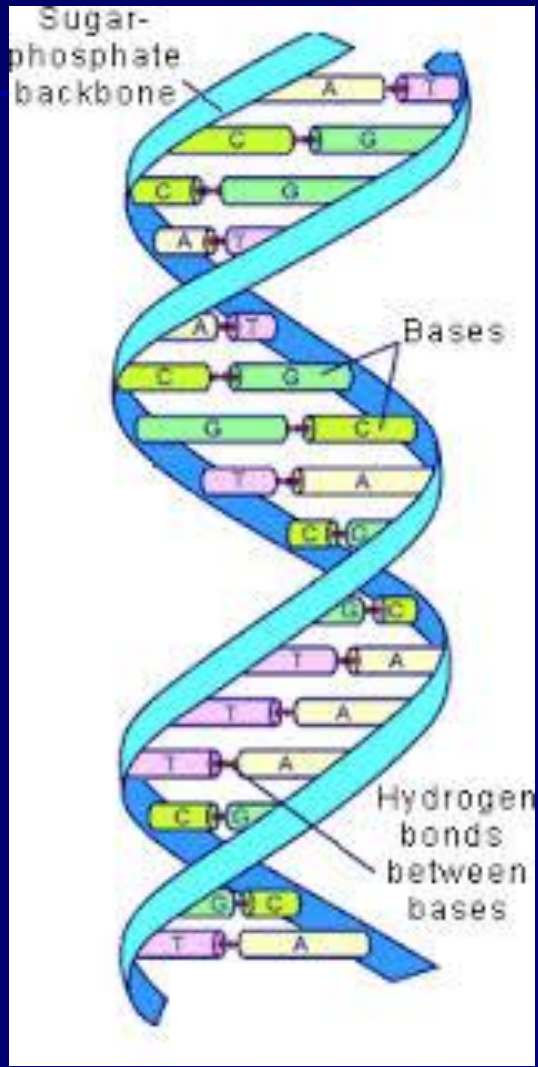
Many beef breeds have indexes which combine EPDs according to economics



TERMINAL	MATERNAL
\$B, \$F, \$G (Angus)	\$W, \$EN (Angus)
TI (Simmental)	API (Simmental)
CHB\$ (Hereford)	BMI\$, BII\$, CEZ\$ (Hereford)
MTI (Limousin)	HerdBuilder (Red Angus)
EPI and FPI (Gelbvieh)	\$Cow (Gelbvieh)
Charolais	\$M (Beefmaster)
GridMaster (Red Angus)	
\$T (Beefmaster)	\$Profit (Topline-Leachman Bulls)

