Genetic Selection of Beef Cattle: Past, present, and future

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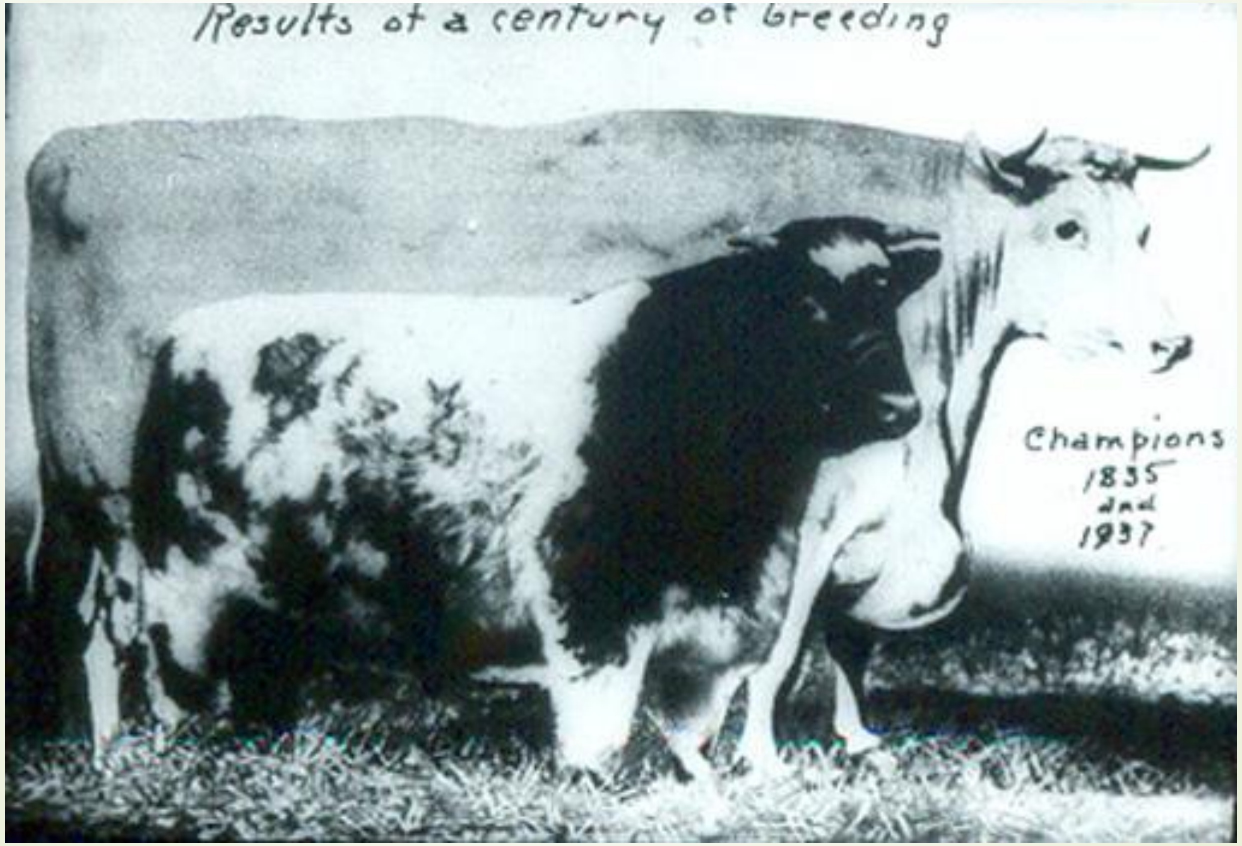
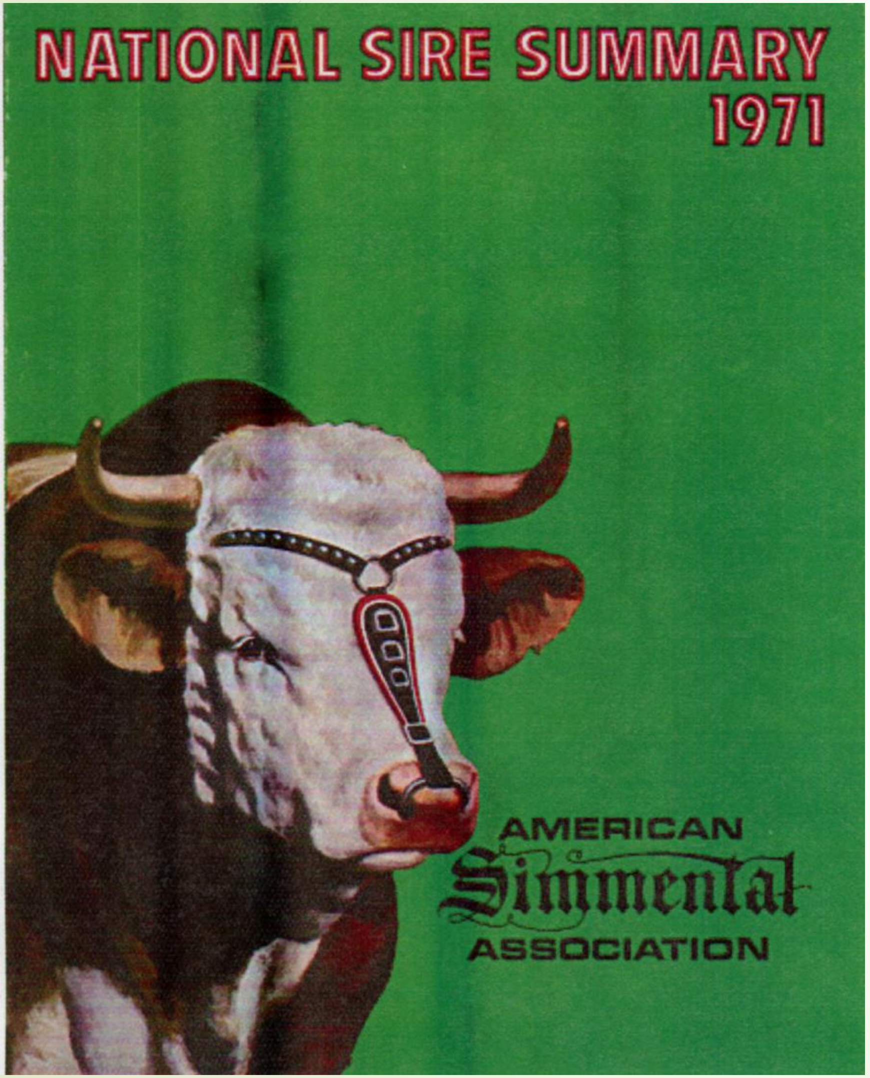
Phenotypic selection—show ring



Genesis of modern beef improvement in the U.S.

