Genetic Technology in Beef Cattle

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Selection

Phenotype/pedigree

- Since (or before) domestication

Statistical Predictions

- Really 40ish years ago
- Think EPD and indices
- Utilizes pedigree and phenotype

Genomic-enabled predictions

- ~ 10 years ago
- Utilizes framework for EPD

Fundamentals

- P=G+E
- Phenotype = Mean + BV + Environment

- 600= 550 + 10 +40
- 600=550 + (-5) + 55

Progeny Inform Us About Parents

Sire

+30 lb

+15 lb

-10 lb

+ 5 lb

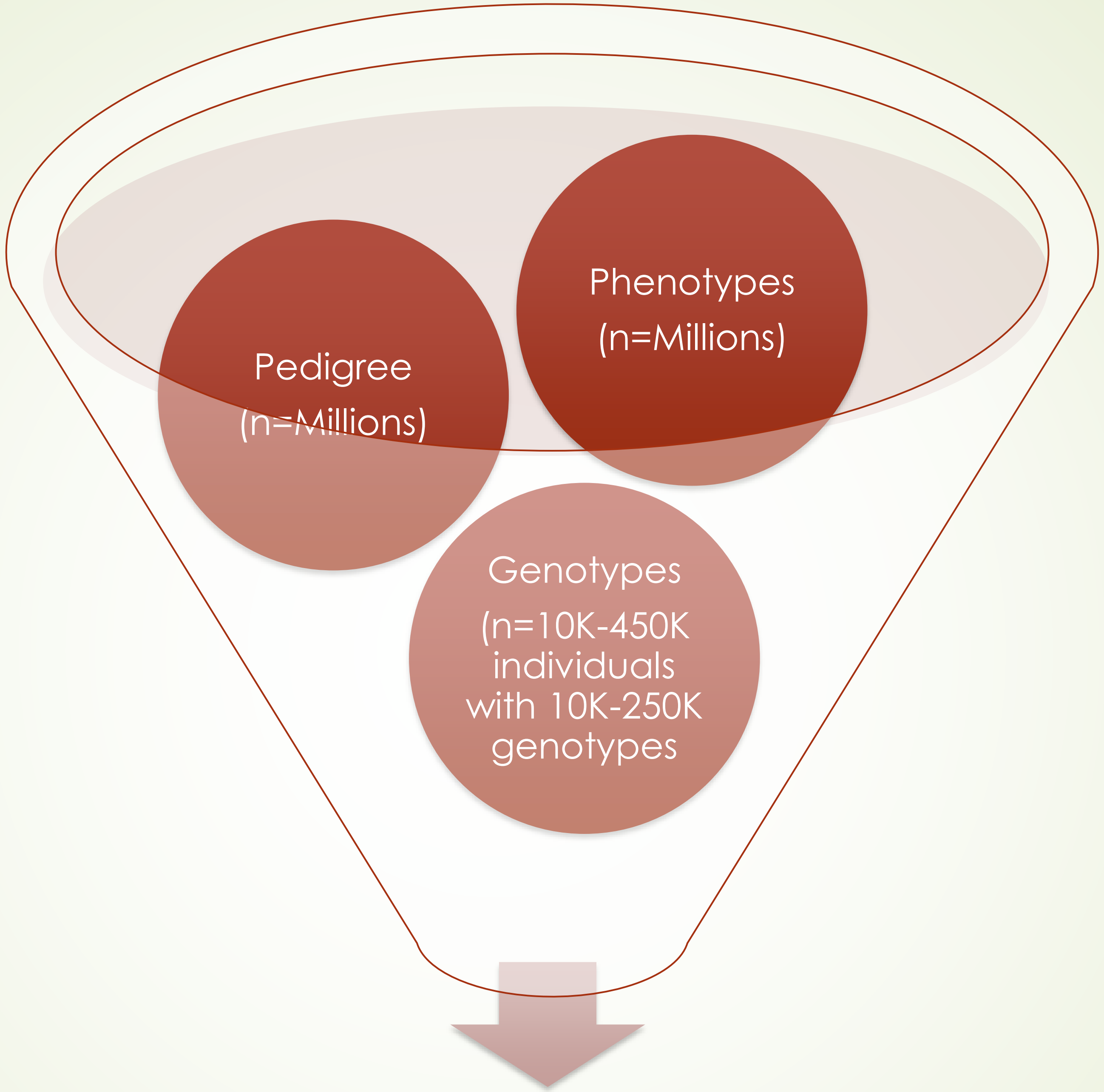
+10 lb

Progeny +10 lb

(EPD is “shrunk”)