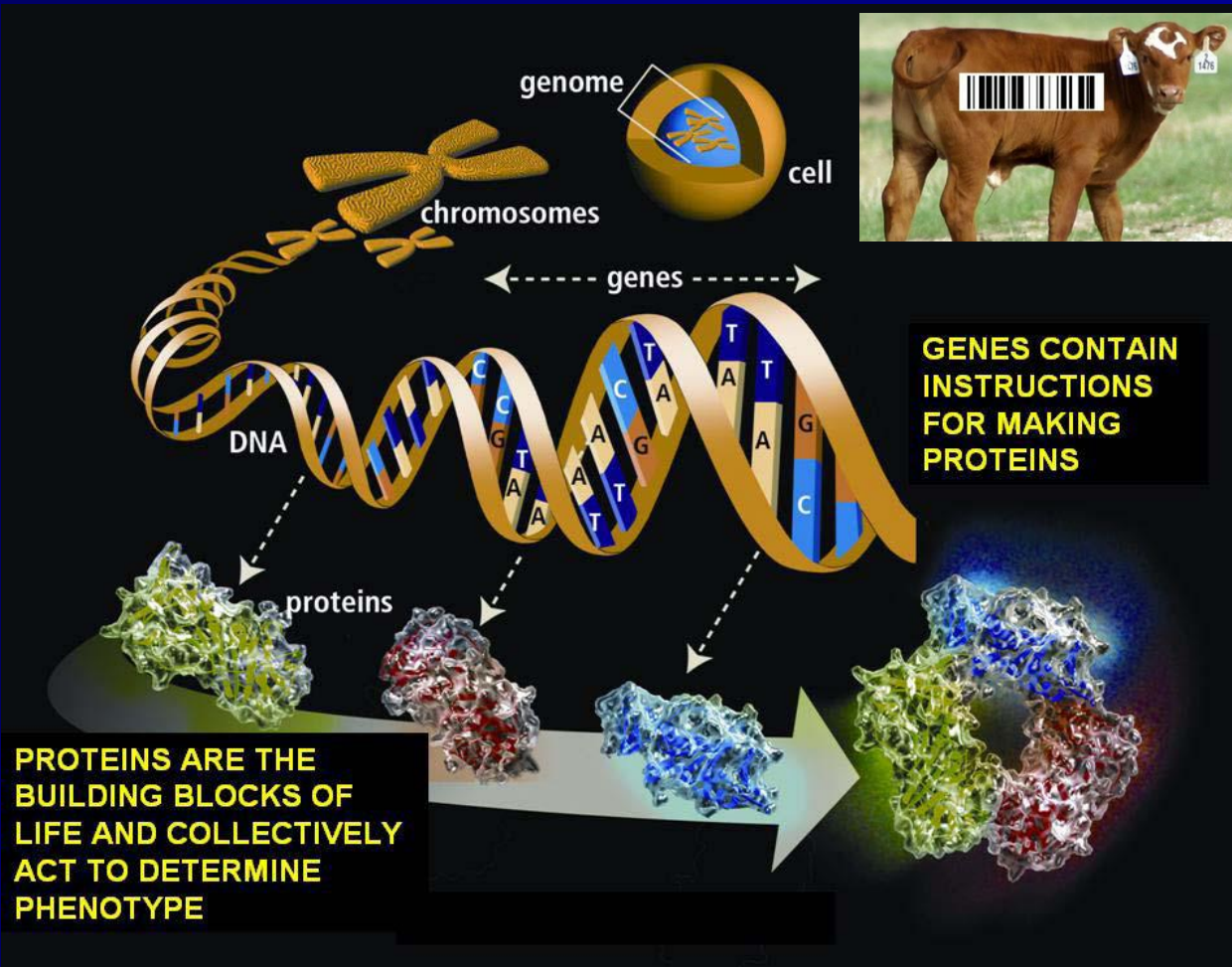


Genomics





The bovine genome is similar in size to the genomes of humans, with an estimated size of 3 billion base pairs.



Human & cattle genomes are 83% identical



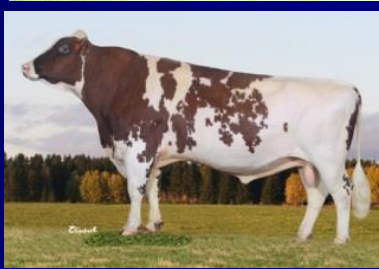


1000 Bull Genomes Run 6

2703 Sequenced Animals, 11x

~55 Breeds: Dairy, Beef, Dual Purpose, Crosses, Composites

2703 x 11 x 3 billion = 90,000,000,000,000



Slide courtesy Ben Hayes, QAAFI



1000 Bull Genomes Run 6

86.5 million single-nucleotide polymorphisms (SNPs) and 2.5 million small insertion deletions