- 1930-35 “Genesis” of Performance Recording: US Range and Livestock Research Station, Miles City, MT
- 1935-45 Beginning of measurement in New Mexico and California
- 1941 Central Bull Testing: Balmorhea, TX

First Simmental Sire Summary

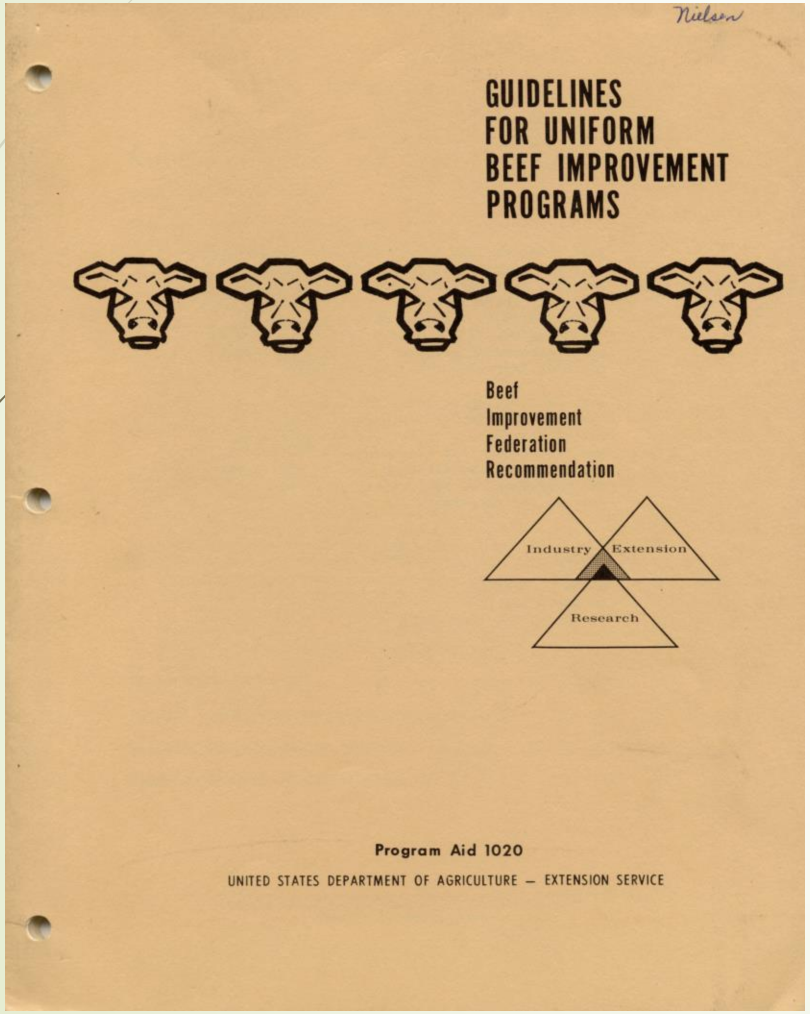


NATIONAL SIRE SUMMARY
1971

AMERICAN
Simmental
ASSOCIATION

1971 (done at Boeing and led by Paul Miller)

BIF Guidelines



Nielsen

GUIDELINES
FOR UNIFORM
BEEF IMPROVEMENT
PROGRAMS

Beef
Improvement
Federation
Recommendation

Industry
Extension
Research

Program Aid 1020

UNITED STATES DEPARTMENT OF AGRICULTURE — EXTENSION SERVICE

1st Edition 1970
measurement, adjustment
herd guidelines
central test guidelines

2nd Edition 1972
some initial thoughts on
sire evaluation
reference sires and
no. progeny
performance pedigree

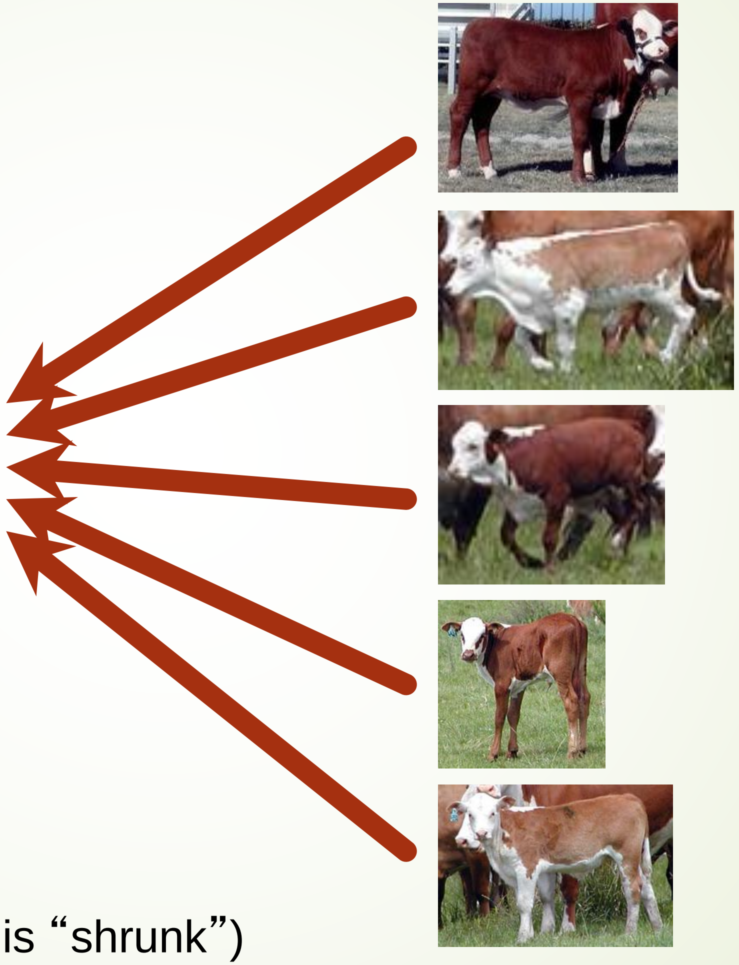
Best Linear Unbiased Prediction (BLUP) Animal Model

$$\begin{bmatrix} X'X & X'Z \\ Z'X & Z'Z + K^{-1}\alpha \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{a} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \end{bmatrix}$$

- This is the framework in which we have worked for decades.