Sire EPD +8 lb

Slide Adapted from Garrick



Genetic Prediction

Breeding Value Estimation

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

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

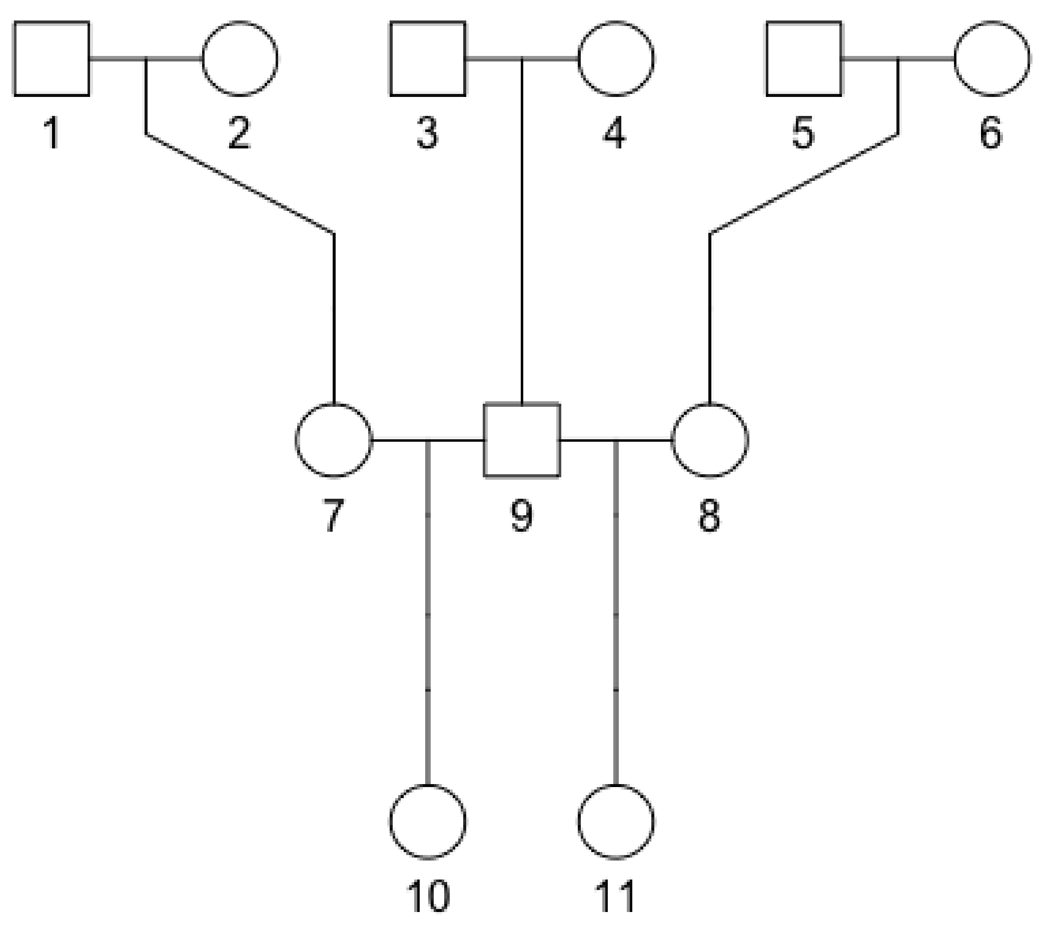
- Estimated Breeding Value (EBV)=genetic merit of an individual; EPD=genetic merit of an individual as a parent (1/2 EBV)
- Φ=Mendelian sampling term
- Genomic data
  - Account for part of the Mendelian sampling term

Relationships

- Pedigree information was the primary method to incorporate relationship information into genetic prediction and is still the backbone.
  - Usually deep
  - Prone to errors
    - ~10%
- Genomic data now augments pedigree, allowing for deviations from expected degrees of relationships
  - Cleans up pedigree errors

Pedigree Relatedness

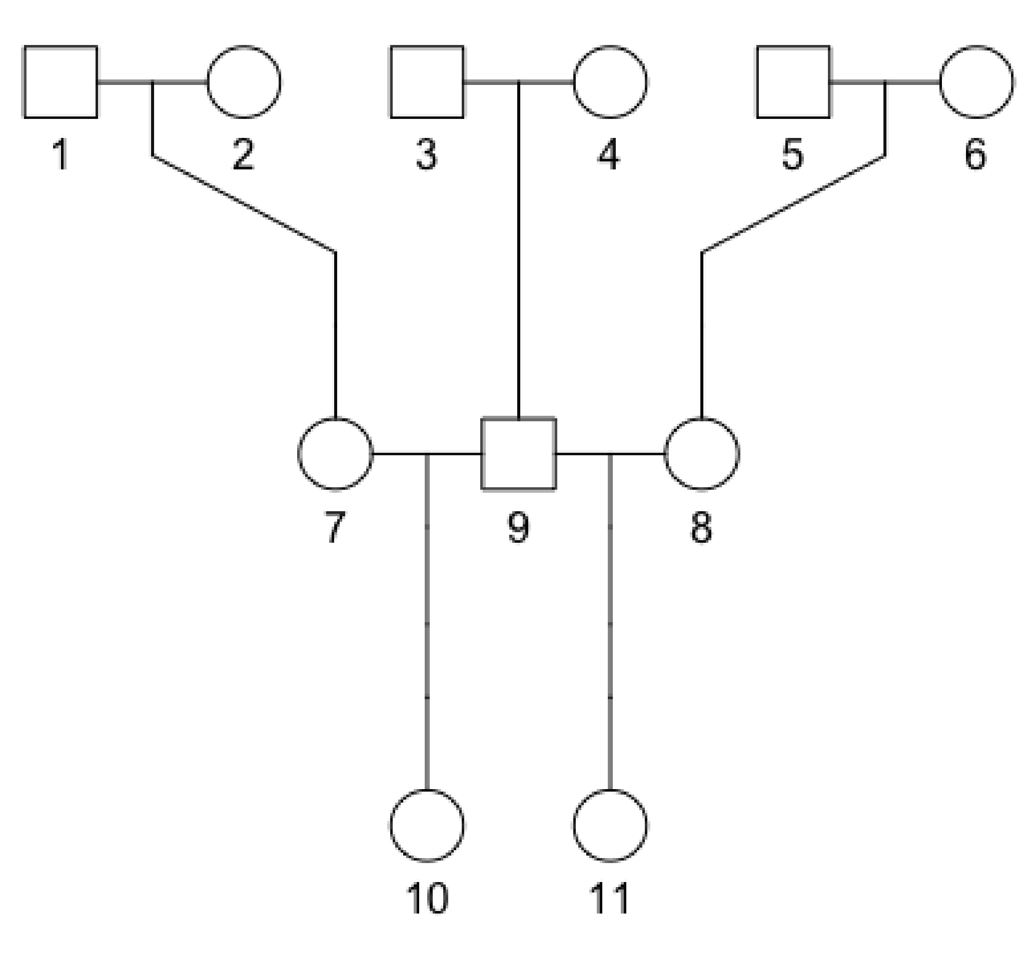
- The **expected** (averaged across loci) relationship between individuals.