Run 6 – Taurus only

44.7 million filtered variants

43 million SNP, 1.7 million Indel



Run 6 – Taurus Indicus

86.5 million filtered variants

84 million SNP, 2.5 million Indel

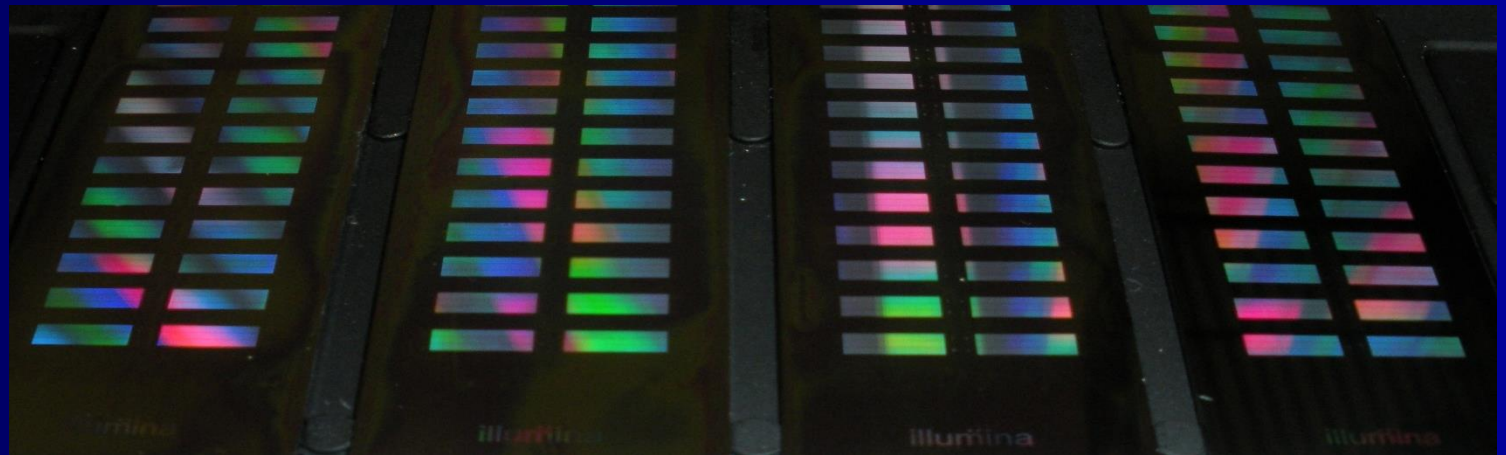


Hayes, B. J. & Daetwyler, H. D. 1000 Bull Genomes Project to Map Simple and Complex Genetic Traits in Cattle: Applications and Outcomes. *Annual review of animal biosciences*, doi:10.1146/annurev-animal-020518-115024 (2018).



High-throughput genotyping technology enabled the development of high density "SNP chips"

The 2009 sequencing of the bovine genome allowed for the development of a 50,000 SNP chip, also known as the "50K"





We can use these SNPs for “genomic” selection?

TRAINING POPULATION

1,000s animals }
– Phenotypes
– Genotypes

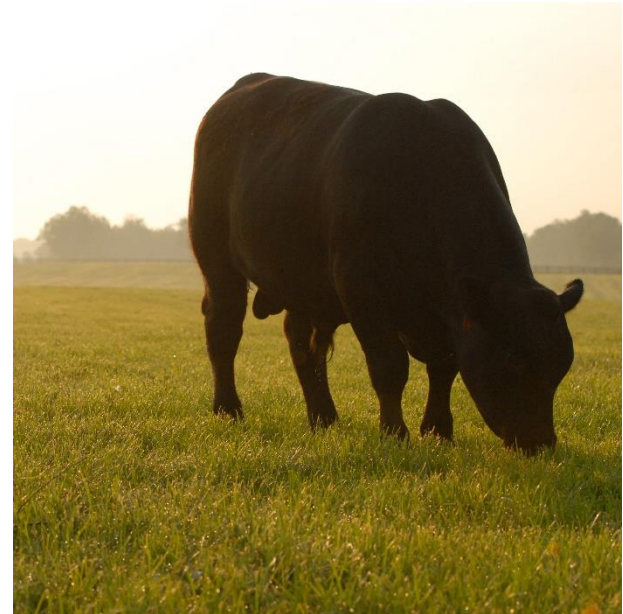
Training = estimate the value of every chromosome fragment contributing variation in a population with phenotypic observations

Prediction = the results of training can then be used to develop prediction equations to predict the merit of new animals (e.g. young bulls)