Progeny Inform Us About Parents

Sire



+30 lb

+15 lb

-10 lb

+ 5 lb

+10 lb

(EPD is “shrunk”)

Sire EPD +8 lb ← Progeny +10 lb

What Is a Selection Index?

- Selection on 'aggregate merit' (Hazel, 1943)
- List of traits that influence "satisfaction"
- Relative Economic Value (REV) of each trait
  - Increase in satisfaction with one unit change in a trait, all others held constant
- List of characteristics to be measured on animal
- Relationships between characteristics (phenotypes) and traits (genotypes)

Why Do We Need Selection Indexes?

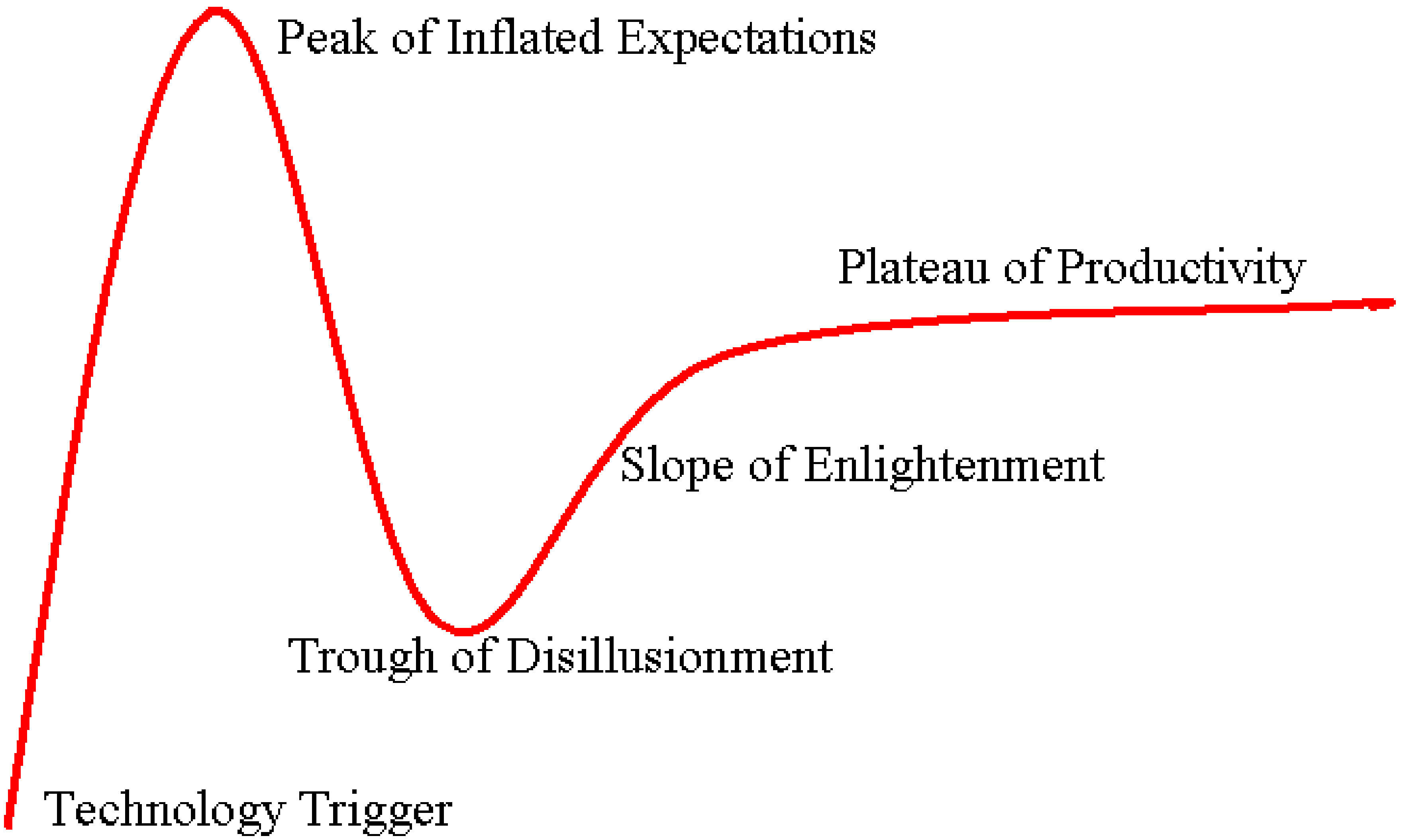
"There is no easily accessible, objective way for breeders, particularly breeders in the beef and sheep industries where ownership is diverse and production environments vary a great deal, to use these predictions intelligently."

-- *R. M. Bourdon, 1998*

What influences net profit?

- HCW = 59.5%
- DMI=19.3%
- MS=11.1%
- REA=5.5%
- FAT=4.6%
- What’s missing?
  - Ochsner et al. (2017)

Gartner Hype Cycle



Peak of Inflated Expectations

Plateau of Productivity

Slope of Enlightenment

Trough of Disillusionment

Technology Trigger

Dark Ages

	CE	BW	WW	YW	MCE	MM	MWW
Adj.		90	700	1320			
Ratio		101	107				
EPD	9	-1.0	25	49	3	11	23
Acc	.29	.37	.30	.27	.18	.19	.23

	YG	Marb	BF	REA
Adj.		4.65%	.23	12.5
Ratio		106	100	95
EPD	.21	.44	.05	-.39
Acc	.32	.31	.33	.34

REA	TEND	MARB
7	6	8

Genomics

- 2004—First Marker-Assisted EPD
  - ASA--Tenderness

- 2009—Release of genomic enhanced EPD
  - AGI
  - A move away from “validation” to “evaluation”

- 2012—Genomic enhanced EPD for many breeds

Breeding Value Estimation

- Progeny receive half of their genetic material from each parent (PA)

$$BV = \frac{1}{2}BV_{(sire)} + \frac{1}{2}BV_{(dam)} + \Phi$$

- Φ=Mendelian sampling term
- Genomic data
  - Account for part of the Mendelian sampling term

Blending

$$EBV_i = \frac{1-R_i^2}{1-r_g^2 R_i^2} MBV_i + \frac{1-r_g^2}{1-r_g^2 R_i^2} EBV_i$$