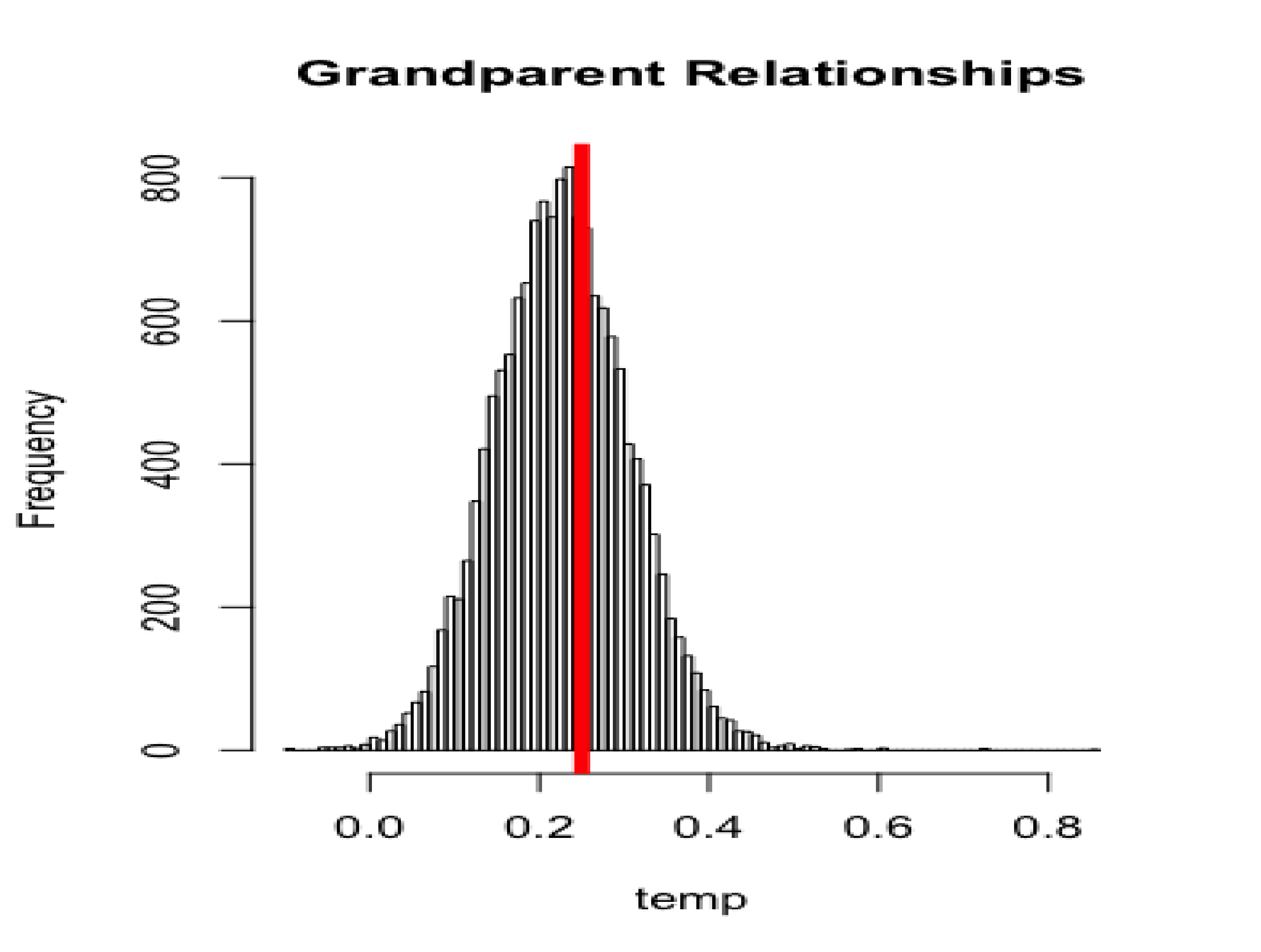
	1	2	3	4	5	6	7	8	9	10	11
1	1	0	0	0	0	0	0.5	0	0	0.25	0
2		1	0	0	0	0	0.5	0	0	0.25	0
3			1	0	0	0	0	0	0.5	0.25	0.25
4				1	0	0	0	0	0.5	0.25	0.25
5					1	0	0	0.5	0	0	0.25
6						1	0	0.5	0	0	0.25
7							1	0	0	0.5	0
8								1	0	0	0.5
9									1	0.5	0.5
10										1	0.25
11											1