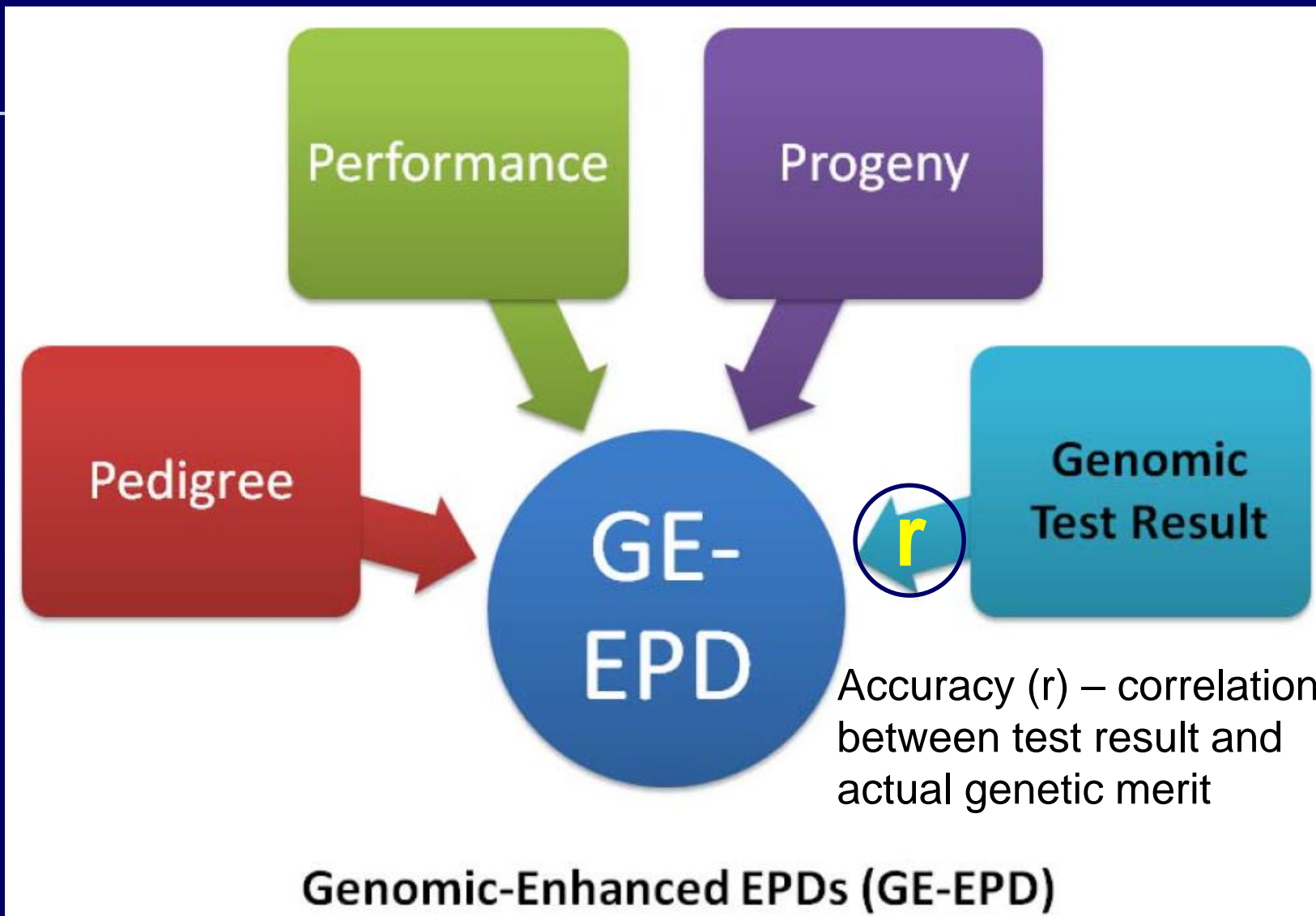
Angus: Current implementation size

- 7.7M birth weights
- 8.4M weaning weights
- 4.1M post-weaning gain records
- 1.5M heifer calving ease scores
- 112K carcass records
- 1.8M ultrasound records
- 19K individual intake records
- 237K docility scores
- 57K heifer pregnancy observations
- 199K mature cow weights





Information sources for EPDs – DNA just one source of data for GE-EPD





Genomics in National Cattle Evaluation (NCE)

- Currently several breeds are using genomic information in their national cattle evaluation programs
 - Angus
 - Red Angus
 - Limousin
 - Simmental
 - Beefmaster
 - Hereford
 - Gelbvieh
 - Charolais
 - Santa Gertrudis
 - Brangus
- Other breeds are trying to incorporate genomic information
- Virtually only National Cattle Evaluation traits – only traits with enough data





How much do genetic tests cost?



- ~ \$13-20 for parentage testing
- ~\$20-\$30 per animal for a single mutation test for a disease or trait
- \$75-90 for the high-density SNP chips for genomic-enhanced EPDs.
- \$45-50 for the low-density imputation chips.

Breed associations work to include that genomic information to provide genomic-enhanced EPDs (GE-EPD) that have improved accuracy due to the inclusion of the genomic information in the EPD calculations.

If multiple tests can be performed on a single DNA sample or a large volume of samples is tested then the cost per test is reduced.

Additional costs can include the cost of DNA cards, sample collection, sample storage and shipping and sample processing, again depending on sample type, test and application.



There are several tests that are being marketed for use on commercial cattle that are not directly part of a breed association genetic evaluation program.