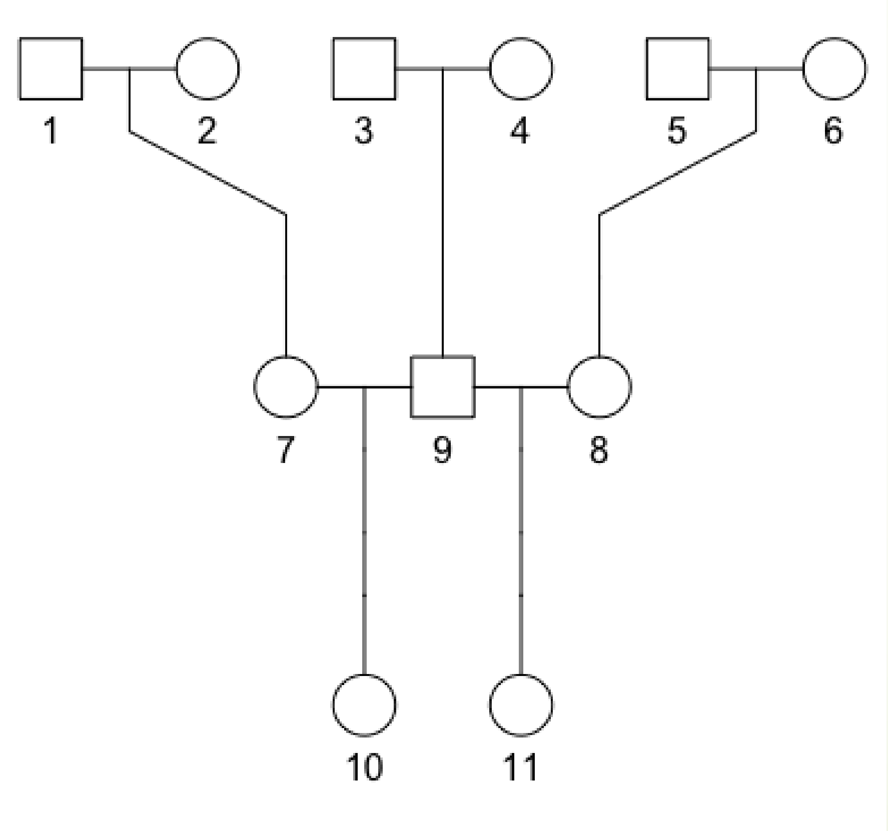
Predictions of who is the better parent

Relationships

- Pedigree information was the primary method to incorporate relationship information into BLUP and is still the backbone.
  - Usually deep
  - Prone to errors ~10%
  - Computationally feasible
- Genomic data now augments pedigree, allowing for deviations from expected degrees of relationships
  - Cleans up pedigree errors
  - Better estimates of relationships
  - More computationally demanding

Pedigree Relatedness

- The **expected** (averaged across loci) relationship between individuals.

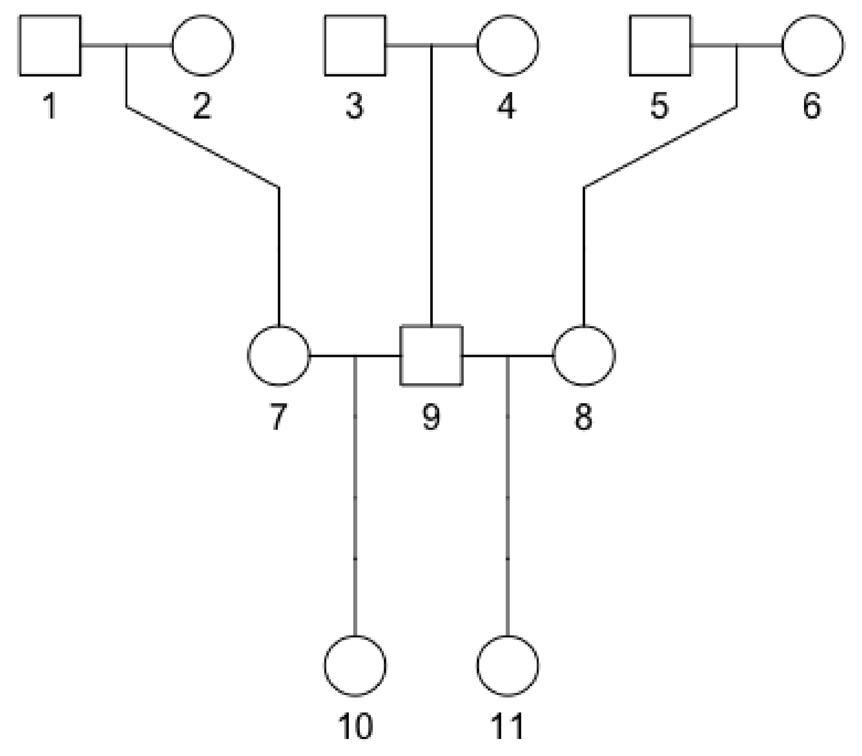


	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
1	1	0	0	0	0	0	0.5	0	0	0.25	0
2		1	0	0	0	0	0.5	0	0	0.25	0
3			1	0	0	0	0	0	0.5	0.25	0.25
4				1	0	0	0	0	0.5	0.25	0.25
5					1	0	0	0.5	0	0	0.25
6						1	0	0.5	0	0	0.25
7							1	0	0	0.5	0
8								1	0	0	0.5
9									1	0.5	0.5
10										1	0.25
11											1

Slide provided by
Jeremy Howard

Genomic Relatedness

- The **realized** (averaged across loci) relationship between individuals.