Genomic Relatedness

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



	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

Methods Used to Incorporate Genomic Information into EPD

- In all cases shown to be more accurate compared to historical methods
- AGI and American Breeds (via John Genho)
  - ssGBLUP via UGA software
  - Uses approximately 50,000 markers to infer relationships
  - Blend pedigree and genomic relationships
- AHA and IGS
  - sHybrid via BOLT software (Theta Solutions)
  - Identifies subset of markers that are actually used

Progeny Equivalents

TRAIT	AAA	AHA	IGS
CED	28	17	25+
BWT	21	8	22
WWT	26	12	25+
YWT	21	9	25+
MCE	18	4	4
Milk	33	15	19
STAY	No EPD	----	15
Marbling	9	3	8

Accuracy, h^2 and Progeny Counts

Approximate number of progeny needed to reach accuracy levels (true (r) and the BIF standard) for three heritabilities (h^2)

Accuracy		Heritability Levels		
r	BIF	h^2 (0.1)	h^2 (0.3)	h^2 (0.5)
0.1	0.01	1	1	1
0.2	0.02	2	1	1
0.3	0.05	4	2	1
0.4	0.08	8	3	2
0.5	0.13	13	5	3
0.6	0.2	22	7	4
0.7	0.29	38	12	7
0.8	0.4	70	22	13
0.9	0.56	167	53	30
0.999	0.99	3800	1225	700

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!
  - Increased information can make EPDs go up or down

Purchase bulls with GE-EPD

- Genetic change is driven by sire selection in commercial herds
  - ~80% is due to the bulls used the last 4 years in self replacing herds,

  - Increased accuracy enables more informed bull selection decisions.
    - Think possible change.

Possible change example

CED EPD = 9.0
ACC. = 0.20

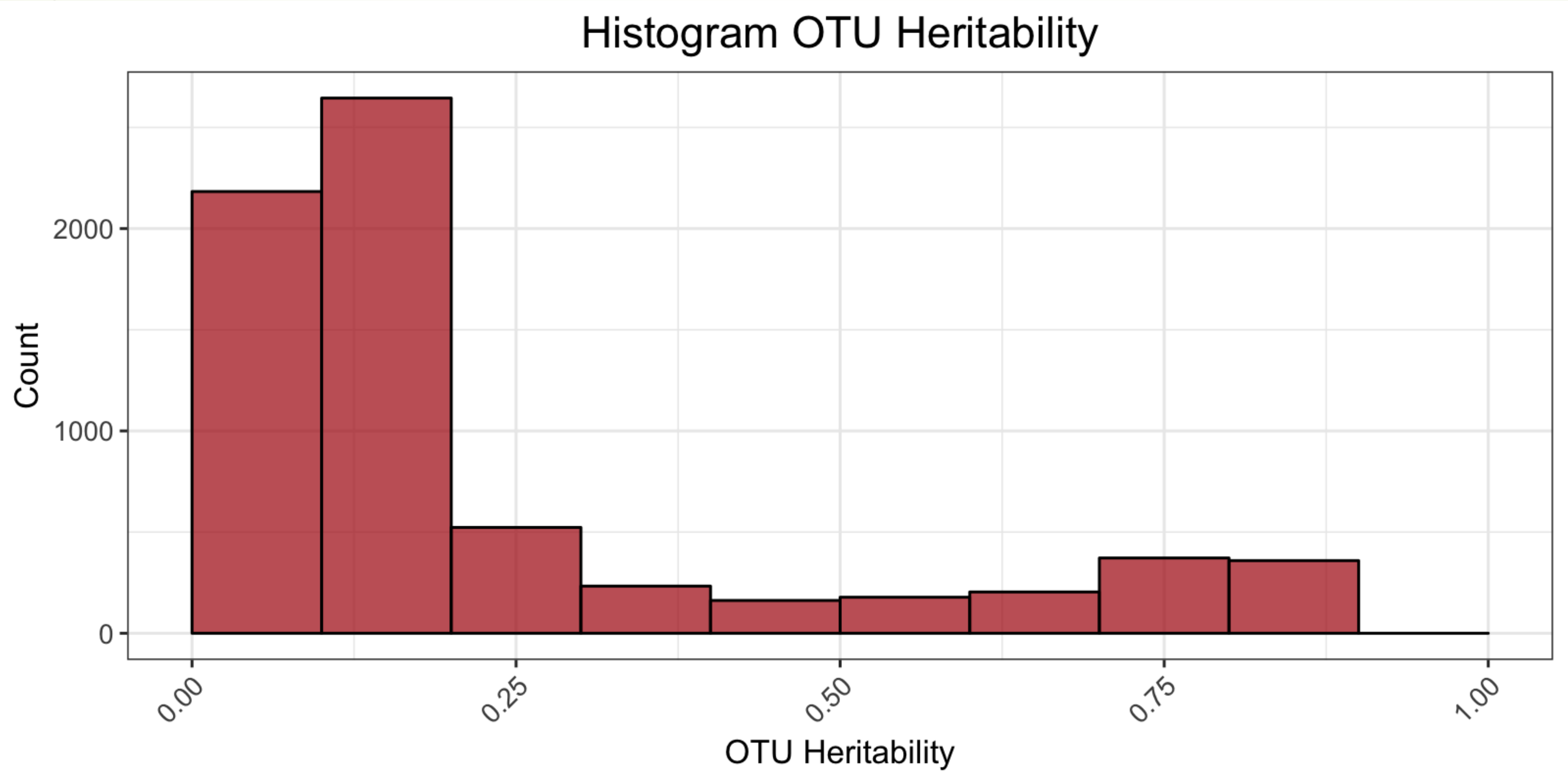
- Possible change +/- 6.2
- 68% confident his true EPD is between 2.8 and 15.2