- **GeneMax Advantage** (\$39) and **GeneMax Focus** (\$17). Distributed by Angus Genetics Inc. (AGI) and marketed by Zoetis® for cattle that are at least 75% Angus.
- **PredicGEN** (\$19.50) is a test marketed by Zoetis® as “a heifer selection tool for straight-bred or crossbred British/Continental animals”
- **The Igenity Beef Profile** (\$29) marketed by Neogen® as “DNA profiles for crossbred and purebred cattle.” Predictions for weaning weight, yearling weight and hot carcass weight for a total of 16 traits scored on a 1–10 scale, plus two new selection indexes. “The Igenity profile was designed and validated for crossbred or straightbred cattle with backgrounds of **Angus, Red Angus, Simmental, Hereford, Limousin and Gelbvieh**”
- **There aren't yet any independent, peer-reviewed papers documenting the field performance of these tests for commercial cattle.**



Crossbreeding

- Should always be a consideration for commercial cattle producers
- Greatest benefit to reproduction and longevity
- Rule of thumb – no females with $>75\%$ one breed!





Website: eBEEF.org
YouTube: eBEEF
Twitter : @eBEEF.org



eBEEF was developed as part of USDA NIFA grants
 # 2013-68004-20364
 #2011-68004-30367
 #2011-68004-30214



Take Homes



- DNA testing can be used to identify parentage, genetic defects, and to improve the accuracy of breed EPDs
- Tests have not been shown to work well in predicting genetic merit of crossbreds
- Economics of testing commercial cattle needs to be carefully considered – will depend on a number of factors – return greater on males than females



Thanks for inviting me!

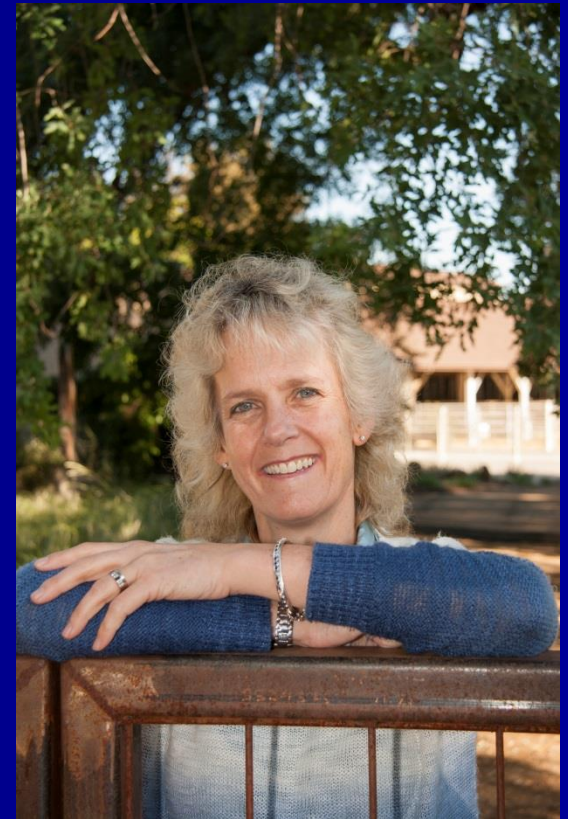
UC DAVIS ANIMAL SCIENCE

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United States
Department of
Agriculture