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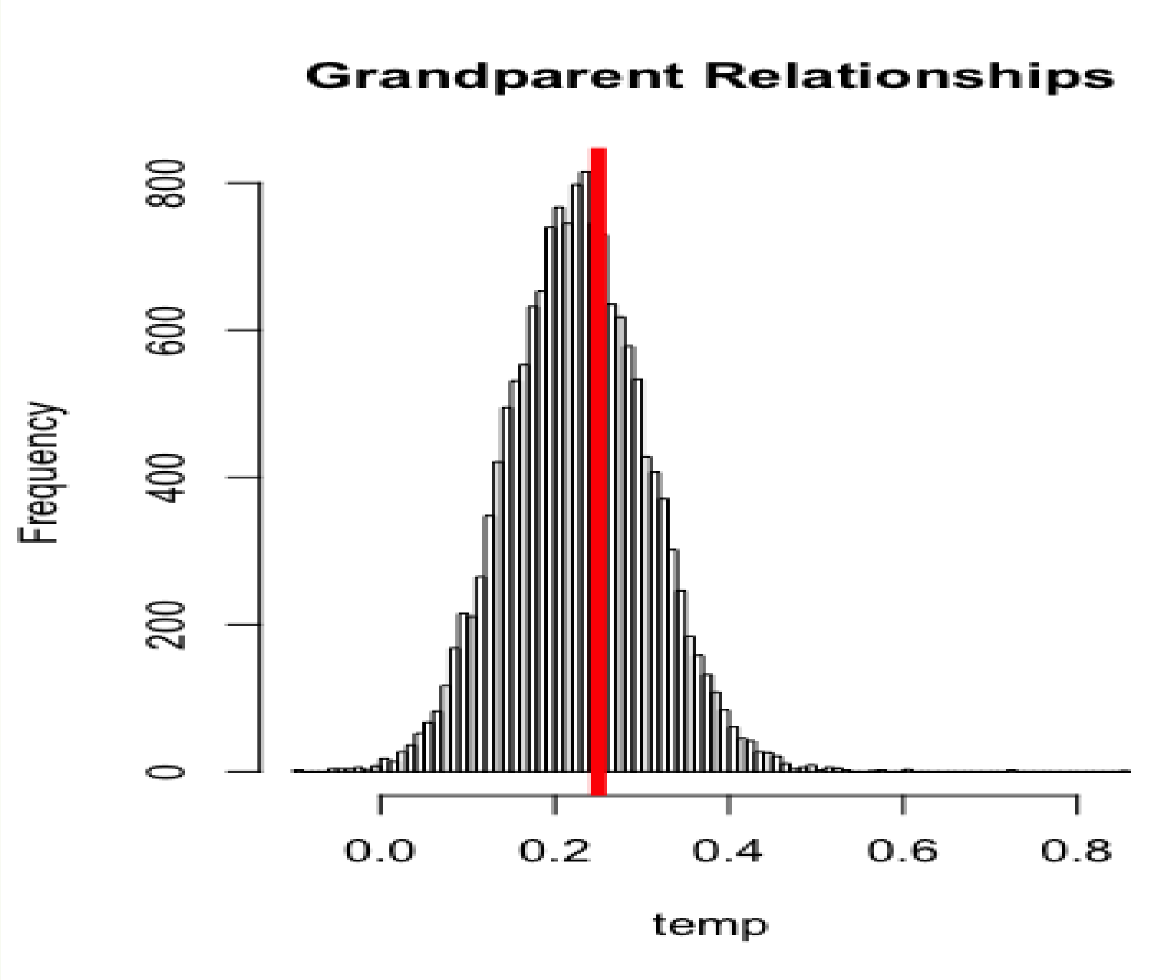
Jeremy Howard

	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**
1	0.99	0.01	0.01	-0.13	0.12	-0.04	0.49	0.01	-0.09	0.2	-0.04
2		0.81	0.00	-0.18	0.09	0.08	0.41	0.1	-0.03	0.11	0.06
3			0.8	0.16	-0.03	-0.01	-0.09	-0.06	0.46	0.14	0.24
4				1.03	-0.09	0.13	-0.12	0.05	0.57	0.25	0.27
5					0.95	-0.04	0.09	0.5	-0.1	-0.05	0.41
6						0.85	0.00	0.43	0.11	0.16	0.09
7							0.95	0.09	-0.08	0.44	0.04
8								1.11	0.06	0.13	0.58
9									1.04	0.52	0.51
10										0.99	0.23
11											1.03


Grandparent Relationships
Frequency
0
200
400
600
800
0.0
0.2
0.4
0.6
0.8
temp

Progeny Equivalents

TRAIT	AAA	AHA	IGS
CED	28	17	15
BWT	21	8	21
WWT	26	12	22
YWT	21	9	24
MCE	18	----	3
Milk	33	----	18
STAY	No EPD	----	25
Marbling	9	3	5