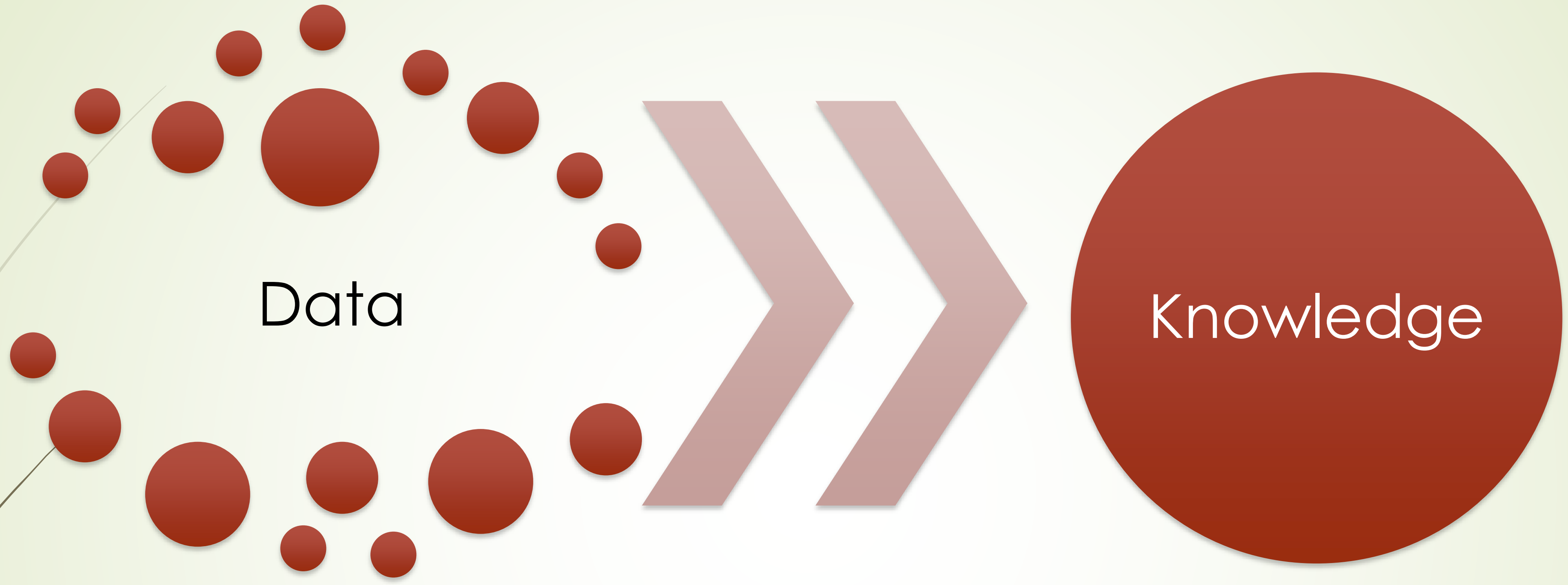
- What if ACC increases to 0.4?
- 68% confident his true EPD is between 4.3 and 13.7

Use genotypes to the fullest

- Improvement in accuracy of EPD
- Parentage determination
- Tracking inbreeding
- Identification and management of lethal and sub-lethal haplotypes
- Breed identification
- Estimating retained heterozygosity (heterosis)
- New trait development
- Identification of putative causal variants from sequence

Heritability Across OTUs





Data is constantly growing

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

Requires turning data into tools

Tools

Decisions

Increasing list of EPD

Requires turning tools into impactful decisions

Decision making process

Breed

- Perceived strengths
- Quantified differences

Breeder

- Reputation/popularity
- Value/service

Data

- Visual appraisal
- Qualitative traits (color, horn/polled, defect carrier status)
- Phenotypes
- Ratios
- EPD
- Breed/organization indexes

Terminal Sires: Traits of Importance

- Calf survival
- Male fertility
- Disease susceptibility
- Calving ease direct
- Growth rate
- Feed efficiency
- Carcass quality/composition

Maternal Traits of Importance

- Female fertility
- Maternal calving ease
- Maintenance requirements*
- Longevity
- Maternal weaning weight (Milk)*
- Disease susceptibility
- Adaptation
- Temperament

Clearly define breeding goals

- Genomic selection 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.