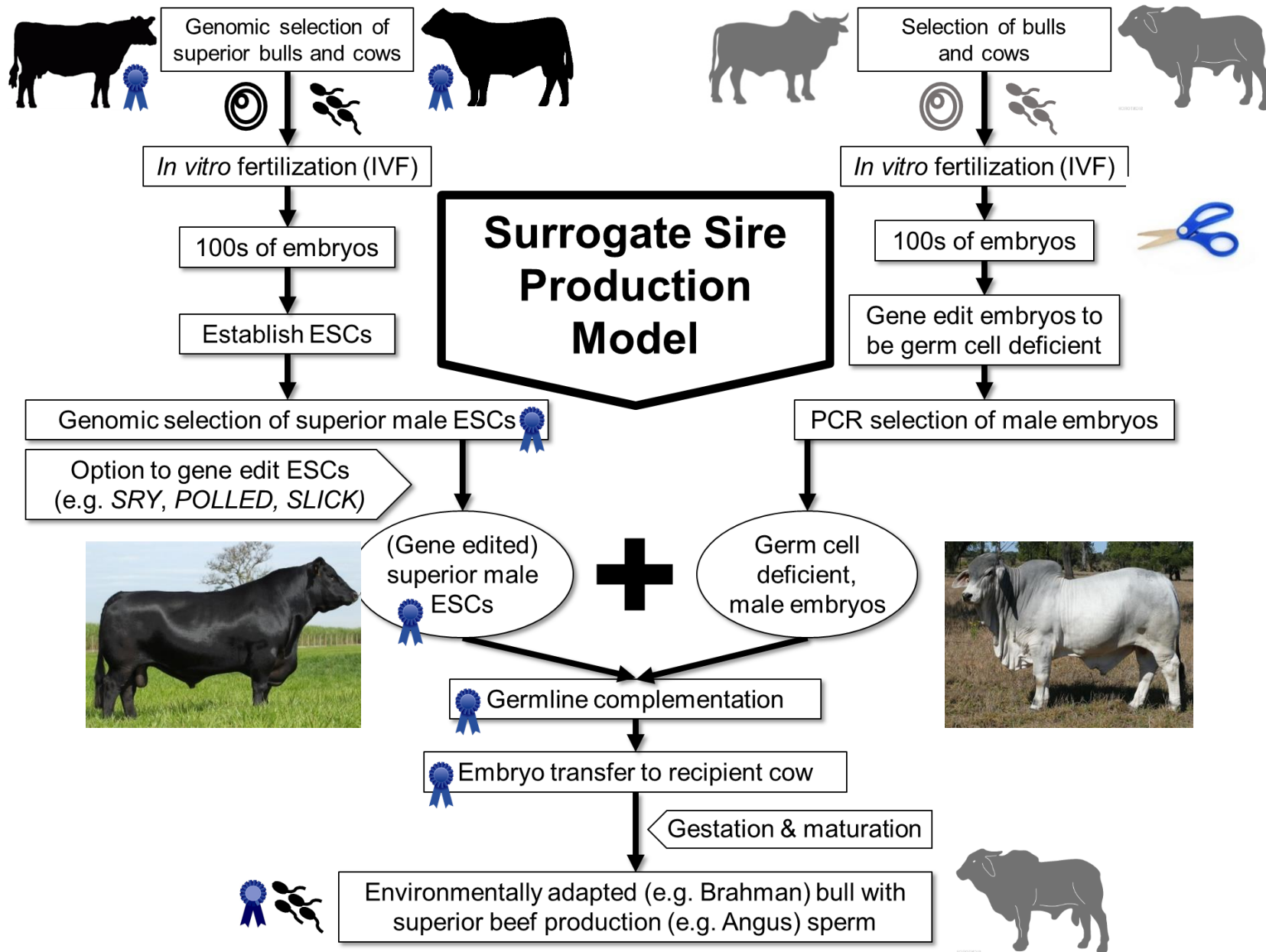
National Institute
of Food and
Agriculture





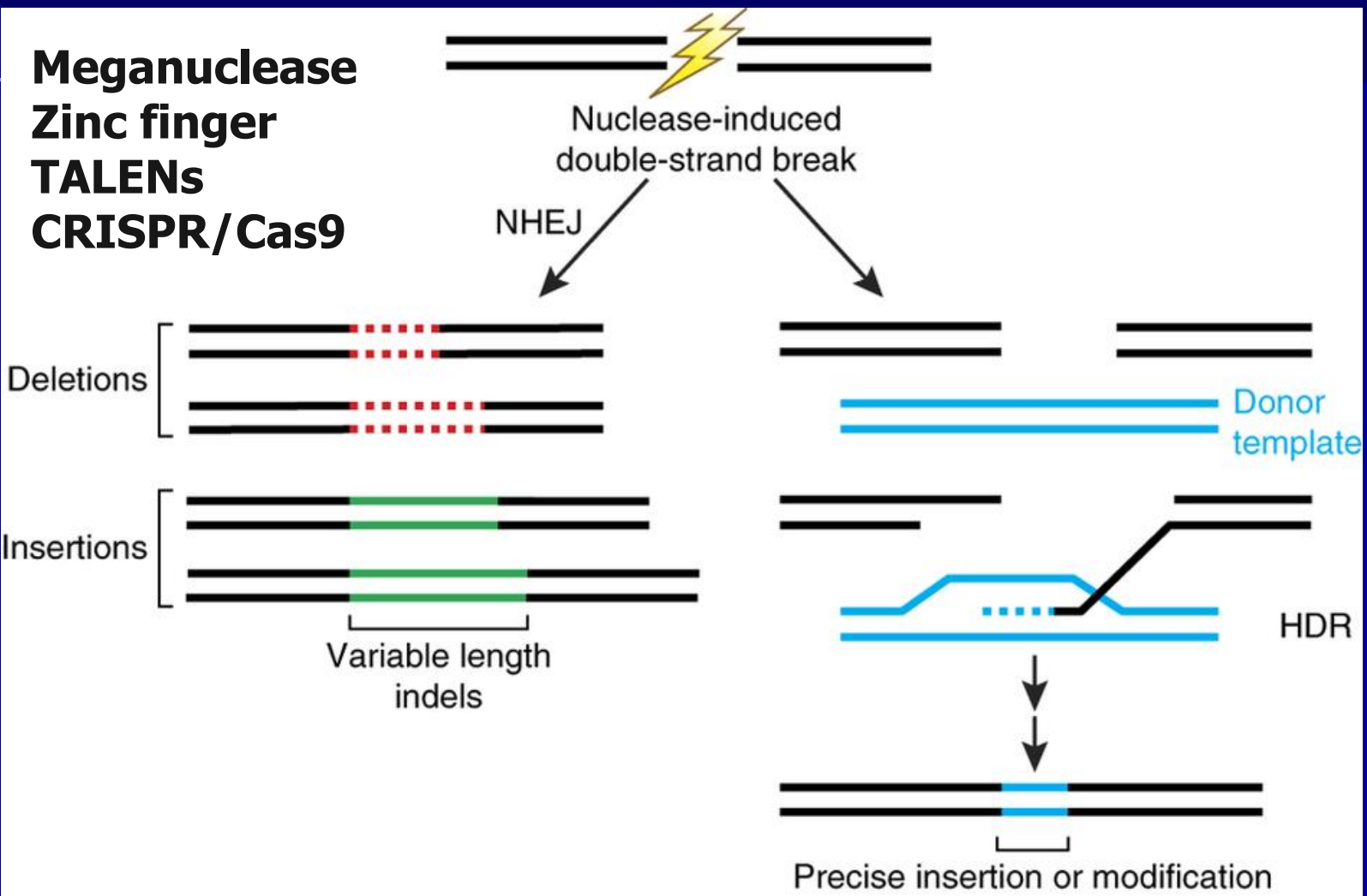
Germline: Efficient beef production (e.g. Angus)