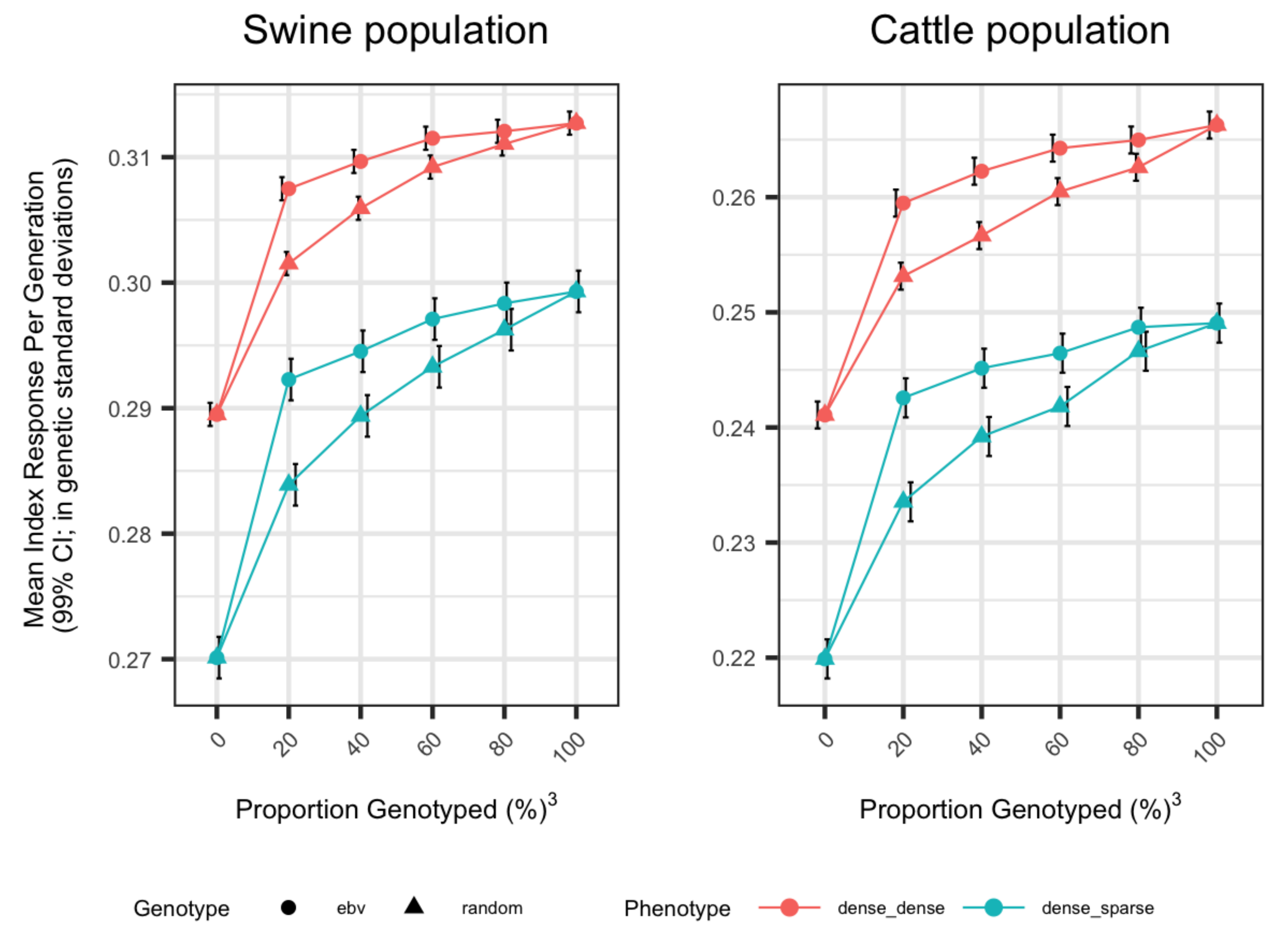
Increased Accuracy-Benefits

- Mitigation of risk
- Faster genetic progress

$$\Delta_{BV} / t = \frac{r_{BV,EBV}\, i \sigma_{BV}}{L}$$

- Increased accuracy does not mean higher or lower EPD/EBV!
  - Increased information can make EPD/EBV go up or down

Delta G should be thought of per $ invested!



Howard et al., 2018

Sequencing Is Just Beginning

- Best chance we have at:
  - Predicting across populations
    - Single variant (birth weight)—r_g ranged between 0.17 and 0.34
  - Developing MAM products
    - An objective, but the highest hanging fruit

What is gene editing?

- A category of new methods that can be used to precisely edit or change the genetic code.
- Molecular scissors called nucleases are used to cut DNA at a specific location in the genome based on recognition of the target DNA sequence.
- This enables us to add, delete, or replace components of the genetic code.

What examples are there in livestock?

- Genetically hornless Holstein dairy cattle.
  - Holstein "horned" allele→ naturally-occurring Angus "polled" allele
- Pigs with a single base deletion in a gene that may enable resilience to African Swine Fever Virus.
- Pigs protected from porcine respiratory and reproductive syndrome (PRRS) virus.
- Changes in the *myostatin* gene in sheep and cattle.

Does this replace “traditional” genetic selection?

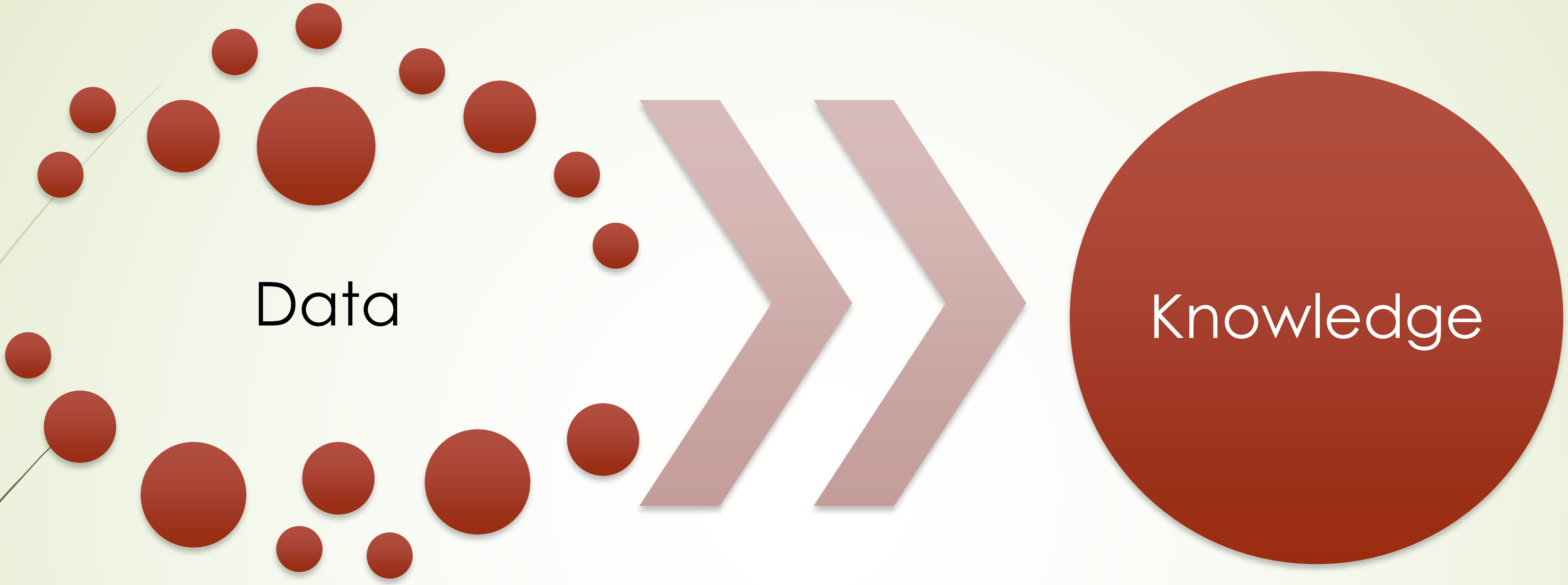
- Can save time
  - Avoid the need to introgress using traditional backcross
  - This can also avoid the introgression of undesired mutations
- The majority of ERT are very polygenic
  - Potentially changes the intercept from which we make “traditional” progress.
- Even if disease resistance is achieved there are several other traits in the breeding objective
- Simply one tool to add to the toolbox
  - But potentially an important one.

Commercial Data is Important

- Improvements can be made by increasing the number of ERT that have EBV
  - Input traits
  - Fertility
  - Health
  - Carcass
- Genomic selection will only be fully realized when we collect traits for which genomics could be most helpful.