Independent Culling Levels

CED = 20 WW = 60 STAY = 15 MARB = 0.50

	CED	WW	STAY	Marb	Index
1	22	62	18	0.8	20.50
2	21	60	16	0.5	20.55
3	20	60	15	0.6	19.35
4	18	70	20	1.0	21.64

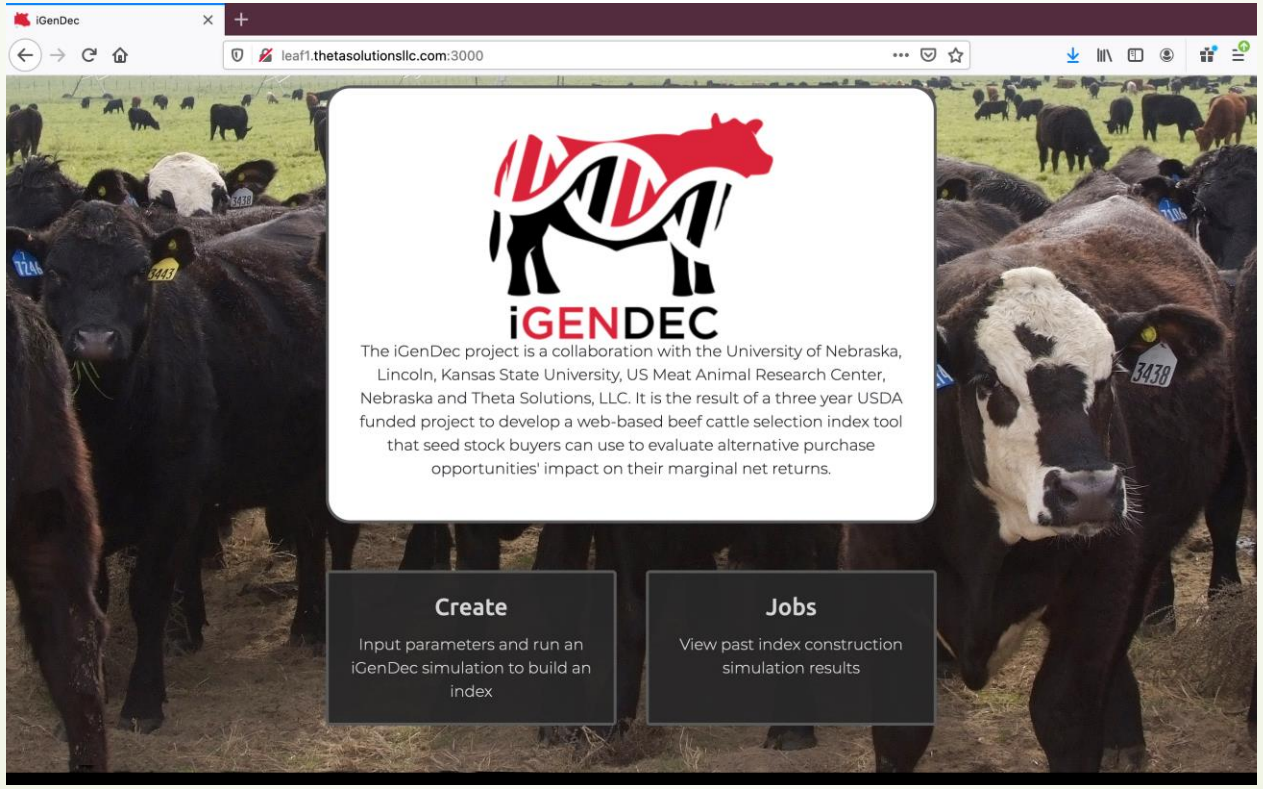
Use selection indices

- As the list of EPD grows, multiple-trait selection becomes more complex.
- Use indices that best fit your breeding objective
  - Do you retain replacement heifers?
  - What is the sale point of your animals?