Surrogate line: Environmentally adapted (e.g. Brahman)





Will gene editing allow an additional inflection point in rate of livestock genetic gain?



Sander JD, Joung JK. CRISPR-Cas systems for editing, regulating and targeting genomes. *Nat Biotech* 2014;32:347-355.

Gene Edited Polled Calves

Naturally-occurring bovine allele at polled locus



Carlson DF, Lancto CA, Zang B, Kim E-S, Walton M, et al. 2016. **Production of hornless dairy cattle from genome-edited cell lines.** Nat Biotech 34: 479-81

Precision Breeding Offers New Alternative to Dehorning Cattle

https://www.youtube.com/watch?v=-Qks_LMmodw

Editing is the Cherry on Top of Breeding Sundae

It will be able to introduce useful alleles, and potentially bring in useful novel genetic variation to improve livestock rapidly, without “linkage” drag



Genome Editing

Somatic cell nuclear transfer cloning

Genomic Selection

Embryo Transfer

Artificial insemination

Progeny testing

Performance recording

Development of breeding goals

Association of like minded breeders

Cracking the genetic code for complex traits in cattle

20 February 2018

A massive global study involving 58,000 cattle has pinpointed the genes that influence the complex genetic trait of height in cattle, opening the door for researchers to use the same approach to map high-value traits including those important for beef and milk production.



The University of Queensland's [Professor Ben Hayes](#), who heads the global 1000 Bull Genomes Consortium of 57 researchers from 30 institutes, said it had previously been a major challenge to identify variants in the genome affecting complex traits, due to variations within multiple genes, and behavioural and environmental factors.

"To overcome this issue, the consortium pooled large genomic datasets and phenotypes collected from 58,000 cattle around the world to gain the clearest picture so far of their genetics," Professor Hayes said.



"We needed access to vast resources of data in order to demonstrate that the genes affecting a complex trait like height can be accurately identified.

"By applying the same collaborative big data approach, it may now be possible to identify genes associated with high-value complex traits that are really important to the industry, such as beef and milk production, feed efficiency and reduced methane emissions."

The 1000 Bull Genomes Consortium's findings on height were confirmed by analysing the genetic material of miniature cattle and the DNA sequenced from a 6500-year-old wild auroch bone.

"Aurochs are an extinct species of large wild ox – which were domesticated by ancient humans about 10,000 years ago and bred to be shorter – and are the ancestor to all cattle breeds," Professor Hayes said.

"From analysing the DNA of this animal, we could predict its height, and then verify our prediction with the fossil records of auroch skeletons."