Clearly define breeding goals

- Emerging technologies should increase the rate of genetic change.
- The rate of ”improvement” towards a specified goal should be the objective.
- This requires clearly defined goals whereby trait maximums or minimums may not be ideal.



Data is constantly growing

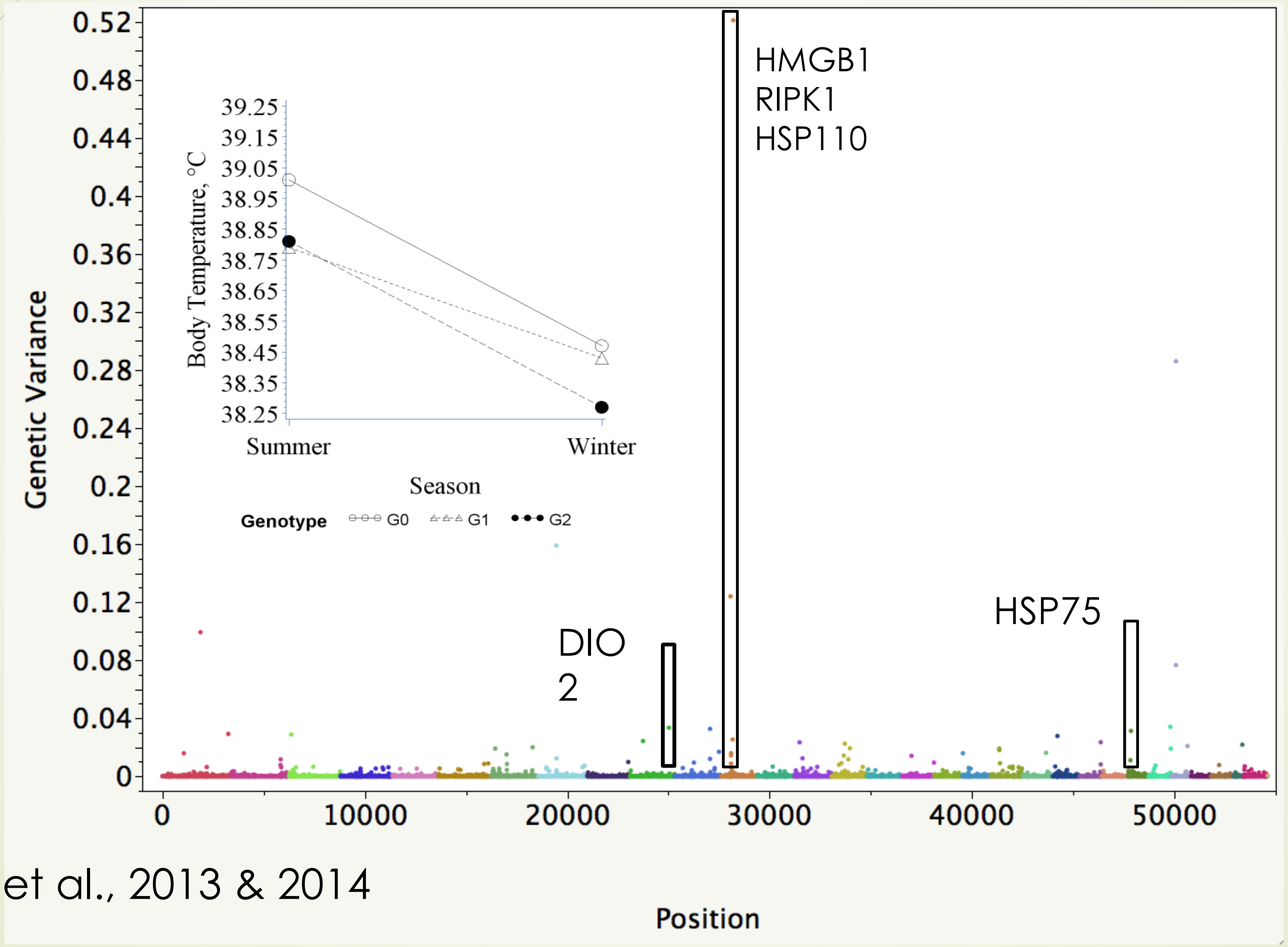
(more animals, more traits, more genotypes, sequence data)

Requires turning data into tools

Everybody is talking about GEMS

- Genotype
- Environment
- Management
- Societal concerns

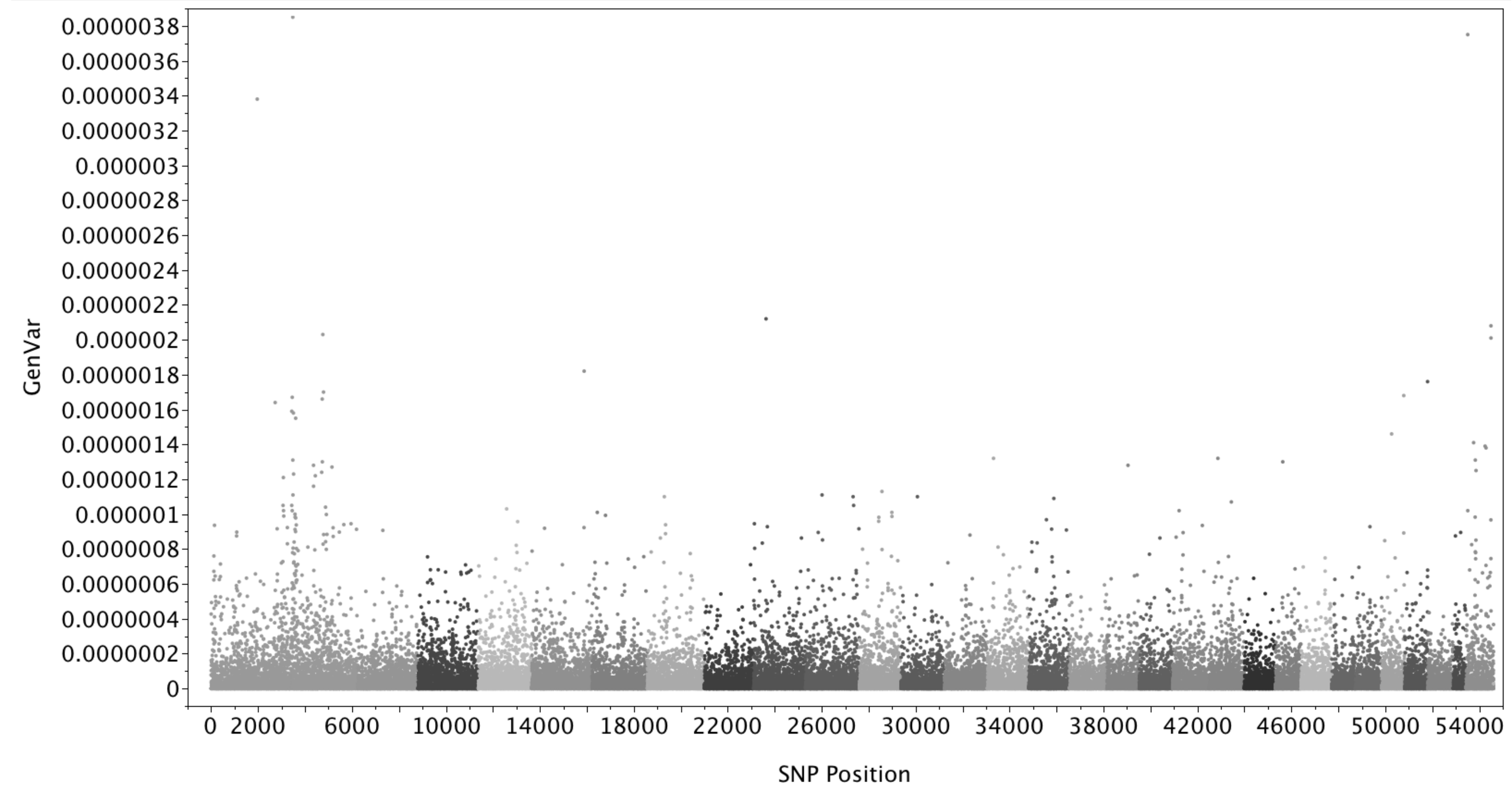
Body Temperature During Heat Stress ($h^2 = 0.68$)