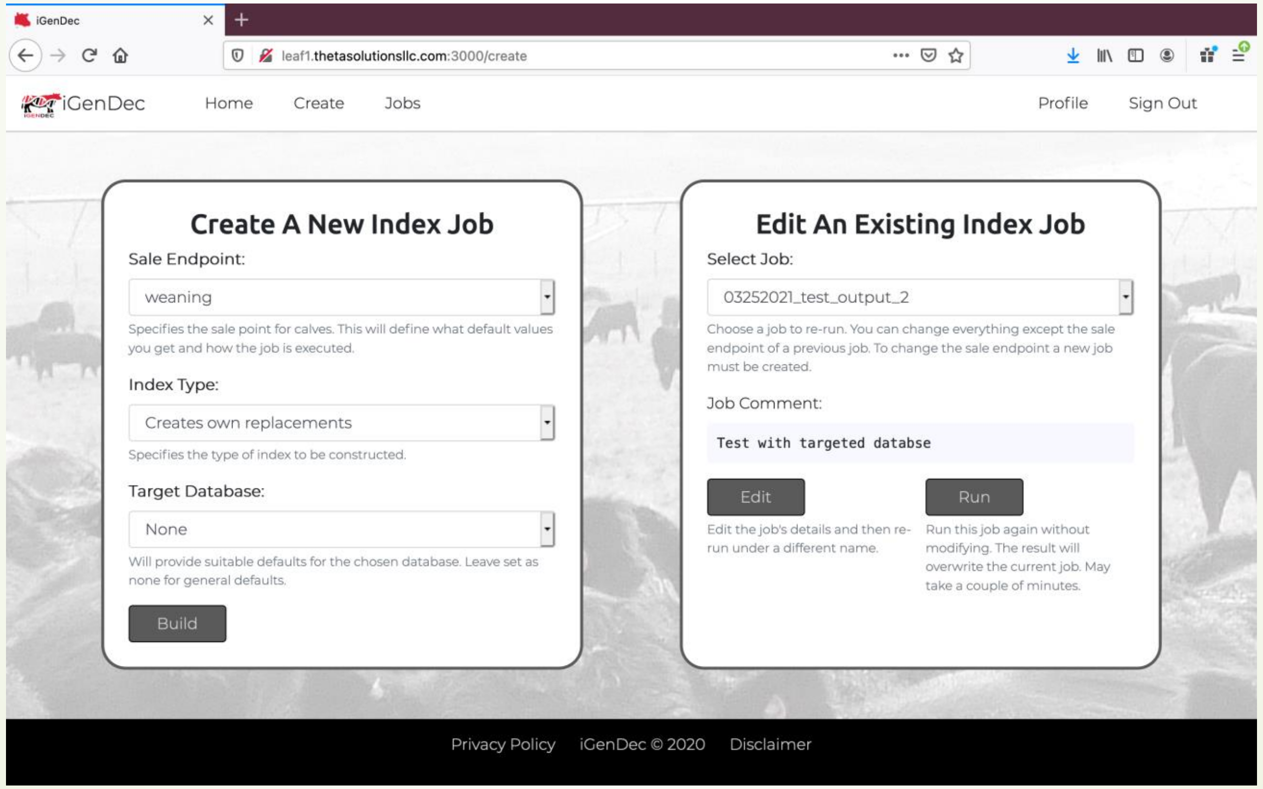
Selection index in a nutshell

- Tool to enable informed multiple-trait selection
- Based on:
  - Breeding objectives
  - Economic parameters
  - Relationships among traits
  - Population (herd) means
- Designed to improve commercial level profitability
- New (~ 10 years) to the beef industry but “old hat” to other industries