Bouwman AC, et al. 2018. **Meta-analysis of genome-wide association studies for cattle stature identifies common genes that regulate body size in mammals.** Nat Genet. Feb 19. doi: 10.1038/s41588-018-0056-5. [Epub ahead of print] PubMed PMID: 29459679.

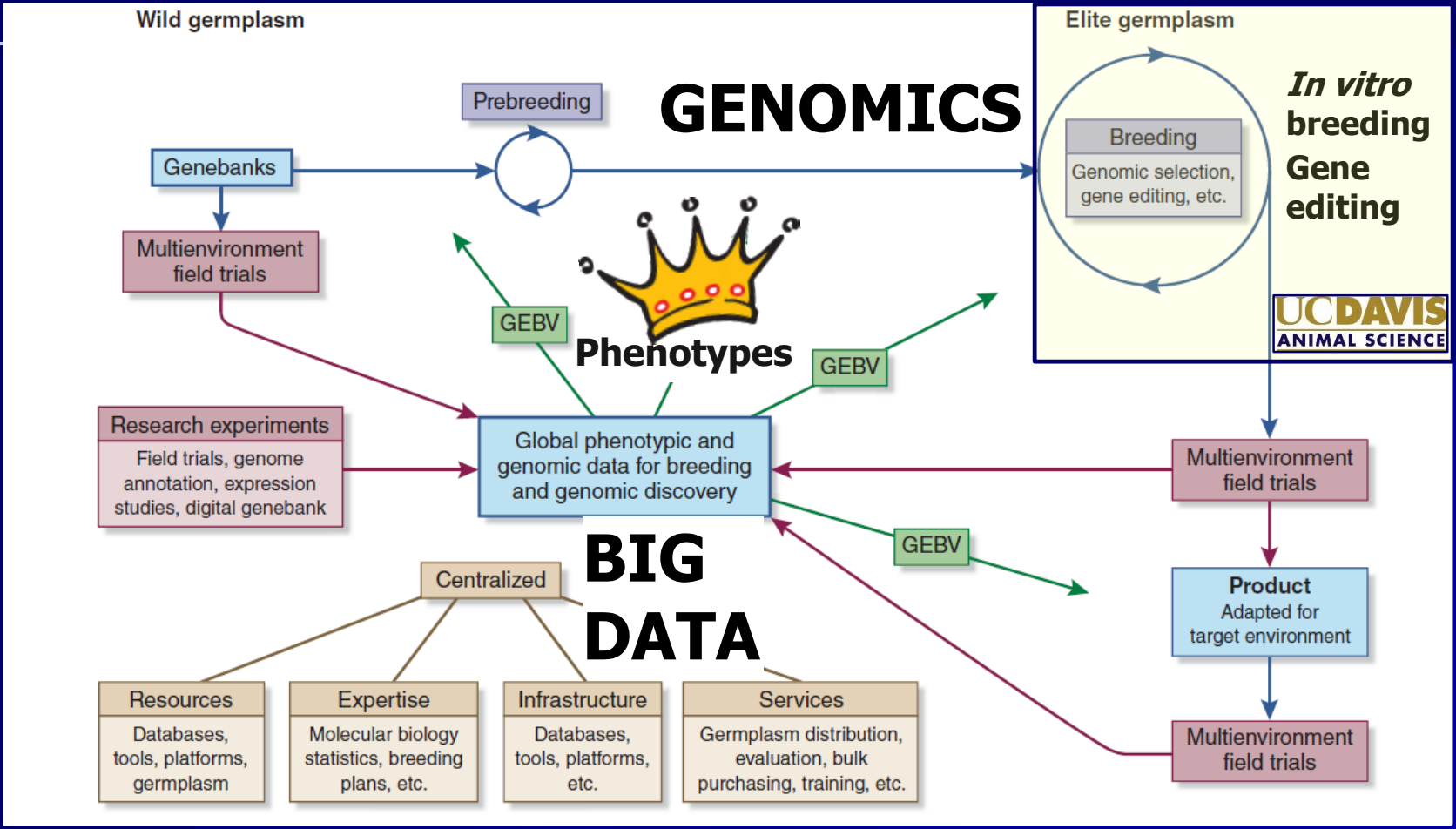
Van Eenennaam 2/2019

Animal Biotechnology and Genomics Education





Strategy to combine big data and genomic selection as a unifying approach to deliver innovative “step changes” in the rate of genetic gain at scale



Hickey et al., 2017; Genomic prediction unifies animal and plant breeding programs to form platforms for biological discovery. Nat Genet. 49:1297-1303.