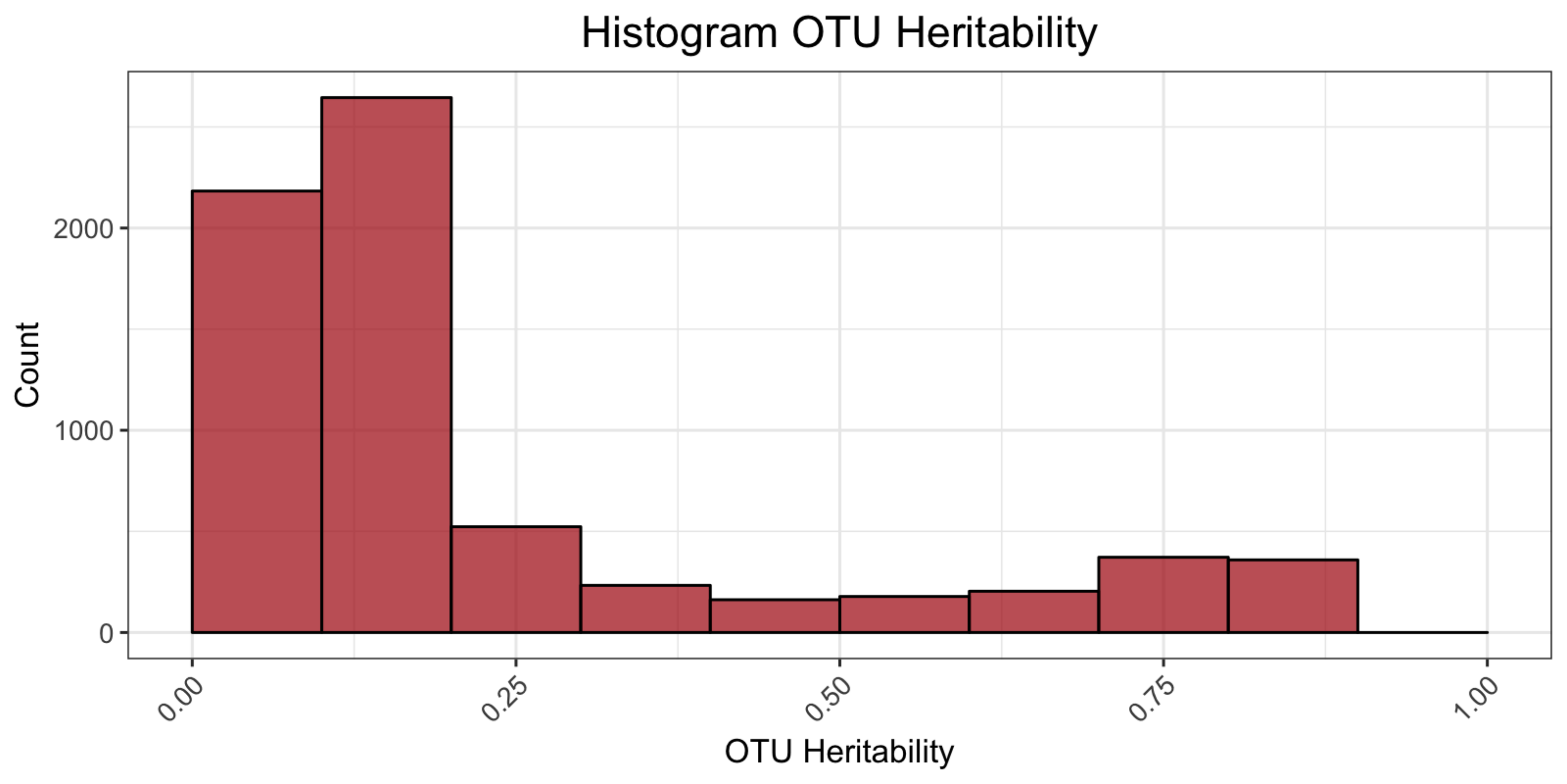
(Howard et al., 2013 & 2014

Iron Content in Beef (h^2 =0.35)

(Ahlberg et al., 2014)



Heritability Across OTUs



Final thoughts

- Use the tools we have, and be aware of the advantages of emerging tools.
- SCIENCE and ECONOMICS should rule the day, not reckless bias based on opinion.
- IF you have not yet capitalized on existing genetic improvement tools, then the only way for you to benefit from new technologies is if someone takes decision making power from you.
- Do not make it harder than it need be.
- Be an educated livestock producer and educated consumer.
  - Consumer of science