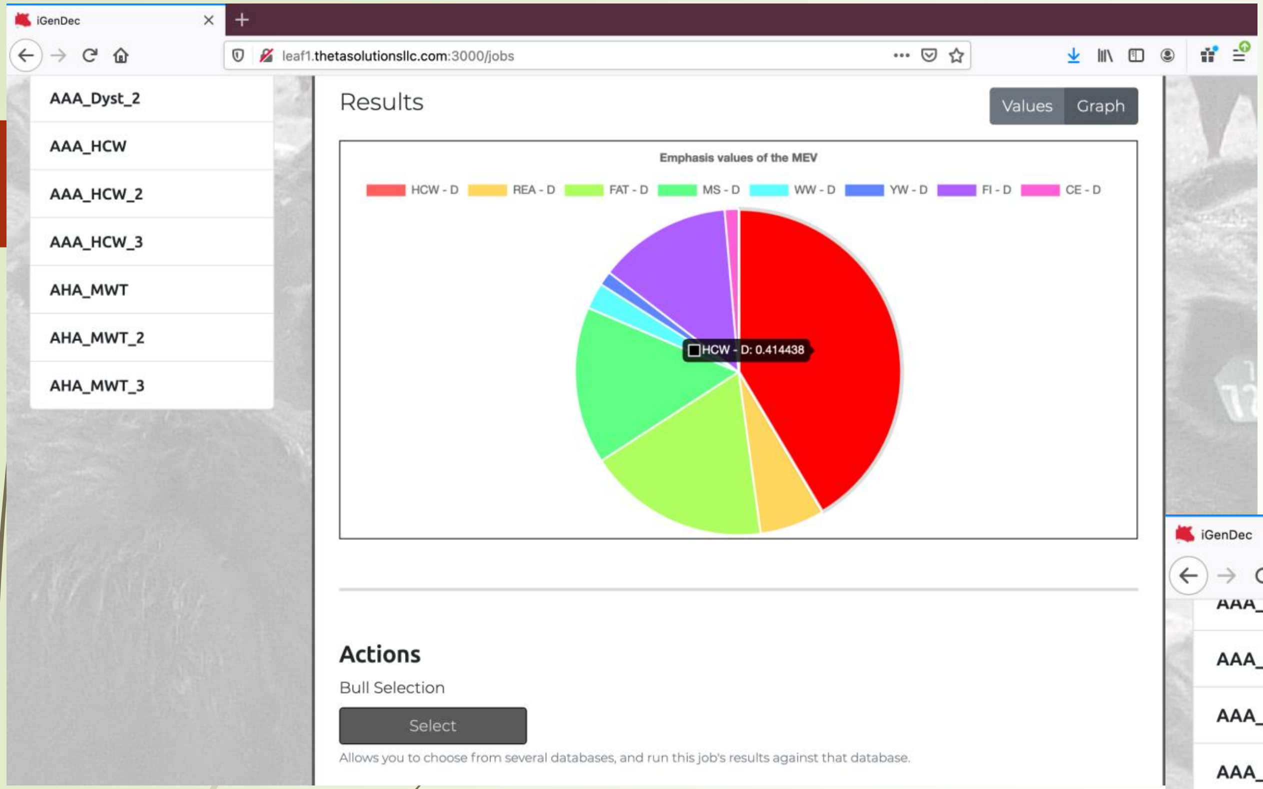
User Interface

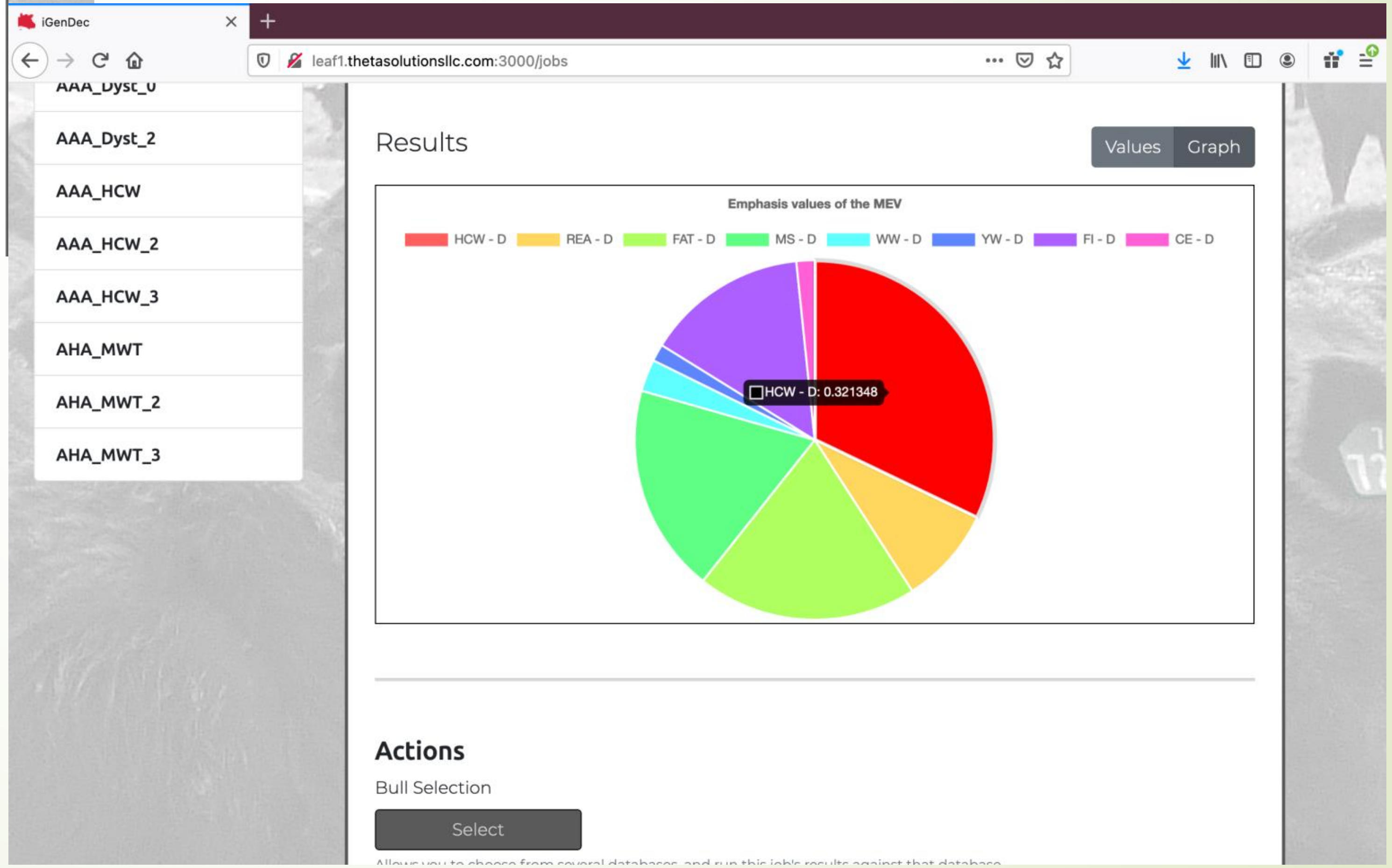


Breeding Objective



Changed hot carcass weight average from 850 to 950 when the discount threshold was 1050





iGenDec Impetus

- The impetus for this project is **not** the belief that currently available selection indices are so inherently flawed that they are of little value.
- We believe that allowing beef cattle producers to take part in the creation of their own selection index has the potential to increase the rate of technology adoption.
- The other primary improvement is in the ability to combine multiple partial solutions (e.g., additive and non-additive genetic effects) to enable sire selection across breeds in an economic framework.

Improvement of Herd Efficiency

- [Dam Weight*Lean Value of Dam + **No. Progeny***Progeny Weight*Lean Value of Progeny] - [Dam Feed*Value of Feed for Dam + **No. Progeny***Progeny Feed*Value of Feed for Progeny].

- By simply increasing number of progeny per dam through either selection, heterosis from crossing, or better management, we will increase efficiency of production.

Adapted from Dickerson 1970

Summary

- Data is constantly growing
- Genetic evaluations are becoming more accurate
- The need for phenotyping has not gone away
- The "old" tools should still be used (e.g., EPD and selection indexes)—they are simply more accurate now

Thank you

- USDA NIFA award number 2018-68008-2788
- www.nbcec.org
- www.eBEEF.org